

Sequence Listing  
from U.S. Pat. No.  
6,348,582 B1

- (iii) NUMBER OF SEQUENCES: 534  
(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US/08/936,165A  
(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCTGA TAATTATTTN GCGATATAAG TCGTCAACGT ACCAATATTA TCAATAGTCA  
60  
CTTTANATNC ATCACCTGGT TGGAAAAATT TAGGTGGTTG AATACCTGNA CCANCGTCTG  
120  
AGTGGTGTAC CAGTTGCAAT AATATCTCCC GGATGNAGTG CAACACATCA TGACATCACT  
180  
ACTATTACAA CAACATATAT CAGAATCAAG TCGCCAGNGT NACCATCTTG TCTAATTTCA  
240  
TNGTGACCTC NTGTAACAAT ATTCACATTT CCAGGTAATG GCAGTNCGTC TTGAGNAANG  
300  
ATTTAAGGAC CCATNGGNTN ANCCNNCAGT TAACTNNGT GGTA AAAATG CTTGATCTTG  
360  
NTCACTGCGG GCTNTGAGAT CAAGTGATAT CGTAAA  
396

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 696 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCTCTATT GCTTNNTTGA TACGTTTCTG TTCTTTAAAT CCAAGATATA CCGCAAACAA  
60  
CATAACAAGA ATGAAACCTA TTATTTGAAT AGGTATTAAT CCATACCATA ATTCATTGAC  
120  
ACTTTTGGCT TTAAACACTG CAGCTACACG AGCCATTGGA CCTCCCCAAG GTNCCATGTT  
180  
CATAATCGCC GCGCTTAATG CTAATAGTAA AATCAATAAA TATTTATTCA TATTTAACGC  
240  
TTTATATAAA GGTAATAATG CAGGAATAGA AAGCAAAAAT GTTACCGCAC CGGCCCCATC  
300  
TAATTGGGCT ATTGTGCCAA TTAAAGCTGT CATTGCACAG ACAATGACGA CATTGCCTCG  
360  
TGTCATTAAT ATTAAGCGTT TGACAAAGCG CTTGAATAAA CCACTATCGT TCATGATGCC  
420  
AAAGAAAATA ATGGCANAGA TAAACATAAT AACAACTNG ATGACNTGAT CTAACCTTTT  
480  
AGCAAAAAAT CCAACCAAAT CTGNCACACT ATATCCTAAA ATCATTGCCC CTAAGCAAGG  
540  
TATGATTGTC ATACCTACAN CTGGATTTAT CTTNNTGGGC AATGAGTAAN CCTACAAC TG

600  
AAATAATAAT NATGNGCCCC ATCACTGTCA ACCACATATT ATCACTATTC ATTTATTTTC  
660  
TCCCTCCACT TNCAATACAA TTTACATTCA CCCCCC  
696

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCTTGNC AA TTCATNGGGT TTTCTGTTTA ATATTTTTCG GGTTCTAANC CCACCATATC  
60  
AAGTGATTCA TCTACTCTTT TATCAATATC TTTTCTTCC CACTTTTTC A TTTGTGCCAC  
120  
TTTGTGCAAA AATTTCTTTT GGGCCTCAAA TGGGGNATAA TTCCAATCTN CCTCCAANAC  
180  
GTANCCAATA TCCCAACGCA TTTGTAATA CTGGATAATC ACTTATTGGT TTATCTTTAA  
240  
AATAAATATA ACCTTCACTT AAGTGAATGA GTCGATTAAT CATTTTAAAT GTCGTAGTTT  
300  
TTCCACAACC TGAAGGTCCA ATTAGCACAA AAAATTCACC CTCATTAATA TTGAAACTAA  
360  
TGTTATCGAC AGCAACATGT TTGCCATAAC GCTTAGTTAC ATTTTAAAC TTAATCACTT  
420  
TGCCACCTCT TTTTCTCTCA TAGCATAAAA CCGAGATTAT ATGTATGTAT TCCCTATTTA  
480  
ACCACGTTTA TTACAATTTT CAAATTTAAA TGATTTATCC TTGAACTTTT TTAACAAAAT  
540  
AATGAATAAT AGGTAATCTC CAGTTAAGAA ATAGTGTTAT TTTACCTT  
588

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGCAGNCT TTANAATTAT TTNAATGATG ATTAGCAATG CATATACGAT TAATTCGATT  
60  
ATGGNTTATA TCTNNATTGA TTAANTCACT TATATTTTAC AAGTGTGTTG CTTTGGAGCG  
120  
TCAACGATGC TATCACATAT TACGGCATAT GAAATTTTAT CTGAAATTCG NAAAAAATTA  
180  
GCTCAAAAAT TAATGCGCCT CCCTTTAGGN GTAGTGGAAT CTAAGAAAAT AGGTGAATTA  
240  
AAAAATATAT TTGNCGATAA GGTTGAAACA ATAGAATTAC CTTTAGCACA TATGATTCCCT  
300

GAAGTTATNG GAAACTTACT TGTGGCAGCT GCTATCTTCT TATACATAAT GNTCATNGAT  
360  
TGGCGTATTG GATAGGTGNC TTANTAGATA ACGATACCAA TNTCAATTTN CGCTTCTAAA  
420  
AAAGTNATGT CTTGGATTTT AATGAGANAA TTTGCTGGAC AAANTGAAAT CCAATTTNTN  
480  
TTTTTNATTT GNCGNAATGG  
500

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCCTGTTGT CCCCNNGGGT CAATAGACCC CGACATACTT TNNGGCTTCT GAAAATAAAA  
60  
TTTCAGGNNC GCACTTTAAA GATGGACGTC GATGTCGACT AATGTGATGA CNGCCTTTCA  
120  
TCTTTTTAAA AANTCATTAA TTTCCCTTCT TGTTTAAAC GTACATANAA GAAATACGCA  
180  
TACGGTACTA ATAAAATAGT TGTATATGTT GCGTGTGTTA ATAATAATAC ACCGATTAAT  
240  
TCAGGAATGA TGTTTAAGAA GTAATTTGGG TGTTTTGGTA ATTTTATATA ATCCAGATTT  
300  
AATAATAGGA TGTTTAGGTA AAATGAATAA TTTTAATGTC CAAATACCAC CTAAAGTTTT  
360  
AATAACCATA AATAACATGA TATAAGCAAA GATTAATATA ACTAAGCCAA TACCATTTGC  
420  
AAAGCTAAAT GTATCTTTAT TAATAAATGC CTCTACACCA GCCAATACAT AAATTAAAAC  
480  
GTGTGTTATT GCTAAAACT TCGAATTTTT AACGCCATAT TCAACTGCAC CGTCTGCTTT  
540  
TAATTGTTTT GAGTGANTAA TACATATCTT TAAGCTGACA AGTCTGATAC AGAGAAAGAT  
600  
AAGTAATATA GATAGANTCA TGATGTCCTC CGTCATTATG TCATATGTAT AAGCGTTGAT  
660  
TTTGACAACA TAAAGTATTT TATAGATAAA ACTTGTCACA TACTATTAAC TATTTATTAA  
720  
TTTTAGTACA TAAATATGTT TCTAAGTATG TGTTTATGTT CAGTATTTTG GATAATTTAA  
780  
TAATTTTAAG GATATTAAGC GCTTACAG  
808

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAATTCTT ATTCATTTAT AAAATAATAT TCGTATGATT TGATGTTTTA ATTAGTCCAC  
 60  
 CATTTGATT TGTGCTATGA TAATAGTGTT AAGTAAACGA AATAAGGGGT TATTAAGTTG  
 120  
 AATAACTACA AAATTGGCCA ACATATCAAG GTGCGTGTA CTGGTATTCA NCCATACGGT  
 180  
 GCGTTTGTTG AGACCCCTAA TCATACTGAA GGACTGATTC ATATATCAGA AATTATGGAT  
 240  
 GACTACGTTT ATAATTTGAA GAAATTTCTA TCAGAAGGAC AAATTGTTAA AGCTAAAATT  
 300  
 NTGTCTATAG ATGATGAAGG AAAGCTTAAT CTATCATTA NGGATAATGA TTAATTCAAA  
 360  
 AATTATGAGC GTAAGAAGGA AAAACAATCA GTATTAGATG AAATCAGAGG NACAGAAAAA  
 420  
 TATGGGTNNC AAACACTTAA AAGAACGCTT ACCAATCTTG GATAAAACAG GCAAAGCGAG  
 480  
 CAACTCGAAA CNGACTAAAG GAACAAGATA AATCCGNACC CGAAAATCAA ACAAAGGGTC  
 540  
 TTGAAATGAA AGTTTCTTAG ACTATAAAAG AGATTAGGTA TCTATTAAAT TTTATTAGAT  
 600  
 ACTAATCTCT TTTTGTCTAC GATAACGTAA TATGATTGAT TCTATTTACA CGTACAAATG  
 660  
 GTTTAAGGTG ACATATCCAT TATCTTTGTT AGATAGAATC GTTGATTTGC AATATTGTAT  
 720  
 GTGGATTTGT TTTTTTTATT TATTTTAGAA ATGAGAACTA CAACTTAAAG TATTAAACGA  
 780  
 ATTGCAACTA TATAAACAGA TAATTG  
 806

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTACGGCATA CCATGCGAAA TAATTGTTGA TTCTAATGCT ACAATCGGTT GATTGTTCTC  
 60  
 CCGTGCTTGC TGAACCTCTC GAGAATACTC AATATACTTG TGTAATTTG CCATTTTTAT  
 120  
 AATCCTCCAT ATCGTGATAA AGTTGCTGTT GATCTAGGTT GTGCCTAACT GTATATTTCTG  
 180  
 TTTCTATCGT TTTCTNTGCG TTAACCATAC CAGCAATTAA TATATCTACA GTAGACATCC  
 240  
 CATTTANCCA GCTATATACT ACTGCAGCAC AGAATGAATC GCCTGCACCT GTAACATCTT  
 300  
 TCACACTATG TGGATGGCAT AACTGACTTG ATGATTCTTC CTCACCACTN CGGATAATTA  
 360  
 ATTCTTNCAC GCCATNTGTC ACAATAACAT TTNTACACCT AAATCATTC AGCGGTTTTA  
 420  
 GCAGCTATTT NTANATCAAC AAGTAGATTC TTATTTNTAA NTTAAGTAT GGTCTGGCN  
 480  
 CANCTTNANT CGGGGATAAT CCAATCAATA GCATGTAATG AATCAGGCAT ATTTTTCATT  
 540  
 TTTGGGGAAG AAACCGTGGT GATAACTAAT TTGATTTGAT GTTTCGTGGT ATAGGCACAT



600  
 AAGAAGTTTA ATGCCTCTTT GCCTAAATTC AAATCGACAA TAATGCACTT AGCCTTTTTTC  
 660  
 AATAAGTGTG AACGCTTAAT TAAAAATTCA GCGTAATGT AGTCANACAC TTCCATATCT  
 720  
 GCTAAGCCAT ATGTCATGTC GCCTTCTTTA CTAATTAAAG CTGTATATGA ACCTGTACTC  
 780  
 GCATTTTCAA ATTGTTGAAC ATGANCCCAA ATTCATAAAT GGTGTGGNCA ATCGTTGAAT  
 840  
 CATTTCCCAN TCACTATCTT GTCCACTAGC AGATAANAAA GCGACCGTTT CGCCAAGCCT  
 900  
 ACCTAAGTTC TCAGCAATAT TTCTTGCTAC GCCACCAATA GAGCGTGTTG ACGTTACAGG  
 960  
 ATTTGATGTT TCTGCAACTA AATCTTTATG CACATAAAAC TTACGATCTA CATTGCTGCTC  
 1020  
 GCCAATACAA ACG  
 1033

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTTACACAAC AAGTTGTCAN AAATTATTTT TATGATAATG ATCGNNCATT TACTAGAAAA  
 60  
 GTAAAAGAAT TATTTGTAGC TCATCGAGTT GAAAAACAAT ATAATAAGAA CGAAATTTTA  
 120  
 CGCTTTTATT TAAATAATAT TTACTTTGGG GATAATCAAT ATACGCTTGA GGGCGCAGCA  
 180  
 AACCATTATG TGGNACACCC GTGAATAAAA ATAGNACAAC AATGTCTCAC ATCAGAGNTT  
 240  
 NACAAAGCGC TATTTTAGCT AGTAAAGTCA ATGCACCTAG CGTATATAAT NTCAATAATA  
 300  
 TGTCAGAGAA TTTCACGCAA CGTGTTAAGC ACGANCTTAG AAAAAATGAA GCAACAACAT  
 360  
 NATATCAATG ACACACAATA TCAACAGGCT ATGTCACAAC TAAATCGCTA AATACTNGCA  
 420  
 TTCATGTGTA AGATGCTTGG AACTATAATG TAGAAGGTTT AATTGAAATG TCATAATGAT  
 480  
 AAAGTTGAAT TGTTTCTGCT TAATAAATTT TACAGATTTG CTTGTAATCA CACTNTCATT  
 540  
 TTAAAAGATG ATAGTGTGAT TTTTGTGTTAG CATCGAAAAA TATTTAAAGT TAAACATTTG  
 600  
 CTATAGGAAG TGGCTTATTG AATAATAAAA GAGTATTGTA TAAACTTGA GAAAGTAACG  
 660  
 GGGTGATCCA GTGCCGAAGA TTTACTAAAT AGAAGTTCAA AAGAAAAACA AAGAACGTCT  
 720  
 TAATCTTTTT TTAGACGAAC AATTGTGANAN GGNNANTGGG TATAGATATC GATACATTAG  
 780  
 TCAAATTTAA TTTAAAAAAA GGGCAACAAC TTGAAGCTGC TGACATGGNA GAGGTTCAAN  
 840  
 AGTATGATCA TTATCGCATA GGTTTAAACA AAGCAATCCA NTATTTATCA TATAAAAAGA  
 900  
 GAACTGAAAA AGAAGTTATT CAATATTTAC AANAAGAAGA GATATCAGAG CAAGCGATTT

960  
CTGANGTGAT TGAATATTGT TATCGCGAAA AGTTANTCGA CCATCAAGAT TATGCGGAAA  
1020  
GTTTACNAAA TACAANGATT CGCACGACAG ATAATGGACC TANANTTNAT CANCAAAAAC  
1080  
TNTTTCAACC TCGGGTATNG NACCACCTAT CATTGANATG TTTACAGANC TTTCTTAGNG  
1140  
AACAAACAGNN CTTGGTTGAT ATTCATCCAA AN  
1172

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAGGCTTGT CGTCCCATTT AAGCATCACT CCGTTTGTTT TCGCTTAAAA TCCCTTGCAT  
60  
CGATGCTAAC AATTGATCAA CATCTTTAAA TTCTTTATAG ACTGATGCAA ATCTAACATA  
120  
TGAAACTTGA TCAACATGCA TTAACAAGTT CATAACGTGT TCACCTATAT CTCGTGAAGA  
180  
CACTTCCGTA TGACCNTCAT CTCGTNATTG GCATNCAACC TTGNTTGNTA TGTCTTCAAG  
240  
TTGTTGGATA TCTAACTGGT CGGTTCTCAC AAGAACGCAC AAGTCCAATA AGTATTTTNT  
300  
CTCTTGAAAA CTGNTCTCTT GCGCCATCTT TTNNCACAAC TATAAGCTGA CTTAACTTCG  
360  
ATATGTTCAA ATTGTAGGGG GAAACCGTGG TTCCCACAA  
399

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTTATATAT AGTAACAAAA CTAAATTATA AATGACAATA TCATATTTTCG CAATCACTGT  
60  
TAGTAATTTA AATATTTTTTC AAAAACGACA TAATCATCAG TTTGTTTCGAT TTCAACGAAA  
120  
TTACTATTTA AACATAATGG TTTAAAATCA TTATTCTCTC CAAACAGAAT CATCGTAATC  
180  
ACATTAAGGT TGTTCATAGTT TTTTCTTAAG TAAGTTGGCA ATTGTCGCAG CGCACTTGAA  
240  
CCAATACCAT TAAAGCGATA TGATTTATCC ACTTCAATAG CAGCAATGTT CATGCGTTCA  
300  
CCAATCTGCT CCAATGCGAT AAAGCCACCT NTTGGCANCA GCATCATAAA NTTAATGATA  
360

TNTACATNGG CCACTTCTTG AACGACTTTC TTCCTCCAAG CTTTAAATGA CGAACATTGT  
420  
TTNGATCTTA AGTCCAAGTA TTTGGCCGGT CCTTTGCATT GGTCCCTCTTC TTAGTCGNNT  
480  
GATTGAATGA TCCAGACGTC CGTTGGTCCA GATTGGNCAA TTTCCGANTC TACTACTGNN  
540  
TTTGNTGATA AATCAGGAAT CACCCTGACA TTTTGGGAAT GAATCAATNT TTCCNGGCCA  
600  
ATTCCAAACC TGGTTTTTTC CAATAATCGN TT  
632

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATATACAGC ACTCAGAATT TTAATGACAA TTAATGCAGC AGTTAACACG ACAACGCCAT  
60  
TAAATGCTTC TTTATGCTTC ATCACTGATT CTCATGCTTT CTTCAATGCA CTTAACTAAA  
120  
AACTTCAAAC TATCAAGCCA TTGATTTTGT TTCGTAAAG TAATTGTCAT TGCATTATTT  
180  
TGAACACCAA CCTTCATTGT TCTACCTAAA GGTTGTGTTG CTTTGAACAG CACTTCGCCA  
240  
TCAATATTTT CAGTGGCTTT TACAGATAAA TGAATATCAA TTATTTTCCC TTTATCTTTA  
300  
ATCAACGTGA TACCTGAATG TAATGCGTGT ACTTTTATTT CCACTATATC AAGCAAACGT  
360  
GCTACTTCAA CAGGNTAATC CAATTAAACG ATCAATTANT TCATCTTTAN TGTCGATAAT  
420  
TGGGNCAAAT TGTTCCAG  
438

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TACCAAAGTT CTTCTTTAGA GGCTGGGGAA TATNTCCNAA CTACATCACG ACGCACTCGA  
60  
AACGGTTCCT CGTTGGAAAA TCGATGTCAT TTCGTGTATA TTGCACATCT ACAAGTTTTT  
120  
TAAGTAATTC ACTTCTATCC ATTTCCATAC CAACTCGAAC ACTTACTACT AAATCTTTAT  
180  
ATTCTTCAGG ATTACCTAAA CCATATATAC AACTTACACT AGCAATAATA ATTACATCAT  
240  
CGCGTTCAAA TAATGCACTT GTAGCAGAAT GTCGNAGNTG ATCAATTTCA TCATTGATTG

300  
AGGCATCTTT TTCAATAAAA GTGTCAGTAG ACGGTACGTA TGCCTCAGGT TGATAATAAT  
360  
CATAGTAACT TACAAAGTAT TCCACCCTGT TTTCAGGAAA AAATTCTTTA AACTCACTAT  
420  
ATAATTGCCC TGCTNATGTT GTGGTAGGTG CGATAATTAA CGTTGGTTTC CCAACTTCTT  
480  
TAATAACATT ACTCATCCGN CAATGTTTTT CCTCGNGGCA GG  
522

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCGCCACCT GTACCATGCA ACAATATTAG CGTTGGTGCA CCTTTNTTGT CCTTCACGAA  
60  
AAATATGTTT CATCACAAAT CCTCCTCATT CCAATTAATC ATGTTAACGC TTAGTATTAA  
120  
ATGGTCTTAT TTCTGATTCT ATATACTCTC TTTTATTTTC TAAAAATGGT GGCAATGATA  
180  
AACCTNCACC TAATGTTTCA TACGGNTCAT CTTCCATAAA TCCTGGTCCA TCTGNTGAAA  
240  
TTTCTATTAA AATATGCCCC ACACGTGNAT ATAATGCTTC AAAATAGAAA CGATTAAACGA  
300  
TGCCTGAGTT GGTTAATACC TACCTCTTTA TATTNCGGGT GCCCACGCTT CTTATTTGCA  
360  
TCAGGATCTT TCCACAACGA AATGACACAT GATGTACCTC ACCATAACTT GAGGGNGGTT  
420  
GNTGGCCTNN ATCATCTTTT ATTAAGATTA CTGGNCACAT TGGCGNCTTC GCAACTTCAA  
480  
GGTAATGCGA CATATCTTCA AGCGCAATAG GTGGCATAACC  
520

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCCATC AGTGCGACAA CTGAAGTATT TANACCAATA ATGTCATCGA CACTAGTTAC  
60  
TATTATCGTC TTCTTACCAC TTGTGTTTGT ATCAGGTTCA GTAGGCGAAA TGTTTAGACC  
120  
TTTTGCATTG GCTATTGCAT TTAGTTTATT AGCATCGTTA TTAGTGTCAA TTAACTCGT  
180  
NCCAGCTTTG GCAGCAACAC TATTTAAAAA AGGCGTTAAA CGTCGTAATA AACAAATCA  
240

AGAAGGATTA GGTGTTGTTA GTACAACTTA TAAAAANGTA TNGCATTGGG TCACTAAATC  
300  
ATAAGTGGGA TNGGTAATTA TATTAAGTAC ATTAATTTGG GGNTGNAACT ATTGTTTTTG  
360  
GGGGGACCNA GACTAGNCAC TTAGCTTTTT TCCAGAA  
397

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AACCATCTTA CCGATATCAG TACAGTACGG CGTAGGAACG GGCATCCAGC GGATTAGAGG  
60  
TGGTGAAACC AACCTGGTTG TTGATAACGA TACGTACCGT ACCGCCAACT TCATAACCAC  
120  
GCGCTTTCGA CATGTTTCAGG GTTTCCTGAA CCACGCCCTG CCCGGTCACT NTGGGGTCCAC  
180  
CGNGGATGGT GATTGGNAGN ACTTTGTTGN TGCTCGGNTC ATCAAGTCTG TCCAGACGGG  
240  
CACGAACAGA ACCGATANCT ACCNNGGCTTA CAATCTCAAN GTGAGACGGG TTAAACGCCA  
300  
GNGCCAGGTG NACCAGGGCG CCATCGGTCT NTAAGTCAGA CGAGAAGCCC ATGTGGTATT  
360  
TCACGTCACC CNTGCCGAGG TGTTCNTAT GTTTACCCGG GGGAAGTCCG TCGNAACAAN  
420  
TCTTTGGGGG TTTTTTACCC CAGC  
444

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCTTG GAGGGCAATT TTGGGCTTGC AATAACAAT CATCAAAATA TTGTTGGTAC  
60  
TATAGGTTTG ATTAGACTAG ATAATAATAT GTCTGCACTT AAAAAATGT TTGTTGATAA  
120  
AGTTTATAGG AATTTAAAAA TAGGTAAAAA ACTTTTAGAT AAAGTTATAA TGACATGTAA  
180  
AGAACAAAAT ATCGATGGNA TNTATTTAGG AACAATNGAT AAATNTATNA GTGCACAGTA  
240  
TTNTTATNCT AATAANGGCT TCCGCGNAAA TTAAGCGAGG AGATTTACCA AGNAGCTTTC  
300  
CTAAATCAGA TGTAGATAAT AGGTTCCATT ACAGCAAANT CNAAAGATTA ANTCGANGCA  
360  
CTGAATAANT GNNATGACAN CCCTCAG

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCCTAG AAGGAGAATT TGTTAGTGGT GTTGCAGAAA AGCAATGGTT GGAAGAAAAA  
60  
GGTTATGAAG TAGACTTTGA ATTAATGGCT GAAATAAATC CAACAAGATT ATCATTAAGT  
120  
GATTGGCTTA AAGTCCAAAA CTATAATAAG TAATGAATGG GGTGCAATCA TGATTCAATC  
180  
AATGTGGTTT AATTTGCATG TGCAAGATTT AGAAAAGAGC GCACAGTTTT ATAAAGCGTT  
240  
AGGATTTAAA ATAAATAGAA ACCCACAAAT GTTAGATAAA ATGGTCGGTA TTCAAATAGG  
300  
TCAAACAACC GCAATTTTAA TAGAAAACAA GCATTTTCAA AATGTAAGTC AGCAAAGCCT  
360  
TAATACTGAA CCAAATGAAG TGATGATTTT TCTAGGTGTG ACACAATGAG AGTTGAC  
417

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCTAT ATACTACTTT GAAAAGGTGT GAGCTTAATG ACAACTTTTA GTGAAAAAGA  
60  
AAAAATTCAA TTACTAGCAG ATATTGTTGA ACTACAACT GAAAATAATA ATGAAATAGA  
120  
CGTTTGTAAT TATTTAAAAG ATTTATTCGA CAAGTACGAT ATTAAATCTG AAATTTTGAA  
180  
AGTTAATGAA CACCGCGCCA ATATCGTTGC AGAAATCGGT AACGGNTCAC CTATACTCGC  
240  
ATTGAGTGGT CATATGGATG TTGTTGGATG CAGGAAATCA AGATAATTGG ACTTATCCCC  
300  
CTTTNCAACT CACAGAAAAA GCTGGCAAAT TATACGGTCC G  
341

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCTCA GGTATAACAC TTCNCATATC TTTACGAGNA ACTTTTCAAA CTAGATACCC  
60  
CTGCACCAAC CAACGTCCAT AATGGTTGAT AGTAATGATG GTCTGCTGGG TCTATAATTG  
120  
CTATTTTCTC TTTTAAGTTN TGATTTTTTC TTAATAGTCT TGATGCTACG GTAACACCTG  
180  
CTGTACCGCC ACCAATAATA ACAATNTGAT AATGCTTATT CATTTNTTCC ACATCCTTAA  
240  
ATTATTTTAA TGATTCTGGA AAATCTTGAT AGCCTTCTCT AATATTCACC ACATTTTCAA  
300  
AACCTNTGCT TTCCAATATA CCCACTGCAA TTGAACCTCT AACACCTGAC T  
351

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCCTGT TTAAGAAACA AGATTAAAG AGCAATACGT GAAAATTTCA AAGTACATAA  
60  
GTCGNATATA TTGGNCAAAG ATATTATTGN TATAGNAAGA CAGGCAGCTA AAGATATGAC  
120  
GACTTTACAA ATACAGNATA GTCTTGAGCA CGTNCTTAAA ATTGGCAAAG TTTTAAATAA  
180  
AAAGATTAAAG TAAGGATAGG GTAGGGAATG AAAACATTAA CCCCTCAACG CATCCCCAAG  
240  
TCTTACCTCA GACAAACGTT AGACTGACCC TAGGGTTAAG ACTTGGCCCN AGGGNTATNN  
300  
TAACTTACTT TAAAATGTTT TCAC  
324

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCCTAT TATCGAATTG CATGCTACCC CTCCTAAAAN CCAAATGCTC TTAATTTATC  
60  
TACAGATAAT TGGTCTTTAT CTTTATTTAA AATATTTTCA ACATATTTAA ACAAACGTC  
120  
TGTTTCTAAA TGTACTTTAT CTCCTAATTT TGTGGATGAT AAAATCGTTG AACGCCTCGT  
180

TTCTGGAATA AGATGAATGT CAAAACCTGTT ATCATGCTTA TCAAATACCG CTAGACTTAC  
 240  
 ACCATCCACA GTAATAGACC TTGCTTAACT AACTGATTAT TAATATGTTG GCTACATTGA  
 300  
 ATCGNAATAA TTGTGGCATT GGTGTTTCAT TTATTTGTGA ANTGTCCTAG TCACTACATG  
 360  
 ACCGAGGAAA AATGTCCACC AAACCTACCG NTACACTCAT GGAAGNTCTA AATTACTTCT  
 420  
 GATTGGCGCT TACANCTGCT AATAGGTTTA TTTCAAGGCT TTATTACTTG ACAGGAAAGA  
 480  
 TGCT  
 484

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAATTCCTTA CTGTATGATA AAGGTATTAC CAAACAATAC TTAAGGGGGA TTATATACTG  
 60  
 TGGNTCAATC ATTATATGAG TTTTGTAGAGG AAAATATAAA TTATCTAAAA GAAAATGGTN  
 120  
 TGTATAATGA AATAGATACA ATTGAAGGTG CAAACGGACC AGAAATCAAA ATCAATGGGA  
 180  
 AATCATACAT TAACTTATCT TCANATAATT ATTTAGGACT AGCAACAAAT GAAGATNTGA  
 240  
 GATCAGCTGC AAAAGCAGCT ATTGATACAC ATGGTGTAGG TGCAGGCGCT GNTCGCACAA  
 300  
 NCAATGGTAC ATTAGATTTA CACGACGAAT TAGAAGAAAC ACTAGCAAAA TTTANNGGAA  
 360  
 CAGAAGCTGC AATAGCTTAT CAAGNCAGGA TTTANTTGGN NATATGGCTG CTATNTCAGC  
 420  
 TTGTCAANGA ATNAAAATGA TGCTATTTTN TCAGATGAGC TTAATCATGC ATCAATTATT  
 480  
 G  
 481

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCCTGT TTAGGTGGTA ACGTTACAGA AACACATACC TTAAATTGC CAGAAGATGC  
 60  
 TGGAGAGCGC CAGATGTTCA TTATTGATAA AAAAAGACAG ACGCCGAAAA AGTACCCAAG  
 120  
 AAAACCAGGG ACGCCTAATA AGACTCCTTT ACTTGAAAAA TAATGCATAA TCCTTTACAA



180  
CTAACATAAA AGGAGCGAAT GGATAATGAA AAAACCTTTT TCAAAATTAT TTGGTTTGAA  
240  
AAACAAAGAT GACATCATTG GACATATTGA AGAAGGATCG CAATAGTAAT GTTGAATCCA  
300  
TTCAAATTGA ACGTATCGTT CCCAACCCGT TATCAACCCA AGACAGGTGT TTGAACCCAA  
360  
ATAAAATTAA AGAACTTGGT GAATCAAATA CAATGAACAT GGGTTTACTA CAAACCTATT  
420  
GTTGGTAAGA CCGATGAGAA GATATGTTTG AAATTATTG  
459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCNNNA AAGATACNAT NCNATTTAAA TGGATATCAT TCCAAGAAGC TGTAGATAAG  
60  
AATCGGGAAC NAATGTCTCT GTTTAATGAA ATTCTTAAGA GTCATCAAAA GACTCCANTT  
120  
TTTGATACAT CTAGCTTGCG ACATACTTCG AAAAAATTAT CAACAATTTT AAAAGGGGAT  
180  
TTGTAAAATG AATATTGAAA AAATCGAACA AATAATCAAA TTAGTGAAGG AAAATGATGT  
240  
TAAGAAATTT AAATATAAAA ATTTTGANGA TGAAATAGAA ATTGACTTCA CTGACTCGAA  
300  
TCATTTGGCT GCACACAGGT AATCAATCAA NTCAANGTAT GAACAATAAT GATTTGACAG  
360  
CTTCAANAGC GAATGATAAC TCCGATGTNT CGACAAATTG ATTATCATGA CATTAAANTCA  
420  
CCANTGGNAG GTACATTCTT  
440

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCCCGGGCT GCCACGGTAA CTGATGCCTC CGCGGTACTG GCGACAGATT ACAAATCTC  
60  
GTTGATAAT AATCAGTGGC AGGTCACCCG CCTTGCCAGC AATACCACTT TTACGGTGAC  
120  
GCCGGATGCC AACGGTAAAG TGGCATTGTA TGGTCTGGAG TTGACGTTTA CAGGAACGCC  
180  
TGCCGTAAAC GACAGCTTCA CGCTGAAACC AGTAAGTGAC GCCATCGTCA ACATGGATGT  
240

ATTAATCACC GACGAAGCGA AAATAGCGAT GGCGAGCGAA GAAGATGCGG GTGATAGCGA  
300  
TAACCGCAAC GGTCAGGCCC TGCTGGATCT TGCAAAGCAA CAGTAAAACG GNNGGCGG  
358

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCCTAC CAGACGTCGC AATGGTCTAT AATTTGCTC TAGATAATCT TGAATAATA  
60  
TCTTTTATTG TTAAATATAC TTCTGGTTGT CCAAACATTG CTGTTGAAAT AGCAAAGTAA  
120  
CTTTCTAAGC GCCCCATTCT CGTTATTTTA TTAATAGCGA TACCTACATA TTTGATAATA  
180  
AATGGTAATA CCTTAATATA ATTAAAAATG CCTATTAATA CAGAAATGAA CACTAATGGC  
240  
AGTAACACAT TTAAAAAGAA CGTAAAGCCA TTTNTATTTT GTATATCTCC AAAAACAAAG  
300  
TTTATACCTG CTTTACTAAC ATTTATTAAC CCTTCCAAAA AATGAGCCTA ATGCAGGTAA  
360  
GATTGGTTAA ACCAATCGTG GTGTTCATCC ATTAAATTAC AACAATCCAA CAACTTTGGA  
420  
TTAAATTATC AATTATTAAC NGCCNTTTTT GGAAGTCTAT GTTTTTACGG ATCCCAAAAA  
480

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCCTCT TTCACTTCTA TGATTTTTTT TAACTTCGAA ACGTCAAGTT GTGCATCAGG  
60  
TTCTGCTGTT ACTTCCATTA CATAACCTTG AATCGTTCTT GGTCCAAAAG GTACAATTAC  
120  
ACGCACACCA GGTGGATGA CAGATTCGAG TTGTTCCGGA ATTATATAAT CAAATTTATA  
180  
GTCAACGCTC TTCGACGCGA CATCGACTAT GACTTTCGCT ATCATTATTG CCACCTAGTT  
240  
TCTAGTTCAT CTAAAATTG TGCAGCTAAT ACTACTTTTT TTCCTTTCTT GATATTTACC  
300  
TTTTTATTAT TTCTAAAATG CATTGTCAAT TCATTATCAT CAGAACTAAA TCCGATAGAC  
360  
ATATCCCCAA CATTATTTGA AATAATCACA TCTGCATTTN TCTTGCGTAA TTTTGTGTGT  
420  
GCATAATTTT CAATATCTTC AGCCTCTGCT GAAAGGCTAT TAATACTGNG ATGTTTATGT

480  
CACCTAAATA TTAAGAATGT CTTGAGACGT TTAAAAGATA CTGACAATCA CCACCTGGTT  
540  
TTTCA  
545

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCTNA CCATCCATAG CTGTGNACAC AACATGATCT TTATCAATCA TCATAATGTT  
60  
GCAAAGGGAT TTCTTTNATC AAACCTCAGGT GCATATGCTC GNACTTCTTC CATAGTTANG  
120  
GGCAATTTTCG TTGGGGTTAA AGGGTGTGTT GGATGCCCCT CTGGNNCCAA GCTCTCAGAA  
180  
TAAGTTAACT CATCTGTCTT ATCACTATCT TTTACATGTT GTANCCATGA AAAAAAGTTA  
240  
ATATCTTGTTG GTAATCTNGA AAATTTAAAA CTGTGACTTA TTAATGTGTG TCTGTGAGAC  
300  
ATGTGNTTAT ATGTCACATC TAACTATCT CGACTGTGTA TTANCTCCTT CGNNGTAGTC  
360  
GCTCTGANNA NTAGGGATAT CAANGGTCAT GACTCAACAC ATCTAACAAC NCCTTCTTAA  
420  
NGGTTATTA  
429

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCCTAA TGCANAAAAAN TTCCCCGAGT CACAGTACAA TTTGCCGTGC TTCGGNGGAT  
60  
TACTTTGTTT ATTTTTATTG TGTANCATTA ATAATGAGTT GTCTTAACGA TTGTCGCTTT  
120  
ATAACTACAC GTGCTGTGAC ATCTTTTAAAG AAAAACACAG AAGGCTTGTG CATGTGATTG  
180  
TAATTGGATG NCATAGAGTA ATGATATGCA CCAGNTGATA ATATAGCAAG ATAGTCTCCA  
240  
CGTGTGACTG ATGAAGGTAA TTAGCGTCT TTTAATAATG ATATCACCAG ACTCACATAA  
300  
TTTTCCAGCT ATAGNTACAC TGACATCTGC TTCTACATCT CTTATTTAAC AAAGCAATGC  
360  
TTGATACTGT GCGGTCATAA AGGTGAAGGT TCTTGATATT GAATCACTCA TNCCGCATCG  
420

AGTTGAACAT ATTT  
434

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCCTAC AAGGATTCAA AATAAAATAC AAGTGTTTTG CGAATATTTG TTCGTATAAA  
60  
ATCTTGAAAT CAAAACGCAA AAACGAACAA ACGTGCTTAT ATTTTATCG ATAATACAAT  
120  
TANTTTGTTG TTCTAAGCCA ATTTAATAAT CTTATGAGCA CATNATTTG ACTTCTGTTC  
180  
TTTAATAAAT TTCTAGATTT AGACATTTTA AATTGCTCAG TTTTAAATTC AAAGTTATTA  
240  
TCATAGCCTA TATGGACTAC ACCATCATAC TCTAATAGAA TAATTGCTGA TGACACATTA  
300  
AACAAATTTAT TAACAAATTG CACTGCATCT TTTAATTGCT GCTCAATAGG TTTATTAATA  
360  
TCAACAAAGT TTTCATTGGT GATTAATCAT ACCCTTTAGA ACATCGGNTT AAATCCNCTT  
420  
CTTNCAATCG ATGATATTAA GCACCATTAG TAATACCATC ATTTTACAA AAGGGTCANG  
480  
AATTTTCTTN ATTACAGCTT GGTCAATTAT GTGTCANCTT GAACCATARR DCTNS  
535

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCCTGC ATTTCCAGGA GGATANGAAA TAAGAATTGA GTTATTAATC AGTGGTTTTA  
60  
TTTTTATATT GGCTTCCCTT AGCGATTGTG GTTGATGGTT ATTTAGCTAG AAAATGGAAT  
120  
TTAGTTACAA ATATGGGGAA ATTTGTGGGN TCCATTAGCG GATAAATTAT TAGNTGCAAG  
180  
TGCTTTAATT GTNCTTGTGC AACTAGGACT AACAAATCT GTAGTAGCAA TCATTATTAT  
240  
TGNCAGAGAA TNTGCCGTAA CTGGTTTACG TTTACTACAA ATTGAACAAG GATNTGGTAA  
300  
GTGCAGCTGG NCAATTAGGT AAAATTAACA CAGCAGTTAC TATGGGTAGC AAATTACTTG  
360  
GGTGGGTATT AGGGTG  
376

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCTCAG TTCATGTTGT GGNGACACTT TAAACGGNCT GTGCCAGTAG CGACCCGAGTC  
60  
ATTTCAAGAA TGACCATTTC ACATTTATAT TATAACACTT GTCGNGCGTA ACTGTATAGN  
120  
TTTTCAGNNG TGTTTAAAGT TAAGTTATCT ACTTCGCGCT TTCCTTGGCT TAATTGTGAA  
180  
ATTACATATT GCGCTACGCC AGNTTGGTTG GGAATTTGGT AACCTGTTAT ATCACTTNTG  
240  
GTCAANNCAA TTATTTTTTAA TTTATAATCA CTCATATTAT CTACGTCCAC TCNTTTTATC  
300  
TAAACAATAA AAATGTGTTT NTCTCCCCNT AAATAATAAC AATGGCAGGC TTAATAAAAA  
360  
CAATATTAAA TACAATTTGC TCTTGTCAAA ATTGAAAACC CCCACATAAT ATTATTTTAT  
420  
TTAAGNGTAA GAGGGGGGCA ATCAGGGCTC CAGCATAATG TTAATCTTTG TCGGGTGGGG  
480  
TTCCNGTCTT GGGTNGCCCN AGATGCCAC TCTCTAGG  
518

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATTCCACT AGAAGTTNCA ACATTACGCA TTTTACATTT CGTAAGTGGA GACGGTGGCA  
60  
AGCTAAAGAT TCATTATGAA TTATATCAAG ATAATGAAAA AATGGGTTCT TATCAATATG  
120  
AAATTAACTA TNAGGAGATA GGCGAATGAA TATTATTGAT CAAGTGAAAC AAACATNAGT  
180  
AGAAGAAATT GNAGCAAGTA TTAACANAGC AGGATTAGNA GNTGAGATTC CTGATTTTAA  
240  
AANTGAAGTT CCNNNGNNT NCAAAAAATG GAGATTATGC TACTAATATT GCGATGGTAC  
300  
TGACTAAGAT TGGAAAGNNG TNCTCCNCNC TGNNNATTGC TCANGCGGAA NGNTTGNNNA  
360  
CCTTAGCTCC NGGACACCNG CACATGNAAC ACAACTNGAC ATTGCCTGGC CCCACGGCTT  
420  
CAA  
423

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATGACAAAA TATTAATCAA TTGGCGTATT ATACAAGAGT AATAGACATA TAAAAGTCGA  
60  
ATGTAAC TAC GTGAGTACTG ATTTTATTCT TTGTAAATTA CAAGCATTTT ATATCATAAA  
120  
GTTTGAAAAG AGGTATATTG AAGTGGAGAA AAACGAATAT ACAGCTAAAT ATAATGAATA  
180  
TAGTCAATTA TTAGACGCTA CTTACTCGCA AGCTGTAGCA TACCTTTTAA ATAAATATGG  
240  
CGCTGTAACC GATGATTATT ATAAGGAAAA ATCATACACG CGATTTTTTAA ATGGAGAAAT  
300  
CAAAGTATT TCAAAGGAA AATACACTAG AGCTAGCGAA GGATTATATT GTCATCACAT  
360  
AAGCGAAGAC AAATTCCAAA ACTTATCTTG ACCTAAGATT CATTTCCGAA TTTAAGTACT  
420  
CATACAACGT CAAAAGAAAG AAAACTTAGT GTACTGTGAT CTTATCGAGC ATTTANTTTT  
480  
ACATGCAATT ATTACAAAAG AATCCAATGG CAATTGGGGT GTGGGCTGGA TTATGTCAAA  
540  
TGATCAAACC AACAGTCATT GATTGGGACA TTAGCGAATA TACTCCAAAA CCAGCATGGA  
600  
TGCAAGCCAC CAAAGCACGT GCCTATGTGC CTAGAATATT AGTAGAGAAA CTACTCATTA  
660  
NNATTGACGA TATGTTAGAA GGAATAGAAA TATATGATNT CCNTGAGTCT AGATAAATGA  
720  
TTAANGGAGA TATATTTCTG GNTCGNTGAG ATTGTGNTAT AGATAGNNTA ACCCNNTAAT  
780  
TAAATATTAT TCTATNAAAT AGACCACGCA TNCCTATCTA TAAACGGACA ACGTTTATAA  
840  
ATGAGTTTGC ATGGTCTTGA ATTGTATTAA ATNTCTTNTT GGGTTTTAAT AGNTCACTTA  
900  
GNGGGTATGT CAACATTCTT TNGACAGCTT CACGTGTATT TTT  
943

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATACC TGCACTAATC AAAGTTTCAC CAAAATTTAA AGCTGTGTGA TATATCACAA  
60  
ATCCACAAAA TCCTAAAATA AAAATAACAG GGATATCTCT TAGTTCAGGG GTAGGCAATT  
120  
TCTTTATAAT TACGAACGGC AAGAGAATTA TTGTTGCTAA AATTAAACGA AATGCCGACA

180  
 ATGATTCTGC ACTAAAATCA TTTAACGCAA TCTTTATCAT TGGAAATGCA GATCCCCACA  
 240  
 ATATGATAGT AAATAAATAT GATAGAAAAG TAGTGTCTCG AAGTTTATTC ATTAATATCA  
 300  
 TCACTCCTTT AATTATGTGT TTCTATATTA AAAAATATGA TTTAAATGA GTACAACCAA  
 360  
 TTGGGAATGG ATTTACCTAT CCAATTTTAA AAGGGAGGGA GAAGATGGCT AAATATTAAG  
 420  
 ATATTGCTAG TGACATAAGA GATAAAATAA TCACAGGGGG ATTGGGTTTT ATGGAATGAA  
 480  
 GATACCTCCA CAGAGGCAGG TGGCGATACA AATACAACGT NAATAGAGTG ACGATTATTA  
 540  
 AAAGTATTGG AGTTATTAGA GGCTGAAGGA TTTACTATAC TAAAGTGGGG AGTGGGNACA  
 600  
 TATGTTAATG ACTATTTGAA TGAAGCACAT ATTACAAATA AGTGGTCTGA AATGATGTTA  
 660  
 TGGTCCTCTC AACAAAGAAG TCAGTATACG GTGCAATTAA TTAATAAAAT TGAGACAGAT  
 720  
 GATTCGTATA TACATATAAG TAAAGGTGAA TTGGGTATAT CGTTAATGCC ACATATTCAA  
 780  
 TTGAAAAAAG CCATGTCTAA TACAGCCAGT CATATTGAAG ACTTATCTTG TGGGTATATA  
 840  
 TAATGGCTAT GGTATATCA AGGTTAAGAG ATATTATCCG GNTGAACGAA TTGTCAAAGC  
 900  
 AAGGTATTAA ATTGTAGGTA GAGGAAAATT GTAATGGATC AACTCCAGGC GCTTTTACAA  
 960  
 TGCCANACCA ACTTNTTATC TTATTGGGGT TTNTAGGGTC AAAGATGCCA TAATAATTC  
 1020  
 GGATACAACC ATCATATTTT CCACTCTACA AANTGTTTGN GGAACAAATG GAATTTTAGA  
 1080  
 CATATTGATG TCCCNTATT ATCAAATTTA ATGAAATTA  
 1119

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAAATGTT CTAGAGATTT AGGTATCGAA GAACCCAGGA TTAAGACGAT TAAAAGAGCN  
 60  
 ACTATGATAT TAGGATTATC AACATATTTA CTGCTGTGTG CAAGAAGTAC GTGCTTGGAC  
 120  
 AATTTAAACC AGGTATGACT GCACCTCAAT GTGCTGGTAT CATTCACTACT GATTTTGANC  
 180  
 GTGGATTAT CCGTGCCGGA AGTAACAAGT TATTGATGAC TATGTACAAT ATGGCGGCGA  
 240  
 AAGTGGCGCT AAAGAAGCGG GCAGACACCG ATTAGAAGGT AAAGAATATA TTATGCAAGA  
 300  
 TGGCGATATC GTTCATTTC AATTTAATGT ATAAACGATA GAGTGAAGTT AATTAAATAG  
 360  
 TATATATGTA GAAGAGGCGG AATCAATTGT TCGCCTCTTT TAATTATGCG TATAATTTAT  
 420  
 TAAAAGAATG GAATGATTTT ACTCGCGTAA ATAATATCTT GAGTGCTGAA AAATTGTTTG

480  
CCTTCGCCAG TATAAGCAGG CTCTAAAACA AGATTAGCCT TTGCACAATA AAGCCATTCA  
540  
GGATGAATGC CACTATTAAG TATCTCTTGG AATTCGATAT CAAGCTTATC GATACCGTCG  
600

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGNAA ATGTTGGCTT TGGCGCAATG AAGAAGCAAC CACCNTCTAA AAGCTAAGTT  
60  
AANCTTATTT GAACACATGA TNNCGANTGC ACGTACATCA NCAGAACAAG GAATGCTTGT  
120  
NTCTGCGGNA ACAATGCTCA NNCANAGTAC GCTACCCACA TTTACGAAAA ATACATCAGC  
180  
AAGTCGTTCA TGATATGAAA TGTAGCAGAC ACGAGATTCA CCCTNTGTNT CCAGCTGACT  
240  
TCGCAAGTCA NNNAAATGTG TTAACCTCTAG CGGAAATGAA AAGGACAATT CATGATATAT  
300  
TGGATTTTCAAG AGATGAAGAT ATTTGGGNTT GTTATTTGGG TACTTTGGCT GTGTCTCCAN  
360  
GCTTAANGGA TGATGANGGT CANNNGTTAC TATCACGTNT ANGAAATGCT TACAATNNNT  
420  
ACGANTAGAA ATGACCCGGA TGGCGNGGNC NGNTAAATTG TCAATGNNTT NAAAGGTAA  
479

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGAGCTTAG TTCATTTTAA AGTAAAGAGT TTTTGTATG TAAAGTATAT TAGTAAAACA  
60  
CAGATTACTT GTCTCTGTGA AATTAATACG TTTATACTAA AAGATATAGT CTTTCTAGAA  
120  
AATCTGTTAA TTAATTGTGA ATTTTGTAGAA AATTTAATTGA ACAGCAAAAT ATGGATTGTT  
180  
ATAATTTAAG TTAAACAAAT TCTTATACAA TATTATTAGG AGGCAATCAC CATGTCACAA  
240  
GCAGTTAAAG TTGAACGACG AGAAACATTA AAACAAAAAC CAAATACATC TCAACTAGGT  
300  
TGTGGGTAAA TATTTTACTG ATTATATGTT GAGTTATGAT TATGATGCAG ATAAAGGATG  
360  
GCATGATTTG AAGATAGTAC CTTATGGGCC TATTGAAATT TCACCTGCTG CACAAGGTGT  
420



TCAATTATGG TCAATCGGTA TTCGAAGGAT TAAAAGCATA TAAAAGAGAT GGGGAAGGTT  
 480  
 GCACTTTNCC CCNNCCCGAA GAAAATTTTA AGCGTCTTAA TAACTCGTTA GCACGATTAG  
 540  
 AAATGCCTCA AGTAGACGAT GCAGAATTGT TAGAGGGGCT AAAACANTTA GTTGATATAG  
 600  
 AAAGAGATNG GNTTCCTGAA GGGGAAGGTC AATCATTATA TNTTCGNCCA TTTGGTCTNG  
 660  
 CAACAGAAGG GGGACTNNGC GTTGGCGCAT CACATCAGTA TNAAATTTAT TAAATTATNT  
 720  
 TATCTTCCTT CAG  
 733

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACTTGTGCAC TGCCAATAAT AATTAATCCT TTCATATTTG ACCCCTCTTT TTTTATTAA  
 60  
 ACTTGTGTGTT CACGTAATAA TTTCATAATA GCTTTTCCAA CACCACTATT TTCATTCGTA  
 120  
 TCTGTGACAT ATTTGCTAT TTTTTTAACT TCTTCTGCAC CATTTTCCAT CGCAACTGGA  
 180  
 TAGCCAACTT TCTCTAACAT TGATAAGTCA TTTAAATTGT CACCTATTGG CATGACATCT  
 240  
 TTCATTTCAA TCCCTAATCT TTCGGCAATT GTTTCTAGCG CAATACCTTT NGGTGCATCT  
 300  
 GAATGCGTTA TTTCTATATT TCCTCTCGAA GATGATGATA TAGCTAAATT CGGAGATTCA  
 360  
 GCTAAATTT TACTAGCTTN GGCAATTTTT TCTTAAATTT CCATCAAATG CTAATATTTT  
 420  
 CATAATTAAT TCAACAGGTA TGTTTTCAAT AGGATCATAA TTATCAACAA CTTTCAACGG  
 480  
 TNCCAATATC TATGCGTCTT TGNATACCAT CTTNAATACG CTCAACGTNT GGATGTTGAC  
 540  
 CTGCACGCTC AGCAATATCT ATGTAAATGT CTAAATCTCT TGGGGGATCT TCCAGTATAA  
 600  
 ATCGCACGAC TCGGNTATNC TGGATAATAA GTACCTGNAT CTTTTAAAAC ATNTGTAATG  
 660  
 NGGTGTACTA ACGATTTATT ANGGNGTGAA GTGCTCATTA CATTGAAAGT TTCATCACGT  
 720  
 TCTTCAGNAC CATTGAGACA AATATATGGT ACTGNTAAAT CTGTGTCAGC AANTGGTGCT  
 780  
 TGTGCTTCAA AAAATGCTCG ACCTGGCACG AGCGATAACA ACCGTTATCC CTTGTTCTTG  
 840  
 AGCGTATTNA NTCGCATCAA TATTAGGTTG AGAAATTTCA TNTGCTGCAT TAAGGTAGCG  
 900  
 NGCCATCCAT ATCAGNGGNT ATTAGGTTTN TCANTATGTT NCCNCGCCCN CGNCTTTCGT  
 960  
 AAATTTAAAA TCTTGTCTT AAATAAGAAT ATATACTCAG CGCACATACT TTTCTATTAA  
 1020  
 CATTATATTT GTCATTAATT TATCATATAA TGTAATTCTA ACAAATTTTA ATTAGTATGT  
 1080

ACTATCGTCT TAATTGGTGG ATTTCTTATT GGCTCTTAAG TTTTAAAAA ATGTTGGTTA  
1140  
ATAATGGTGC TACATGCTTC TTTTAAGGTA CAACCTTTAT CAACAAATTG GACGGATGAT  
1200  
TAAAAATTAG GTTNGGTTGG AAATAAATTC AATTAACTT GCTACTACAA ACCACRRDC  
1260  
TNS  
1263

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATTATGCCTA TTTGACACAT TATTGAAATT TTTAATATAC CCCTTATACG TTACGGCTTT  
60  
GTACTGTGTT TAGGTATATA AAGCTTTGAC ATATCGATAT TCTCCAACCTC TAACAGCTTA  
120  
ATTTTATTAT TAATCGTTCC ACCGAATCCT GTTAAGCTAC CCGTTTTACC GACAACACGA  
180  
TGACATGGCA CGATAATTGA TAATGGATTA CTTCCGACTG CACCTCCAAC CGCTTGGGCT  
240  
GACATTTGTG GCTTATCAAG CACCTTACCT ACTTTTGTGG CAATAGCACC ATACGTTGTT  
300  
AGAGTCCCAT AAGGAACCTG TCTTAATTCA TTCCAAACAC ACTGTTGAAA ATGACTACCT  
360  
GTTGGCTTTA AAGGTATTGT GATTTTCAGGA TTGTCAACCT TTAAAATACG CGTCTTAACC  
420  
ACTGTGTCGN CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA CCAACACCTT  
480  
GTTGATTTTC AAACAAACAG CGGTCAGATT ACCCATCACT CAAAAGTCCA ATCGTCTACA  
540  
GCGATCATAG TACTCTATCT CCATAAATCC CCCTTTTCTT ATCATACGCC TATG  
594

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATGGGAAGT TCAATACCCA TAATGNCAAG CACCCTTGCA TTTAATTGCA TTTTCCNACC  
60  
GTTATTACNG GCCCCATCTC CAACAATATG TAAAGTTAAT ATCTGCATAA TCTTTTTTTA  
120  
AAGACTTCTT TTGCTGTTAA GAAATCAGCA AGANCTTGAG TAGGATGATC TTCATCAGTT  
180  
AAACCATTCC AACTGGTAC GCCTGAATAT TCAGCTAAAG TTTCTACTGT TCTTTGTGTN

240  
 AAACCCGCGG TATTCAATGC CATCATACAT TCCACCAAGC ACACGTGCAG TATCTTTAGT  
 300  
 TGTTTCTTTT TTACCCATTT GTGATCCAGT TGGGCCTAAA TAAGTTACAT TTGCACCTTG  
 360  
 ATCATGCGCT GCAACTTCAA ATGCACATCG CGTTCTTGTA GAATCTTTTT CAAATAACAG  
 420  
 TGCAATATTT TTATTTTTTA ACATAGGCTT TTCAGTGCCA ATATATTTAG CACGTTTTAA  
 480  
 ATCCTCGGAG AGNGTTAATA ATNNGNAATT C  
 511

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTGCCTTTTC TCTATCTGAT AAACCACGCT TTATTAAAAT TAAATCTCCT AACCATACCC  
 60  
 CGTCTAAATT ATCTGGAAGT ACATCAGCCT CTCTTACTTC AATATAATCA TGTTGTATTA  
 120  
 AAGTTTCTTC ATATAATCCC ATCTGATACA TCCTTTACTT ACGTTTACTT CTTATATAAT  
 180  
 CTGCATAATC TAAAACTCTT TGGCATT CATCTGTCAA TTCTCCTTCA AGGTGAGCTG  
 240  
 CACGATGTTG TACTTCGNTT TCTGGTTGTC TATTTNNTAA TAGTAAATAT TCTGGGGTAA  
 300  
 CTTTCAATGC ATTGGCAATT TCAGCTATAT CCTCCATAGG TATTTNTCTG CTACCGNNTN  
 360  
 CGTATCGGGA TAAGGTAGAT TTATTGACAC CTATCTTAGG TGGAAAATCA GGTAATTCA  
 420  
 CATTATTTNC TTTTCGGAGG TTGGGTGATT AATTTANCTA TTTCCGCTGA AGTNCTCATA  
 480  
 TTCAAATTTA CTCCCGTTTA TTTATACAGT ATAATAACAC TTCCCATATT AGGAAACACT  
 540  
 AGCATT  
 546

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTATATTATG TTCTGTTGGA CCCAGTAAAA TGTTGCAATG TATGATAAAA AGCCCTTGTT  
 60  
 TCAATTAATC GAAAATCGAC ACCAATCGTT TCATCATCAT ACGCTAATTC TAATGAAACT  
 120

TGTGTGTTCC CCACTGCAAC TTCTTTTACT TTATTGGGAA TATTTAATAA TTGCTGCTGC  
 180  
 ACTGCTTGTG GGTATCGGT ACTTATTATG AAATCTAAAT CTTTGCTCAT TTCTTTAAAA  
 240  
 CGACGGAAGC TTCCTGCAGA TGAATATTGA TCGATATAAT TTAATGTATC TATATAATCA  
 300  
 ATGATTTCTT GATTAAGTCT TCTCATTGGA TCAATTGGAT ATCTATCTTT CTTAGCACAG  
 360  
 NGGGGTTTCA CAGCTTCTAA TATGGTGTGG TCCGNTTCTT TTAGCAAATC CGCTTAATTC  
 420  
 ACTTAACTTN TCCCAATNTC ACAANCAACT TGGAAGTGAC GCTTNTATCA ACAAATATTC  
 480  
 CAACTCTTTA TATAGCTTAG CAATTTCTTG GTTCCAAGTC TGGAANTTTC AAAAGTGGAT  
 540  
 TAAGACCTCC CGGACTTCTT CCCGGTAATG GT  
 572

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGATGCACTC TGTTAGCATT ATCTTTAAAC ATTAAATATG GATAACCTGA TTGTAATTGT  
 60  
 GTNTGCGCAA TTAAATTCAA CATTTACGC GCATTCTTTT TCTTTTCTC AACATTTGGG  
 120  
 TTTGCAACCA TGTCATCATA ATATTTTCT AAATCGATAT CGTCTAATGT CACACCATAT  
 180  
 TCTTCTTTAA CTGTATGAGG TGCAAACATA TAAAAGTCCT TACCTTCTTT AGCTAAATCG  
 240  
 AAGAATTTAG ATGGAACAAT TAAACCAGTT GATATTGTAG ATAAACGTAA ATCTTCATCC  
 300  
 GCATTTACTT NNTTAGTATC TAAAAATTCT TCTACATCAT AATGGAAGAT ATTTAAGGTA  
 360  
 CACAGCACCA GCACCAGGGC GGTGGACAA GTTGGATCTG CATAGCTAAA GCCACCTTCA  
 420  
 AGTGACTTAG CAATAGGTAA AACGCCTTNC GCTACGCCTT TAATTCCTTT AATTGCTTCA  
 480  
 CCACGTGCAC GCAATTTAGA TAAGTTAATT GCAACGCCGC CCCCAATTTT ACTTAATTGG  
 540  
 TNGNGCAAGG NGGANTCAAT AAAGTTAANT TGAATTTAAG NTGNCAACCC ACTTCTTNNA  
 600  
 TNNGAAACAT GACTAGCT CACCACGACG CGCACGGNCT GCGTTTAAAA ATGTTGGTGT  
 660  
 CGCTGGNTGA TATCTTTGTT CAACCATAGC AGAAATAAAT TGTTTAGCTT GTGCTTTATT  
 720  
 ACCATNTGCT AGGTATAAAG CAACAATGGC AACGTGTTGA TTATAGCTT CTAAGTATTG  
 780  
 ACTTTTATCA TTTGTTNCA AAGCGTAATC TTTGAAAAAT TTAGTAGCTG ACATATAACT  
 840  
 TGCAAAATTA AACGAGATTG ATNTGGATA ATCAGTGATT TCAATTAGAT CCNCTTCACT  
 900  
 ATAAATATCA AACACATTGA AATAAAAATC GGTGTCTTCT AAATAACGTA AAACGCTCGA  
 960

TTTCAATATT CGAAGAAGAT NGCGTGGGCT TTTTACTTCT TTCTTAAATT AAGCTTACNT  
1020  
AAAGGTTCCCT TGGGGCTTTT TTCTTAAACT TAAAGGAATC CCATCTTCCT CTTCCCGGTT  
1080  
NGGGGACCCC AAATATTTTA CTCAAATATT GATGG  
1115

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTCCATGGAG GCATGCGCAC AATCTGCATT GTAATTCATA CAAAATGTT CACCGACTCC  
60  
CAACCGAATC CACCGAAAAT GCCAACATCT AGAATCGGTT GCACATCATG TTCAACACAT  
120  
TCTTCGTGCA ATAAATTAGA GAGTTCATTA TTGATGCCAT AACCGATGCT AATTGTATCN  
180  
CCATAAGTTA AAAACTGAGC AGCACGTCGG AGAATCAATT TCCGACTANT AAAAGGTAAT  
240  
GCGGGTTCAG GTATTCCATC AATTCGTTCT TCTCAAGACA AGGCTGGTAA ATAATGACTC  
300  
TGAATTACTT GGCGGTGATT CTTTTCATCT TCTGTGACGA ATACATAATC GACAAGATTT  
360  
CCTGGGATAA CAACTTCATT CGGTTTTAGG TGATAGTCGT CAACTAAAGC TTTAACTTGN  
420  
ACAATAACTT TCCCATGATT GGCTTTCGCG TTTAATGCGA CATGATAACA CTCGCTCAAG  
480  
TACGCTTCTT GAGNTAAATA AATGTTACCT TGTTGATCTG CGTATGTTCC TCTCAGTAGT  
540  
GCCACATCAA CGCTAGGGAA TGTGTAATGT AAGTATGTTT CATCGTTGAT GGTTACTAAT  
600  
GAAACTAAAT CATCAGTTGT TCGTGTATTT ACTTTACCGC CACCGTATCT AGGATCAACA  
660  
GCTGTGTTTA ATCCGATTTT AGTAATAACT CCAGGTAATA ATTGATTACT CTGACGATAA  
720  
TGAGTTGCAA TGATACCTTG TGGTAAAAAA TAAGCTTCAA TGTCATTATT TTTCATTGCT  
780  
TGTGCCGTTT TGGAAGAAGC CGTTAAAATG CTCATAATGA CACGTTTAAT CATGCGACGT  
840  
TCTATAAAAT CATCTAAATC CGGTGCGGCA CCTAAACTAT GGATATCATT CGCTAATATA  
900  
AACGTTAAAT CTTTGGGCGT ATGATATGTG TCATGTTGCG CTAACACAGC ACGTAGAACT  
960  
TCGGCGGGTA AGTTGGCTAC AGCTAATGCT GGTAAACCAA TCACATCACC ATCTTTAATG  
1020  
ATATGTTGTA AGTCGTGCCA TGTGATTTGT TTCAAGCAAG TCACCTCCAT CACATTTGAT  
1080  
AAAATATAGC GTTTTTACAC TTTGTGTAAA CCCTTACAAG AAG  
1123

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
CTCCATTTGC ATTTGGGTCT TTAAAACTAA ACACATACTT ATAGTTGCCA TTATGTTCTT
60
CAATAGAATA ATCATTATAC ACTTTATTAT TACTACCAA TTTATTTGCT TCATTATTAG
120
CCGCATTTAA AGCTGTTTGG AAATTTGGCA ATTGCTGTAA AGCTTGAGTT TTATTTCCAT
180
TAAACGGATA AATTTGACGT GCAACCGGCG CGGCATTTTG TCCATAATAT GGTGCAACGT
240
AACTTGATTN TTGATTATTA CTTGATTGGG TTATTATTTG TTTGGGTNTT GGGTCATTGT
300
TTGTTGCATT TGAATTAGA TTGTTGCTGG TTATCGTTTG CACTATTATC TTTATTATCT
360
TTGNTTACGT CTTNACTATC ATCTTNATTG TCTTTCTTAT CTTNAGATGA ATCANTTGNT
420
TTNTTATCTT GTTGNTCAGT TCTCGCTTTA TCATCTTTTT CTNNATTACT GTCTTTTTGG
480
TGGNGCACTA TCTTGACCAC ATGCAGCTNA AAATAATGAT AATGCTAGTG GACCCTGTAN
540
CTAATCTTTT CATACATATC TCCTCCTATA ATTCGATATT CATTGAATAA GCTTGAAATA
600
CATATCTNCC ATGTGTATCA TTTCATGGCT TGTTACCANA GACGTCAACA TTAATATGAT
660
TTGANTTATC ACAATACCCA TAACTACAAT CTAAGGTTCT TTTTATTATA CCCTAATTTT
720
TGTTCATTAT TATTTAATTT TTGTGAATTT TATGTTTTCT ATAAATTTAA TTATTTTACT
780
TTAACAATTC ATTACGCATT TAGCATTTCA AGGCATACAC AATAGGAATT CCGATGATTT
840
CATTTTATCT TGCTGCAAAA AACAATCATT ATTACTTCTT TTTTCCATAA TTAAATCTTG
900
TATCCCGTTA CATCACCTGG TNTGGAAATG ATGTTCAACC CAACCACTTT TAAATCCAAG
960
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
TTGGCCCTTT GGAGANTCCG GATTATTGAT AAAGATATTC CTAGCGTTCG CTAAGCATAG
60
TTATGTGATG GANAATAGTC TTGTTGAAGA GTTGTTC AAT ATTGCCTCGN CTGTCGCTCC
120
AAGTAATGAT AAGCAGGGTG TTTTANCGAT TATCGAACAA GAAGTATTGN NCAAGTAGGT
180
AGCACATCAT CAATGAAGCG GCTATCATGA TACCTAAATA CATGTTNNAT GNAANCTTTG
```

240  
 NATACCGAAT CATCNAACAT TAATATATCT CCAAACAGGT TAGCCAATAA TCCCATAGTA  
 300  
 AAATAAGCCC ACTACAATCA GTTGAATAGA TGATAAAATA AAGCAGATTT TAATCAANCC  
 360  
 GATTTTGATA CAGATAAACA ANATANNAAN CAAAGGCACA TGGTGC GCCT GTGCTTTTAA  
 420  
 ATATATATTA ATTTAAACGT GTTTCACATG TACCCAAGTT GTTAATNGAC AAGATAATTG  
 480  
 CTGCGTTTAA ANCCACCTT CCAACAAGGT TTTGTACCTG CTTTCATCAGA GAAGAAACCA  
 540  
 ATATGTGGTG TTAATAAAT TCCTTTCATG TTCCGATTAA CTCTAATAAT GTTTTATCGT  
 600  
 CAATGTCTTT ATTAGTCCAG TCATTTGTGA AGTATGCAGC TTCATTTTCA TAAGTATCAA  
 660  
 TCGCAGCACC TAACAAAGTA CCATCGTTCA CTGCAGCGAN TAAATCAGGT GTATTGATGA  
 720  
 CTGCACCACG TGCTGCGTTA ACTAAGATTG CACCTTTTTT CACATGATCA AACATTGCTT  
 780  
 TATCGAATAA ATGATAGCTT TCTTTGTTTG CTGGAACATG TAAAGAAATA ATATCGGCAT  
 840  
 CTTTAATAGC TTCTTTAACA CTATCTTTAT AAGTTAAAAA GTCTAAATCT TTATTAGGAT  
 900  
 AAGCGTCATA AGCTGTAATT GTAGCACCAA ATCCTGCATA TATTTTAGCT GTAGCAGCAC  
 960  
 CGATACGACC CGTACCGATA ATTGCAACAG TCATATTTTT AACTGGTTTA GACATGATTT  
 1020  
 CTGCTTGCCA AGTAAAATCA TGTGTTTGTA CACGGCGTTC AATATCTGGG AAGCGACGCA  
 1080  
 CTAATTGTAG GGCGATAGAA ACAGAATACT CTGCAGTGTT TCAGGGGAAG  
 1130

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCAGTATCAA TAGTAGTTGG TTCATCATTG CCAAACACCT TTTTCAAATT ATCATTTTCA  
 60  
 AGTTGAAGCG CTACATTTTC TTCTACTAAT TCAACTGCAA GTGCCTTTAA TTCTGAAGTT  
 120  
 TCCTTTGAAA GTTGATTGAC ATTCATTTCT AAACGCATTA TTTTTCAAA TATTTTCATTG  
 180  
 CGATCCAAAT GTAATAATGC CTCCTTAATG CATAGTTTCT ATTTCTTCTA ATTTATATTC  
 240  
 AAGTGGCTGT TCATGTCCCT CAAGCTTCAC CTGCATAGAA ATGTCTAATA TATTTAAAGC  
 300  
 AACTACTTTC CCGGTTACCA TCAGGCGTTT CAATTGCTTC ACCAATATCA GGTAATTGTG  
 360  
 CACGTACTTC CTCATAATAG TCATTTTCAT ATTTTAAACA ACACATCAAG ACGACCACAT  
 420  
 GCAACCAGAA ATTTTAGTTG GATTTAATGA TAAATTTGGG TCCCTTAGCC ATCTTTAATC  
 480  
 GATACTGGGT TCAAAATCCC CCTAGAAAAT GTAGGAACAA CATAACGACC TACCCACAAG

540  
GGTCCCGATA CCGCCAAGCA ATTGGGCTTC AAT  
573

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCTTAAGAAG CACCTTTACC AATTCCGCCA AAATCTGTAA ANTCAAATGT AGTAGGTAAT  
60  
GTTTTTTTAG GTTGAACCAT TTCTTCTAAT TTAAGTAGTC TTGCATCTGN CACTTCNACA  
120  
ATACCCACAT TTGGGTCNAT AGTTGCGANC GGATAGTTTN CTCCCAAGGC ACCCGCCTTT  
180  
GTAATTGCAT TAAATAATGT TGATTTACCA ACGTTTGGTA AGCCAACGAT ACCTGCTGTT  
240  
AAAGCCATGA ATCATTCTCC TATCTTNGTG TATCATCCTG AGATACGATG ATTTTTTTTA  
300  
GTTTTTTATC AAACGTTTGA CGTGGAATCA TAATGCTTCG TTGACAATTT TCACACTTAA  
360  
TTCTAATGTC AGCACCCATT CTAATAATTT TAAAACGATT GGTTCCACAC GCATGTTGTT  
420  
TTTTCATTTT TACTATATCA TTTATTCCAT ATTGNGACGC CATTAAATAT GACCTCCATG  
480  
TATTATAAAC TACTAAACAC CGNTTTCCT ATGATTAAAA GGTGTCATTA TTGGNTGTGG  
540  
TGTCTTGATA CCTTCTTGTA AAAACATTTT GTGGACTTCT TTACGAATAA TACGCGCACC  
600  
AGAGAAACCN TCACCTGGTA TTGTTTCTGC TGAAACCCNT AATATTACTC TAGTATCTTC  
660  
AAAGGCATCA ATACCAATCA CAACAGGATC ACTTACAAAT AAATNNATAT TTAATACGCA  
720  
GAGGATGGTA AATAATGTGT TTAATTTCTT CTCAACATTA TCAATATTTT CATCTACAGA  
780  
TACTGGAATT TTAACAATTG CTGGTTCCAC TCGGNAATTG AGTAANTCGG TATTCACCCC  
840  
NTNCTACTAT TTGGGAAGAT TGRRDCTNS  
870

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TAAGATATTA AGTTATAAAA ATGATTTGAA AAATAAAGTA GAAACTTAA ACAATTTAAG  
60



TCCAACATAAT ACNATGTTGC GTGGATATGC AATTGTTAAT AAAAAAGACG AAGTCATTAC  
 120  
 GAGTACTAAA GATTTAACAG AAAATGATCA ATTGACGTTA ACAATGAAAG ATGGCTTAGT  
 180  
 AGATGCAAAA GTTACGAAAG TAAGGTGTAA TAATGACTAA AGAAACGCAA AGTTTTGAAG  
 240  
 AAATGATGCA AGAATTAGAG CAAATTGTTC AAAAATTAGA TAATGAAACA GGTATCTTTA  
 300  
 GAGGAATCAT TAGATTTATA TCAACGTGGG TTTTGAAACT ATCAGCAGCT TGGTGACACA  
 360  
 ACTTTTAAAA AATGCCGANA AAAAGGNGAA TGACTIONATA AAAGAAGAAG CTGAGATTGT  
 420  
 TAAAAATGAC GATCTTCCGA NTGANTTAAT TATAGANGGA NGTCAATATG ATNTCCGGTG  
 480  
 GCGATAATTA NCCCAGNAAT GGTTCTCNGT NGGAAGGAG  
 519

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCAATCGCNT GTNTGACTGT NTTGTCACTG ANAGCGTTAT CTTNTTTACC AGANTTGACA  
 60  
 ACTNACATTN TCGTANTCAT AGGTTGACTA CGCNTAACTT GATAGTCACC TGTATCTTTT  
 120  
 AATTGTTTTA AAGAGTCTTT GNCTAAGCTA TCCGTACCTC TATCATCTGT GAGCCANAGT  
 180  
 CGTTTCACCT TTTTTCATTG ATAGGAATGC TGTTTCACCA GCAGGCATTA CTTTGTCTTG  
 240  
 TACTTTGTTA AGTTAAGACT TTTCGCCCCA GTATTGATCA TTTTGTAA AGTCTGCAGA  
 300  
 CTCATCTTTT TTGTGTTTAC CTAATTTAAA TGGACCAGTA CCATCGAACT TTTTAACGCC  
 360  
 ATCTTTTGTT GTACCGTTTT TAAAGTCTTT TGGAGACACA AATACATATG GACGAGGCAT  
 420  
 CGCTAATTCA GCCAATGCAG GTTGATATGC TTCTTTCAA TTCAATTCAA CCGTGTACTT  
 480  
 ATCTTTAACT TTAACATTGT CAATTAATGT TGAAATCTTT AACCAAGAAT GCAATTTTTT  
 540  
 ATTTTGTGA NCCGCATCAA TATTTTCTT AACTGCGTCA GCATCAAATG TTGNTCCATC  
 600  
 ATGGAATCTC ACATCATCTC TTAAATGGAA TTGTATTAAG TCTTCCCATC TTCAAGACAC  
 660  
 ATCCCATTTT TTAGCTAGGT AAAGGCTTAA TACCATCTTT CGGTGTTACG GTACAAAGCG  
 720  
 GCTCGTARRD CTNS  
 734

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GNGNTNCTTA TNCGATTCAC AGTGAAGTAG GTGATAAGAT GATTGGTCCC AAGCTGAAAT  
60  
CCCCAAAATT GTGCCAATTG ACTATATTTT NCAACAGGC GATATTGTTG AAATACGTAC  
120  
TAGTAAACAT TCATATGGAC CAAGTCGTGA TTGGTTGAAN ATTGTTAAAT CGTCTAGTGC  
180  
CAAAGGTAAA ATTAAAAGTT TCTTCNCAAN ACAAGATCGT TCATCTAATA TTGAAAAAGC  
240  
CCGAATGATG GTTGAAGTTG AAATAAAAGA CCAAGGATTT AGAGTCGAAG ATATTTTGAC  
300  
AGAGAAAAAT ATTCAGGTTG TTAATGANAA ATATAACTTT NCAATGAAG ATGATTTATT  
360  
CGCAGCTGTA GGATTTGGCG GCGTGACATC CTTACAGATT GTTAATAAAT TAACTGAAAG  
420  
ACAACGTATT TTAGATAAAC AACGTGCTTT AAATGAAGCA CAAGAAGTTA CGAAATCATT  
480  
GCCTATTAAA GACAACATCA TTACTGATAG TGGTGTCTAT GTAGAAGGTT TAGAAAATGT  
540  
ACTTATCAAG TTGNCAAAAT GTTGTAAATCC TATACCAGGT GATGATATTG TAGGTTATAT  
600  
CACCAAAGGT CACGGCACGA AAGTACATCG CACTGATTGC CCAAATATTA AGAACGAAAC  
660  
TGAACGACTA ATTAATGTTG AATGGGTAAA ATCNAAAGAC GCAACTCAAA AATATCAGGT  
720  
TGATTTAGAG GTAACGCGT ATGACCGAAA TGGCTTGTTG AATGAAGTAC TACAAGCTGT  
780  
TAGCTCGACA GNCGGCAATT TAATTAAAGT TTCAGGACGT TCAGATATTG ATNNNAATNC  
840  
AATAATAAAT ATTAGTGTC TGGTGAAAAA CGTGAATGAT GTTTATCGTG TGGTAGAAAA  
900  
GACCAAACAA CTTGGTGATG TTTATACAGG TAACAAGAGT TTGGGAACAA GAGGGTCCAA  
960  
AAATATTGAA AGTAGGTGGT ACAAAGAGG TTAAAGAAGC ATCGGGTGGA CGAATTGATA  
1020  
CATTAAATAA TCAAATCAAA AAAAGGATAT TGGTTTATTA GTCGGGGATC CGGNCAAGAA  
1080  
CTCTACAAGA GCAAAGATGC AGATGTAATT GCAAAGAAAA TTGCTAATGC AAGATTATTT  
1140  
GAAGATGACA ATAATAAATT AAACTTTAAT ATCCAACAAA TGAATGGTGA AATACTATCA  
1200  
GTTTCACAAT TTAATCTCG  
1219

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACTAAAATGA TTAAATTACT TATCTCTTTT CATCTGATTG ATTATCGAAA TTTCTTCCTT  
 60  
 CTAAACCTGC TAACTCTTCT TTAGAAGCTG NAGGTGCTTT CATTTCAAAT ATCTCATTCA  
 120  
 CTACTGTGTA ATCGGAATAT CCTAATCTGG CAATAGGTTT AATCGACTTA ATGTCCAATT  
 180  
 TACCATTATC AAGAATAACC NTATCGGCAA TATGAACTTG GGCAACTCTT CCTATAACAA  
 240  
 TATCTACGGT AGATACTGGG TCTCCTGGCG GAATACGAAT CGGGTGAACG GTACTCACAT  
 300  
 NCAAAATGTA CTGGCGATCT TNGACTCGAT AACCNNGGGG CTTCTATACA ATGNTNCTTN  
 360  
 CGGGCACAAC CGGNATATTN AAAATNCAAC CCCCCNCAGG TGGGTAGGTG CCTTCCGACG  
 420  
 GATAAATTAA CAGGCTTCTC TTAAATCAT ACGGTGGCCA TGTNCCAATA CAAACCCACC  
 480  
 CCGGTTTCTT CCTGGAAT  
 498

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTCAATGA ATATGATGAT ACTGATAAAA TTTTCTCTAA CCCATCAAAC AAGAAAACAG  
 60  
 AAGATTATAT TTCAGGAAGG TTTGGTTGAT ATATAATGGC AATAATTAGA CAGCGATATC  
 120  
 AGGAGCAACT TGATGATTTA ATAAAGGAAT TACGTCGGTT AGGTGCAAAT GTCTATGTGA  
 180  
 GTATTGAAAA TGGTATAAAA TCATTAAGTA TTGACGATAG AGGCTTTGNA CGACAAACAG  
 240  
 TTAAAAACGA TAAACATATC AATCAATTAA ATTATGATAT TAATGAGCGA GTTATCATGT  
 300  
 TAATTACAAA GCAACAGNCC ATTGCGAGTG ATTTGCGTAT GATGATTTCT TCAANTAAAA  
 360  
 ATCGNCTCCG ATTTAGAAAG AATAGGAGAT AATGCATCGA GTATTGCCAA TATTCGATTG  
 420  
 CGTACAAAGA TTACAGATGA TTATGTGTTA ACCCGTTTAA AGACAATGGG TAAATTAGCT  
 480  
 ATGTTAATGC TAAAGGACTT AGATCAAGCA TTAAAAAGA AAGATACCGT ATTAATAAGA  
 540  
 GAAATAATTG AGCGTGATGA AGATATCGAT GACTTATATA GTCATATTAT TAACGCAACG  
 600  
 TATCTTATTG ATAACGATCC ATTTGTCGCT GCACAAGCTC ATTTAGCAGC AAGACATTTA  
 660  
 GAACGTATTG GTGATCATAT TATTAACATC GCTGAAAGTG TTTATTTTAA TTTAACAGGT  
 720  
 ACACATTACG AACAAATAAC TTAAAGTTAT TACTATAAAA TCCCTTACGA TAAATATATA  
 780  
 TTTCTATCAT TCATAAACCC TCAAAAAAAA CCAAGATTCT CACAAATTAG NAATGNGTGA  
 840  
 AAANCTTNGN GNTATATTTT GGTTCCTACT TATTAAATNG GTCTCGCATC TTAGGNTATT

900  
TGGNTTGGTC AATTTTCATCT TG  
922

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCAATCGGTC TTATCTTTCA ACACGTTTGA TTGTANCGGA TATCACCCGG TTCATAAATC  
60  
CNAATCGTT GTAATATATT TCTCTTTATA TTCATTATTT CTAGGAATCC ACCCCCNCCG  
120  
TGCGGGCAAG TTTCTGGGAA ATTTAACAGC TATCCAGCCT TTCAACAAAT AAATCTGAAA  
180  
TTCGATGTTT TAAAATTTCT GCTTCTTGAT GTACTTCTTC CCAATTATAT TTCAATATTT  
240  
CTATTAAAAA TAATTCTAAT AGTCGATGTC TCTTAATGAT ATCAAGCGTA TCGGTTAAAC  
300  
CATCCTCTGT TAATCTAACA CCTTTGTATG GTTTTGTTC AACATAGCCT GCTTTTTCAA  
360  
GACGTCCTAC CATTTCACTT ACAGATGGAG GCTTAATATT TAAAAATTGA GATAAGATTT  
420  
TATTTGTCAC AAAGTTTTTA TCGCCATTAA TTCGTAAGGA TTTGCCTTTA AAATAAGTCC  
480  
TCTTTTTCTT CAGNTAACAT ACTTTCACCT CAACAGACAT TGTCTATATT ATATCACGAA  
540  
TTTACTTGAC ATGATAAATA TTCTCAGTTT ATTANACAAT TAATTAGGTT AGCCTAAACT  
600  
TTTAATTAGG AGGTATAAAC GTTTGTTAGA AACANAAGAT TTAAATCTGT TTTTAGGTAA  
660  
TAAGCATGTA CTAAAAACA TTTCTTATC GATACCAGCA CGAGCGGCGA AATAATTGGT  
720  
ATCATGGGCC CGAATGGTGC TGGTAAATCT TCCCTTATCA AGTCTTTAAT TGGTGAATTT  
780  
AATGCTACCG GTACTAAATN GTTNTATAAC AAACCTATAC AACAACAACN GCAACAGATT  
840  
ACATATATTC CACAAAAAGC ACATATTGAT TTAGATTTTC CTATAAGTGT GGAACAAGTG  
900  
ATTTTATCAG GTTGCTACAA AGAAATTGGA TGGTTTAGAC GACCTAATAA ATCAGCAAGG  
960  
GATTAAACTC AAACAGTTAT TAAGCGATTT AGAATTAGAA TCTTTTACGT CATCGACAAA  
1020  
ATTTCAAGAA TTAAGTGGGT GGGACAAATT ACAACGGTGG TGCTTANGTA GGAAAGAGCA  
1080  
TTGGATGGTC CCGAAAAGTG AAGGTTTATT TTCTTTAGAT NGAGCCCGGT TGGTCGGGAA  
1140  
TTTGGATTTT AGGGTAGCGA AAAAATTAAT CAATGACAAA AAATCCGAGA ACTTTAAAC  
1200  
AACAAAGGA  
1209

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATTCATNT TATCTATCGG NAATCATTTG TAATACATCT ACTAATTATA GTGTTTTATT  
60  
CGATAATATA ACTGCATGTA CATCTANAGA AGCCTCTTGC CTNGAAATCG CACCGTCAAA  
120  
CTTAAACTA TAACCTATTA AATCTGCTTG NGTGNCATTA CCACTCACAG NACAGCGATT  
180  
AAATGATGCA GTAGCAACCA AATCGTTTCA TGCACTTNCA CATAANTACG ACTGACATTA  
240  
NGCTGTGTAG ATGTACCTGC TTCTANCTCG CCAAGAACAT CTTGGANTNC GNGNTNGCTA  
300  
TTTGGNGCAA TGTCANCTTC ATCCATNGAG CGCTCAATAG TGTCAGCTGC CAGAGCGGCA  
360  
TAACTGCTT  
369

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCTTATTATA AATTAAAGAA AGGTAGTGGT TTCTATGAAA TACAATACTA ATGTTAAACA  
60  
TACAACTTTA GAAGCGTTTG TCACAACTGT CAATGATTTG GGTATTGAAT TAATTATCAA  
120  
TGAAGCACTT CGAGAGGTAA GAAAACGACA GCTCATAGAA CTTATAGATG ACGCACTCGT  
180  
CAATAAAGAT GAAGCAGCAT TTAATCAATA TACGGCAGAA TACAAAAATT TGGAGGCATT  
240  
TCTCGGTGNA TAACATTGAT TCGAATTC  
268

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTATACAACT AAAGTAATTC ACAATTCAAA CTTTGTAAAG GGTGTACAAA GTGAAAGTAG

60  
 CAGTCATTAT GGGCAGTTCT TCCGATTGGA AAATTATGCA AGAGAGTTGT AACATGTTGG  
 120  
 ATTATTTGGA AATTCCGTAC GAAAAACAAG TAGTATCCGC ACATCGTACG CCAAAAATGA  
 180  
 TGGTTCAATT TGCTTCTGAA GCGAGAGAAA GAGGTATAAA CATTATCATT GCAGGCGCTG  
 240  
 GCGGTGCGGN ACATTTACCA GGTATGGTTG CATCATTAAC GACGCTACCA GTTATTGGTG  
 300  
 TGCCGATTGA AACANAAAAG TTAAAGGGT ATTAGATTCT TTTATTATCA ATTGCTCAAA  
 360  
 ATGNCAGGAG GGTATTCCNG NTGGAACGAC TTGCAANTGG GTGCAGNAGG GTGCTTAAAA  
 420  
 ACGCAGGTAT TCTTGGCAGG AAGAATGTTA AGTNTTCAA ANTCTCTTT TGGNNGGANA  
 480  
 ANTTAATCAA GNTTGATCTT CCGNAATCAA AA  
 512

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCCTCGC ATTTAATTGA ACTTTATAAT ATTTGTAGTC ATCCACAAGC  
 60  
 AAATATATAC ACTCCCAAAG GTTTACATAA TTCCAAATTA GACACACAAC GGTGGATTGA  
 120  
 AAAATGGCAA AACCATTGGC AACAATATCA ATTTGGTTAC TTTGTATTGG TGAAAAAAT  
 180  
 AGATTGTAGT GNTATTGGTA TTTGTGGATA TGAATATCGA CAATTAAAGC AAGAAACAGN  
 240  
 ACTAANTTTA TTTNATAAAT TACATCCAAG TTTTGGNGGA CAAGGGGTAC GCATGTGAGG  
 300  
 CTNTTACAGC AATCACAAAT T  
 321

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGCAGGACTC GTGCCGCTCC TGCACAAGAT GTAGGAGCAT TTTTATATTT AAATAACTAG  
 60  
 AGTAATTAAC GTAAAGGCGT GTGATACAGT GAAAACAATT GATTAAATTA ACACCGAAGC  
 120  
 AAGAAAAGTT TGTGCTAGGA CTCATAGAGG GCAAGAGCCA ACGGAAAGCA TATATTGACG  
 180

CAGGGTATTC GACTAAAGGT AAAAGTGATA ATTATATTGA TAGCCGAGCT TTTGAGTTGA  
 240  
 GTAAGAATAG TGCGGGTTTA GATAGGTATG AAGAATTGCG TCAAGAAGCA GGTGAACAA  
 300  
 TCAAAATGGA CACGCCAAAA GGGTTTTGAA GAATATGAGT GGGTAAAGAA TGTNGCTAAG  
 360  
 AATTGACATT GNAATAGAGG GGAGGTAAAG GAAAGGGACA GGTTGATGCA TTCCCCCCTA  
 420  
 GT  
 422

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCCCGAGCG GGA CTTAAAA AGGCCACCAC TGTTGTGAC CTANCCTTAT TTACNTTTAT  
 60  
 AAATATAAGG AGGAGGTAGT AGTGAAAGAC TTATTGCAAG CACAGCAAAA GCTTATACCG  
 120  
 GATCTCATAG ATAAAATGTA TAAACGTTTC TCTATTCTTA CTACTATCTC AAAAAATCAG  
 180  
 CCTGTCGGAC GTCGAAGTTT AAGCGAACAT ATGGATATGA CTGAACGTGT ACTGCGCTCT  
 240  
 GAAACAGATA TGCTTAAGAA ACAAGATGTG ATAAAAGTTA AGCCTACCGG AATGGAAATT  
 300  
 ACAGCTGAAG GTGAGCAACT GATTTCGCAA TTGAAAGGTT ACTGNGATAT CTATGGAGAT  
 360  
 GATAATCGTC TTGTCAAGAA GGGTATTTAA AGAAT  
 395

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGTGATTTA TCATTGATT GCATGATTAG AGGGAGGGAT TAAACGTGAC ATATCATGAG  
 60  
 CGTGTTTTAG CATTAGAGC AGANAGTAAN AGNNCCGCAT TTGATTTTCG ATTCGGNAGA  
 120  
 TTTATTTACC NAAGAAGAAT GGCTAAGTAT GTCTCTTGCA GAAAGACNCA AAGCTGANAA  
 180  
 AGCATTTCTGA CACGNAGTTA AAAATATGGA CGATGTAAGA ATGCCCTTCT CAAGTGTCCA  
 240  
 TGACGCCCCA AGTAAAATTA TATAATGTTG TATATTCTGA TANC GG CATT AACGTAATT  
 300  
 TTAAACNAGC TGAAAATGAA GGATTCTAAT ATCATTTTCGT TTATATATAG CAGACATGAT

360  
 AGAATTTTAT ATGTAAATCT TGTAGGTAAT CGTTTTNNAA ATAATATAAG TATGACTAAA  
 420  
 NCCACATCCA ATATAGGACG GGGCTTTTAG TATCGTTCCA GATTTGTGGG GAGTTAGGGT  
 480  
 TTACTTAATT AAAGGGGTCT GCCCTCAATT GCTCACCAAC GAGGGCAAGT TACATCAATC  
 540  
 ACAC TTCAAT TGCCGCCGAC TAGGGGTAGT AATCATTGGC AATAAGAACT AGTTAGTGAC  
 600  
 TAACGGATTT ACGTTCCATA AGCAAAGTGA TACAAACGCT CAGCATCAAT GTAAGGCATA  
 660  
 GAATCAATAG TTAGGTAACC ATCTTTGATG TCACCAATTA ATCCTTGATT TACACCAGTG  
 720  
 TTCACGTAAA TATCATAGCT ACTTACGTCT GAGAAAATAA GCGCTTCAAT CTCTTTTCTC  
 780  
 ATAATCATCA CTCCAATGTT TATATATTAT TTATATAAAC TCTCTCGTCT CTCTCTATTT  
 840  
 ATTAAC TTCT TACAAGTCTA ATATTACATG AATTTCCAAA TAAATAAAGA GGT TTGTGAT  
 900  
 GTATTT CACA AATTTATCAC TATTTTGGAA AATTAAGAAA TAGTTAATTA TATAAAAGTT  
 960  
 TAATAAGTCA GAAAATATGA TAAATGTAG ATGTTCTTTA GACATTAAAA GCTTCTAACA  
 1020  
 TGATACGGAA TATGAGGTTT CTGTATCACA TTAGAAGCTT TTTTGTGCG GTGCTTATAT  
 1080  
 TAATAATGGC ATGAATGAAC GCATGCTGTC TTAGTTTCAG GAATCGGCTA GAATATTAAA  
 1140  
 CTTCCGTTCT TTGAATATTT NTTAATTTCT TACTAATATC ATCCAGTTCA TTCTTCGCCT  
 1200  
 TTTTAACCCA ATCTCCTTGA GCTACATTAT CAAATTCACC TTAAATTTT TTGANATGGC  
 1260  
 TACCTATATT TCACAGCTCA CTTTAGATAT CGAACTTGTT TCTTCAGAGT TACTTGTTAT  
 1320  
 ATTACCAGGT TTTATTTGAT ATTCAGTTTG ACTCATAACT TGTATCCTCA CTTGAAGTAT  
 1380  
 AGTGTA CAGA ATCTGTAAAA TAAATGTTTT CTCTTTTATT TTCTACAAAG GTAAATTCTA  
 1440  
 GATTTTTTGA CCCTACAGAT GAGCCTTTTA AATCACCATC NCCTTTTATT AAG  
 1493

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGATGTGATC CAACCAAGTG ATAGCAATGT ATATGCAGTT GGAGAATGTG CAGAACATAC  
 60  
 CGCCAAAGTT TATGGACTCG TTGCACCACT ATATGAACAA GGTAAGTAA AGCTGATCAT  
 120  
 TTAACAAATA AAGAAACGAA CGGATACAAG GGATCAACAA CAAATTACGT CATTAAAAGT  
 180  
 TTCTGGTTGT GACTTGATATA GTGCTGGTCA AAGTTGTAGA AAATGCAGAA ATTAAAGGTA  
 240  
 TTGAAATATT TAATAGTGTT GATAATAACA ATAAAAAAT CTTTTTAAAA GACGGTAATG



300  
 TAGTTGGTGC AGTATCGTGC CAATATGGTG ATATCGATGA TGGTTCACGC TTTTATAACA  
 360  
 TGATGAAAAA AGGTGAATCC ACTGAAGATT ACACACTTGT ATCATTGCTT ACTAAAGGTG  
 420  
 GAGAAGAGGC ATCGCTATCA ATTGCTGATA TGGCTGATGA TGAAACAATT TGTGGTTGTA  
 480  
 ATGGTGTTGA TAAAGGTACT ATAGTAAATG CGATTACGGA AAATGGCTTT ACAACAGTTG  
 540  
 AAGAAGTAAC GGCTAAAACA AAAGCGGGGA ATTCATGTGG TAAATGTAAA CCGCAAATTG  
 600  
 CTCAAATATT GCAGCACACC TTAGGAGATG ACTTTGTTGC CGCAAAACCT GCTGGTATAT  
 660  
 GTGGTTGTAC TGATTTGACA CGCGATCAAA TTGTAACGCA AATAAGAGCG AAAGGTTTAA  
 720  
 AAACATCTAA AGAAGTTCGA CATGTTTTAA ACTTTAAAAA TAAAGGTGGA TGTCCAAAAT  
 780  
 GTCGACCAGC AATCAACTAT TATTTAAACA TGGTTTATCC ACATGATCAT GAAGATGAAA  
 840  
 GAGAATCAAG ATTTGCTAAC GAACGTTACC ATGCGAATAT TCAAATGAT GGTACATTTT  
 900  
 CTGTTATACC TCAAATGCGT GGAGGTGTTA CAGATGCAGA CCAACTGATT CGTCTAGGAG  
 960  
 AAGTGGCTAA GAAATATCAT GTGCCACTAG TTAAAGTGAC AGGTTGCAA CGTGTTGGTT  
 1020  
 TGTATGGAGG TTAAAAAGA AGAATTACCA AATATATGGG AAGACTAGGT ATGCGTTCAG  
 1080  
 CATCAGCTTA TGGAAGAAA ACACGCTCAA GTTAAAAGCT GTGTTGGGTA AAGAGTTTGG  
 1140  
 GCGATTGGGT ACGCAATACA ACGACAACGA CTTGGGATCC GTTTAGAAAA ACATTTGGGT  
 1200  
 TCAATCGATC AACCC  
 1215

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTACCTCCAA AATCCTTTTA AATCCATGCC CATAGAAGAT GANNCCCAA ATACATTANC  
 60  
 TAAATCGAAA CATTGCCATC CATAACTACC GTCGAAATCC CATCCTCTAT TCTCTAATGT  
 120  
 TCTCAAATAA NTTAATGTAC TGCTATTACT ATTACTTTTA TTATTTGAAG ACACTGTTTN  
 180  
 TGGTNTTGGT TCTACTAATG GTGTCATTGG CACTTTTAAN TNTTGACCAA NAAATANTAA  
 240  
 ATTAGGATTT GCTATATTAT TTGTATTTTG AATATTTGAA ACTGAAGTTT NGTACTTTTA  
 300  
 ATGCNATAGC ACTAAGTGTG TCTCCTTTTT TTACAGTATA GAGTTGTGTT TTTGGAGCTT  
 360  
 CTCTAAACCT GTAGTAACCA AAGTAATTAG TAAGTAACNT TAATCGTTTT CTTCTGATAA  
 420  
 GAATNTTTGA GCTTCCAAGT TTGCAATNTT AANTTCTTNA GTAGGTNCAAT TGTANTTAA

480  
 TAAC TAGATT GTTACNTGG CTTGAGTTTT TCGGAGTATT TGAAATCTTT ATATCTTGAT  
 540  
 TAATTTTCATT TCCGTTTGAA ATTGCTGATT TGTTGTCTAA CTTTAAACTT GTGTCCGATG  
 600  
 TTTTAACAGC ACCTTCATTT TTTATTTTGT CTTTGTCTGT ATTTTATTA GCATTTAACT  
 660  
 CTGATTTTCGC TCGAATACAT TTTGCTCATA CCCTCTTGTA AAATCTTTAG ATTTATCAAT  
 720  
 TTCATCTGCA TATGCTTNGT TCGACATACC CAATGCCAAG  
 760

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATATGCTGAA AATGTATCAT CAGGATTCAA GATATCAATT AAATGATGTG GAATACCATC  
 60  
 CATTTCTTCA GGTGTTACTT GTGCAGTTCC AATATTCATA TGTTTGTAAG CTTGCATAGA  
 120  
 ATCACCGCTT ATGATTTTAC CATTGATACG CTTTCGCGAGT TCTATGCTAA GCTCTGTTTT  
 180  
 ACCTGAAGCA GTTGGCCCCA CAATTACTAC AATAAAAGGC TTATTTTTTAT TCATATTTAA  
 240  
 TTCCACTTTC TTTATTTTTT ATAAAATTGA TTCAACCATT TAAACAAGTC TTCCCAAATT  
 300  
 GTGTCATGAT CTTTTTTTCAA ATAACACTTC ATGACGTTTA TGATGATAAA GATTCACTTT  
 360  
 TAACAATTTT TAATGCCAGC TTCTCTATAT ATATTCGCCA ATTTTAAAAT CCCTTTACCA  
 420  
 TAATCACCTA AAGAATCGGC ATATCCTGAA ACTAATAATA TAGGCATGGC ATGATTTAAC  
 480  
 ATTTTCATAT TTTTAAATTG TGATGTATGT AGCATATAAT AGGCTGTGTG ATATAATAAT  
 540  
 TGATNTGACA CATTAAATCC ACTATATGGA TCTTTAATAA AGTTATCTAC TTCAATTGGA  
 600  
 TTACTAGAAA TCCAATCACT NTGTGTACGT AATGGACGTA TTTTTTTATT AAAACTATNT  
 660  
 GATACTAACT GGTAAACCCA TNCAACTCGT TTCTCAGCAC CATAAATTTG TGTAATCAGT  
 720  
 TGTAACACTT TAACGGTTGG GTAAACCTTT CCATAATTGA ATACATACCA AGGTCACCAC  
 780  
 TTTAAATTA GACCATCAAC ATATTTGCGG ATATTGGTTT CTTACAAAAC AATCTTAGTT  
 840  
 ATACGG  
 846

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
AAGNTGAATT TTTAGTACAA TTTCCACTGT ATTTATCTGT TANCCACTTT ATACCCGCAA
60
TATTTTCGTTG ATCTTATATA AACACTTTTG GCTGCTTTTC CTTGACCNAG GNTAANATTA
120
NAGATTTTCC TTTGTAAGAG TGTGTTTTGT AGTATCATAA ATATGTAANC TGTATNAAAN
180
TCCACCACAT TTTAGGACCT GGTGANAGAT GTCGNAAAAG AANATTTTAA TATTANCTAG
240
TATTATGTTA ATCATANTAA TTAGTGTTGC AAGTATCNAN TTAAAATGA AATATGACGA
300
AAAAGAAAAC CAAAAATCAA TTTATTATAA AGAACAACAA NCGCGCATT CACTTTATCT
360
TAAGCATAAT ACTATAGAAC CGAACACAAC CAANTCTGNA CATTTNCNA AATTGGAANC
420
AANTCCTATG GGAAGTGCTG TGATTGAAGG TTACATAAAT GANAATAAAG AAGATGATTT
480
TGTTGCCTAT GCATCACCTG AAAATAACTT TCAATTTGTA GGTGATTTAN TTNNAAAGTG
540
AAAGATTAAG TGAGTTACTA AAACCAGCGC ATCAATTNNA ACATCNCCAG ATGATATNNN
600
NNAAGAACTA AATANNAAGT AGAGTCACTA ANGTTAGGAG TTACTTTAAT GAACAAAAAA
660
CATGTTTTTG TAATTATTGG TGTCATTTTA TGTATATGTA TAGTTGCATC AGTCATTTAT
720
TTAAAAGTGA AATATGACGA AAAAGAAAAA CAAAAAGCA AAATACTATA AAGAACAACA
780
GGAGCGTATT ACACTCTATC TCCAGCATAA TACCAAAGAA CCCAATACCA TCAAATCTGT
840
GCATTTCACT AGTTTAAAAA GAGGACCCAT GGGCGATGCC GTAATTGAAG GCTACATCAA
900
TGAAANCAAA AAAGATAATT TTAGTGCTTA TGCTACACCA GAACATAATT ATCAGTTTGG
960
TGGTGCTATG ATAGAAAGTG AAAGATTAAG TGAGTTACTA AAACCAGCGC ATCAATTAAA
1020
ATCACCTGAC GAAATCAAAG AAGAATTAGA CACCNAAGAA GGCCACTAGG GTCTTCTTTA
1080
TTTTTGATTT AATCTTCCAA TAATCTATGT CATTGCTATC GAAGGTGTTT CGCAATTAAT
1140
ATCAATCACT TCATCATCAC CAATACTTCC CCAGTTTTGT ACAGTACATT AACACAAGCG
1200
AACCCCATTA ATGTAAATGA AATAATAGTT TAGCCATTAT AAAACATTA TATACCGAAT
1260
AACAAATGGCG AGGACGTGAT TTATTGACNA CTATCAAATT TTCTCANATG TGTGTGATTT
1320
TTTATAANNN AGGGTAGAGC AAGGTATAAT ATCCTTTCAA TCGGTTTTCA TATTTTATAT
1380
ATTTTTTAAA TATAAGCGCT AAATGTTTTA ACTAAAGCAT AGATTGACAA GATGTTATAC
1440
AGAAATTTAA ATTCTATCCA ATATTGTTG AAGTGTAAGT TCACTGGANT GGTATTAAAC
1500
AATGTAAAGG AGAGATTGCA NATGCCGTAT AATTACAAGA AACACAATGG AGAGTTAATG
1560
TCTGTAATGA GCCAAGGTGA AAAGTTTATT CATCCAATCC ACCGGTGAAT GATGAACTTA
1620
GTGCATTGAT TAAAGCTATT AATCTCCAAC AAATTAACGG TTGTCATTAT TGTGTTGATA
```

1680  
 NCCANAANAA AGAAGTAAAG GAANTGGGTG TAACACAACCT GANNATTGAT GAAGTCTTGA  
 1740  
 NNTTTAGACA TTTAGANTTA TTTACTTGAT CAAGAAAAAG TGACGCTTGA AGTTGCAGAA  
 1800  
 ATGNTAAATT CAANCAAGA CNTTAAGAAG TTTGAAATTA TTGACCGCN AAAATCATTT  
 1860  
 TATGATGAAG AACAANTTAT TGATCTTGTC TTTGTTGTAA ACCAAATTAA CGGTTGGAAC  
 1920  
 AGACTAAATA TTATTAGTGA TAGACTATAA TTGTTTCATAT AAATGCAGAG TTTTCATCTCG  
 1980  
 AACGCTATAT CATAACAANT CATGCCACTA TACAGGTCAA ATCTTGTATA GTGGCATTTT  
 2040  
 TAATTTATCC CTTTGAATAC TGTTATTTAA CGAATATCGG TCCACCTGGT CCAACAGGGA  
 2100  
 TACCTAATAA GAACCAAATG ATGACAAATA CTGTCCATAC AATGCTTAGC GCGATTGAAT  
 2160  
 ACGGCATTAA ACTAGAAAGT AAGGCTCCGA GTTTCATGCG TTTATCGTAT TTTTGTGCAT  
 2220  
 AAGTTAATAA TAAAGGTAAG TACGGCATCA TCGGTGTAAT TGGATTGGTA ATTGAATCGC  
 2280  
 CTACACGGTA AATGACTTGC GTAAATGCGG GATGAAAGCC GATAAGGATT AACATTGGTA  
 2340  
 CGAATATCGG TCCTAAAATA CCCCATTTAG CCGATGCGCT TCCGATTAAC ATGTTGACCA  
 2400  
 TTGCACTCAG TACAATAATA CCTAGTATCA ATACAATACC GTTTTGATGT TCTAATAATT  
 2460  
 TGGCACCTTT AACAGCAGCG ATAATTCCTA AATTACTCCA CTTTAAATAC GCAAGTAGCT  
 2520  
 GTGCTGCAA AAACACAATA ACGATAAATG TTCCCATTTGA TCCTACAGCA TCGCCGAACA  
 2580  
 TTTTACCTAA GTCTTTTGTA TTTTAAATTT CTTTGCTTAA AATCCCATAA ACTAATCCAG  
 2640  
 GTACTAAAAA TACGACAAGA ATAATTAATC CGACACCGTT AATTAATGGC GCATCGTCTA  
 2700  
 GTAAGCTGCC TGTTTTAGCA TTTCTTAAAA AACTATGTTT AGGAATAGCT GTAATAATTA  
 2760  
 ATAAAATAAT TGTGACTATG AAAGTGATAT TTGCCCATTT TAAAGCATGT GCTTCTTTGT  
 2820  
 CAGTAATATG TGAAGATGCT TCTTCAGGT CATG  
 2854

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTATGATAGN ATCGGAAAGA TGTATAAAGT TATCTAAAAG TTATACGACA CAAGTACACG  
 60  
 AGGCACATCG CTATGCGGTG TGTCTTNTGG TATGCAATCA AAGAGGTGTA AGAGATGACC  
 120  
 AAGCATAATA ACATTTATTA GCATGGNCGT AAGTCATATC AATACGATTG GTTCTATCAT  
 180  
 TCAAAAGCAT GGAAGAAGTT AAGAGAGATA GCATTAGATA GGGATAATCA TCTTTGTCAA

240  
 ATGTGTTTAC GTGAAGACAT NGTAACAGAT GCAAACATAG TGCATCATAT TATTTATGTT  
 300  
 GATGAAGATT TTAATAAAGC TTTAGACTTA GATAATTTGA TGTCAGTTTG TTATAGCTGT  
 360  
 CATAACAAAA TTCATGCAAA TGATAATGAC AAAAGTAATC TTAAGAAAAT TAGAGTATTA  
 420  
 AAAATTTTAA TAAAAAATA ATTTATTTTT ATAGCCCCCT ACCCATCGGC TTAAATGTT  
 480  
 TTTTCGACGG GTACCGGCGG GGGCCCTTCG CTTGCAACGC GGATAAACTT TTATGAAAGG  
 540  
 GGGTCTTTAT ATGAAATTAA CAAAAAACA GCTGAAAGAA TATATAGAGG ATTATAAAAA  
 600  
 ATCTGATGAC ATATTAATTA ATTTGTATAT AGAAACGTAT GAATTTTATT GTCGGTTAAG  
 660  
 AGATGAACTT AAAAATAGTG ATTTGGATGA TAGAGCATAC AAACAAGGCT GGTGCCGAGC  
 720  
 AATATTGTTA AGAATCCATT AAGCATAGAA CTGACAAAAA CAGNTCAAAC ACTAAATAAC  
 780  
 TTACTCAAGT CTATGGGTTT ANCTGCAGCA CAAAGAAAAA AGATAGCNCA AGAAGAAGGT  
 840  
 GGATTCGGTG ACTATTAAAG TTTTAAATGA ACCTTCACCA AAATATTAA CAACATGGTA  
 900  
 TGCAGAGCAA GTCACTCAAG GGAAAATAAA AACAAGCAAA TATGTTAAAA AAGAATGTGA  
 960  
 GAGACACCTT AGATATCTAG AAAATGGAGG TAAATGGGTA TTTGATGAAG AATTAGCGCA  
 1020  
 CCGCCCTATT CGATTCATAG AAAAGTTTTG TAAACNTCC AAAGGATCTA AACGTCAACT  
 1080  
 TGCATTACAA CCATGGCAAC ATTTTATTAT TGGCAGTTTG TTTGGTTGGG TTCATAAAGA  
 1140  
 AACAAAATG CGCAGGTTTA AAGAAGCTTT GATATTTATG GGGGCGAAAA AATGGTAAAA  
 1200  
 CAACTACTAT ATCTGGTGTT GCTAACTATG CTGTTTCTCA AGATGGAGAA AACGGCGCTG  
 1260  
 AAATCCATCT NTTAGCAAAC GTAATGAAAC AAGCTAGGAT TCTATTTGAT GAATCTAAGG  
 1320  
 CGATGATTAA AGCTAGCCCA NAGCTTAGAG AAAATTTTAG ACCTTTGAGA GATGAAATTC  
 1380  
 ATTACGATGC ACTATATCTT AAAATATGCA CAGGCTTCAG ACAGTGATAA GTGGTTGGTT  
 1440  
 AA  
 1442

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCAGC CGACCGATGA NGGTTATNTG ANATTACATA AGACGTGGTT TNGTNANTCA  
 60  
 AAGCTATGTC CAGTTTGTA TCGGAGGCGT GCTATGAAAA NTAGTTATCA CGCTCANANA  
 120  
 GTGATTGANG ANGTAATTAA GGAAAAGCCA NCAGCACGTT GGTGTTTTTC ACCACTNTCA

180  
 CCAANANNTG CGATAGATGG AGATACTTTA GTAACAAAGT TNGANGCATC TAACTAANGC  
 240  
 ATTTGATAGG TTGAGTAGCA TATNAAAAGG TTAAACANAA TCTNGTTGGA TCTATGCGTN  
 300  
 CAACAGAAGT TNCCGCCTAC CTAAAAATGA CG  
 332

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCATCCGTTT NCNTCATCNC ANGACNTTCN ANANTTAATT TTTACNAGGA GTGACATCTG  
 60  
 TGAATAACAC ACAATCCTCA CCACGCAGTN ATANTATTAT TGCGATTATG TTGTCTGCAT  
 120  
 TAACATATTG GGTGTGTGNA CAATCATTTA TTAATATAGG ACCTCTCGNN GGNCAAACGT  
 180  
 ATCAAACCTC TCCTGCCGTG TTAAATTTAT CTATTAGTTT AACTTCCCTC GCCACAGGTA  
 240  
 TCTTCATGGT GGCTGCAGGT GATATTGCTG ATAAAATAGG ACAANTGAGA ATGACATACA  
 300  
 TGGGTCTCAT AATCAGNATG TTTGNATCTC TTCTATTAAT TATATCGGAC ATCACTGCAC  
 360  
 TGCTCATCAT CGGNAGGAAT TTTACAAGGT CTATCAGCAG NTATCTTGGT TACCCTCCAA  
 420  
 CAGTTGGCGT TTAAATAAT CAATTTAAAG GAGAACATTT AAGACGAGCG ATTAGTTATC  
 480  
 TAATGATTAG TACTGTTGGG GGCATCGGCC TAGCTGGTGT TATCGGCGGT TTAATTGCTA  
 540  
 CAAATTTTCG ATGGCAAATG AATTTTCATCA TTAGTATAGT CATTGNTTTC ATTGCCATAT  
 600  
 TACTTCTAAA AGGCACACCT GAAAAAGTAA GTCAACATAG NCACCGTCAT CCGTTTCGATT  
 660  
 ACAAAGGTAT GTCGATTTTC GCTGTTATGA TTGGTAGCTT TACATTATTG TTAACACAAG  
 720  
 GATTGGAACA AGGTTGGTTT AGTACATTCT CATTCAATTG TCTGAGCATT TTTATCATCA  
 780  
 CTACGCTGAT ATTCATCATC ATCGAACGTC GACATGAAGT ACCCTTTTAT TGATTTCTCA  
 840  
 GTATTACGCA ACCGNCCGNT CATTGGTGCA TTTTAAATA ACTTTGTTTT AAATAGCGGT  
 900  
 CTAGGCGTTA CAGTGGTCTT TTTCATATAT GCTCAAACAC ACCTTGGTTT ATCAGCTGCG  
 960  
 CAATCTGGAT TGNTACATTG GCATATNCCA TAGTGGTAGT TGCGATGATT CGTCTTAGGT  
 1020  
 GAAAAAGCA ACATTACGGT TCGGGTGGGC AAATTGGATG CTCATCATGG  
 1070

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAACAANTGG TAAAACCACG ACTTCNAACT TAATTGGACN TACTTTAAAA GCAAATAATA  
60  
TNCNAATTAT ACNCAATAAT GAAGGTGCTA ATATGGCTGC AGGTATAACT TCTGCATNCA  
120  
TCATGCAATC AACACCTAAG ACTAAAATTG CGGTAATCGA AATTGATGAA GGTTCGANTC  
180  
CACGTGTGTT AANAGAAGTT ACACCTNCAN TGATGGTATT TACTAATTTT TTNAGAGATC  
240  
AAATGGATCG CTTCCGTGAA ATTGATATTA TGGTTAATNA CATNGNAGAG ACAATTAGTA  
300  
ATANAGGCAT CAANTTATTG CTAAATGCTG ATGATCCATG TGNGAGTCGG GTGAAAATCG  
360  
CAAGTGANAC GATTGTGTAC TATGGTATGA AAGCACATGC CCATGAATTT GNACAAATGT  
420  
ACGATGAATG AAAGTAGATA TTGNCCAANC TGTGGTCGCT TATTGCAATA CGATTATATT  
480  
CATTATAATC AAATNGGTCA TTATCACTGT CAGNGTGGTT TCANACGAGA GCAAGCAAAA  
540  
TATGAAATAT CANGTTTTGA TGTGGCACCG TTTCTATATC TANATATCAA TGATGAAAAN  
600  
TNTGATATGA AAATTGCAGG TGACTTGAAC GCTTATAACG CGTTAGNAGC ATATACTGTT  
660  
TNAAGAGAGC TAGGGTTAAA TGAACAANCA AATTAANAAT GGCTTTGAAT ACGTATACAT  
720  
CAGACAATGG TCGCTATGCA GTACTTTTAA NANAGAACGA AAAGAAGCGA TGAATCAANT  
780  
TTAGCTAAAA ATCCTGCAGG AATGAATGCA NAGTCTATCA AGTGGGTGAA CAATTAGAAG  
840  
GCGAAAAAGT GTATGTTATT TCGCTAAATG ATAACGCTGC AGATGGTCGA GATACTTCAT  
900  
GGATTTATGA TGCAGATTTT GGAAAAATTA TCTAAGCAAC AAATTGAAGC TATCATCGTG  
960  
ACAGGTACAC GAGCAGAAGA ACTTCAATTG CGATTGAAGT TAGCAGAGGT TGAAGTACCA  
1020  
ATTATTGTTG AGCGTGATAT TTATAAGCA ACGGCAAAGA CTATGGATTA TAAGGTTTCA  
1080  
CAGTTGCAAT ACCAACTAT ACATCAATTA GCGCCTATGC TTGACAAATTA AACCGTCCGT  
1140  
TTGAAGGAGG GCAATCATAA TATGCATGAA TTGACTATTT ATCATTTNAT GTCAGATAAA  
1200  
TTGAATTTAT NCAGTGATAT AGGAAATATT ATTGCTTTAA GACAAC  
1246

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATTCAAGAA TTATCTATAC TTTAAGCCCG ACTAAAATCT ATAGAACAGC ATTACTAAAA  
60  
GATAATGACA TTTATTTTCC AGAAGAATTA AAGAGTGCAG AAGATCAATT ATTTACAATG  
120  
AAAGCATATT TGAATGCAAA TCGAATCAGT GTGTTAAGTG ATAAAGCGTA TTATTATGCT  
180  
ACAAAGCGTG AAGGTGAACA TATGAGTAGT GCGTATGTTT CACCTGAAGA CTTTTACGAA  
240  
GTCATGAGAT TGATTGCTGT AGAAATATTA AATGCAGATT TAGAAGAAGC TCATAAAGGA  
300  
TCAAATCTTA GCAGGAATTT TTAAATCCGN CATTTTAGTT TTTCTCCGTA CGAATGGCTT  
360  
CTCACTTAAA GTTAAACTTG AAGAGCAACC ACAATGGATT AATGCTCTAG GAGGACTTTA  
420  
TACAAGCAGT TCCAGAACGT GTAGATGCAT TGGTGATGAG TAAATTACGA CCATTGTTGC  
480  
ACTACGCGAG AGCGAAAGAT ATAGACAACT ATAGAACTGT AGAAGAAAGT TACCGTCAAG  
540  
GTCAATACTA CCGTTNNGNT ATTGTAGATG GTAAATTAAA CATTCAATTC AATGAAGGCG  
600  
AACCATACTT TGGAAGGCAT TGATATCGCT AAGCCAAAAG TGAAAATGAC AGCATTTAAA  
660  
TTTGGATAAT CATAAAATTG NTACAGGAGC TAACGGTTAA ATGATTTATG ATTGGCGAAG  
720  
GGACAATTAT GATGTTCAAA GCTTTAAATT T  
751

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCTGTTTGCC CTAATGGANT CGGGTNACAA TNCACGGAGA TCCTTCTTCT CACATCAATN  
60  
TNAAATGGGG TGTTCACCT CATCTTTGAT CTGATGACGA TGACATGCGC GGCATGCAAC  
120  
TTGTCCGNTC AATTTGTTCA AGATCATTCG TACGNATAAA ATTAGTAATN TTAACGTGTA  
180  
TCGGNAATNT TAAATAAATG TTTAATGCTT TTGAGAATAC AGTTCTANCC GNAGACGTGC  
240  
GGGACACTAA ATCACCGGAG ACGCCAAGGT CTTTTATTAA ACCTTGTTCA CTATATTGCA  
300  
TATACTGTGG ATACTGTCNC AACACATTGA NTTGATAAGG ATGTGTTGGT AATAAAATAA  
360  
AATCTTTGGG TATCTCTGAT ATATCTATGT CTGCTAATTG ATACAACACT TTCTCAACCT  
420  
GATCTTCTTT ACCTTCTACA TAGCGCGTGA GCAGAACATC TGGATGCACA GCTAAATAAT  
480  
GCAATTGGAA TGATGTATGA CATTCGGGTG CATATTTCTC TAAATCTGCT TCTGAAAACC  
540  
CACTTGCACT CTTAGGAGTC GGGATGAAAT GGATGACCTA AGTATTNAAG ANTGGTCTGA  
600



AACGATATAA CGATCCTCTA CGTAGGCTAT TGTGTTACTT GGGAAAGAAC GCGCCGNGCG  
 660  
 ATGAATGCTA TTATCGATGN CAAACATAAT TNGCGCCATA TGTTGGTTGC ACTGCCGTTT  
 720  
 GATTATCTGC ACTTTGAGCC ATATGTGGCA AAATACGCGC AATTGCTTCT TTATAAGTTG  
 780  
 TTATTTTTTTT ACTTTTTTCCA TCGATAAGCC ATACCTCTGG ATGATACATA TGATGCCCCA  
 840  
 TCGCAGACCA ATAGCGAAAT TCACCCGTTA AAGTTTCGAG CTCTGATAAT TGTATAGACC  
 900  
 ATTGATGATT TTGAGGTGGT ACTTGATATA AATTTTCTTC TCTAAAATAT TCATTTAAAA  
 960  
 TCGGTTTCGAT AGCCGCATAC GCTGCATGTT GTATTAATTC TTTATTTTGC ACTTTTTGGT  
 1020  
 TTCAACTCCC ATAATTTTCAT TAATGTGTGA TCGGTTGATT TGATTAGTGA TGGTTGAACA  
 1080  
 AATTAAAAAT AAACACTTCTA CTGCAAATAC TACGCCCATA ACGATAAACG TAGTAGCTGG  
 1140  
 TGTAGTATAA CTTGTAATGG CAGCGCCACT AAGACTGCCA ATAATTTGAC CAACAACTAA  
 1200  
 CATACTGTTC GTCGTTCCAA CAAATGTGCC NTTAAGNTGT TGATGACACG CANTCACGAC  
 1260  
 AACAAACATG AACTTTTGAA TCNATGCACT AGATGTTAAT CCTGAAGTA TTCTTGACG  
 1320  
 CATTAAANAC TCTATATTCG TCGCTAAACC TTGCAGTATC GCACTACAAC CACATGCAAT  
 1380  
 CGTGGCAAAT ATAG  
 1394

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATAATATGTC TAATTGACTA ACTTGTTGGA GTCATTTACT ATTTTATGTA TGACATATTT  
 60  
 TAAAAAGTGA GGGTCAAGCA TGTCTTATAA AGCATATCCA CTCTTTAGAG ATATATTAAT  
 120  
 AAATGAATGT ATTTATTTTCG CCTCTAAAAA TAAAAAACTA GTACGCCTAA ATTATAAAAG  
 180  
 TGAAGCGTAT GTAGGCGTTT GGACAGAAGA AAGTGTGGCC GTATCATTTT TAACAAGTCG  
 240  
 TGATATTCCA TNTGATAAAG TTGTAAAAAT GGACGTTGAT CCGCCGNGCT ACTTATGAAT  
 300  
 TAGATGAATT GTGTGATGAA CAAGACATAT TATTATGAAT CAAACAA'TGG AAGAAGAAGG  
 360  
 GCATCTACTA ACGTGGGGCT TGNTACAAAA AGAAGGTGAT GACGGGATTA GATAAAANAG  
 420  
 ATCAAAGATT TGGGCCCAGA TGTTGCAAAT ATGATGAAG  
 459

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
CTGGTGCCTC TTCTAATGAA TTTAGAGATT TTTTACCAAA TCACCATATG CAGTATACGA
60
TGATGAAGTA TGCACGTGAA CATGGTGCAA CAACTTACGA TTTCGGTGGT ACAGATAATG
120
ATCCAGATAA AGACTCTGAA CATTATGGCT TATGGGCATT TAAAAAAGTG TGGGGAACAT
180
ACTTAAGTGA AAAGATTGGT GAATTTGATT ATCTATTGAA TCAGCCATTG TACCAATTAA
240
TTGAGCAAGT TAAACCGCGT TTAACAAAAG CTAAAATTAA AATATCTCGT AAATTAAAAC
300
GAAAATAGAT TAACGACTGA AATCTGAACG CTCATAAGAC TGTCATTTGC GTTCAGATTT
360
TTTTACACAA TATAGAATGG TTGAGTAAAA TATTTTTGAA TATAGTGAAA GAGGGGGAAG
420
TACTGTGATA AAAAAGCTAT TACAATTTTC TTTGGGGAAT AAGTTTGCTA TCTTTTTAAT
480
GGTTGTTTTA GTTGCTTGG GCGGTGTATA CGAGCGAAGT GCTAAATTGA AATTAGAATT
540
ACTACCAAAN TGTACAAAAA TCCAGTTATT TCAAGTTACA ACAACAATGC CGGGGTGCAA
600
CGCCACAAAG TACCCAAGAT GAAATAAGTA GTAAAATTGA CAATCAAGTA AGATCGTTGG
660
CATATGTGAA AAATGTTAAA ACGCAATCCA TACAAAATGC TTCAATTGTA ACAGTTGAAT
720
ATGAAAATAA TACAGATATG GATAAAGCAG AAGAACAGCT TAAAAAAGAA ATCGATAAAA
780
TTAAATTTAA AGATGAAGTT GGTCAACCAG AATTAAGACG TAATTCGATG GACGCTTTTC
840
CGGTTTTAGC ATATTCATTT CAAATAAAGA GATGACTTGA AAAAGTACGA AAGTACTGAA
900
TGACAATTAA TACCAAATAC AAACGGAGAT
930
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
TTTACCTTCC TTAATTGCTT CCAACCCAAT CATCAGCTAA TAATCCACTA CTTTTTCACC
60
CATGCTCTTT CACNAATGTT TTGAACTGCG TTTCCTTTAA CGTCATACCA ACCTGTTTTA
120
CCTACTTTTG TAATATTACT TGCCAACACC ATTTTATTAT TATAAGCGAT TTGGTTAGCT
180
ATCGTGAACA TAGGTTTTAA ACATCGTCTG TGCACCCATA AAGGTATGCC TATCCAGGTT
```

240  
 TTTTGATTAC TATCAGTAGC ATCAGATTTT CAAAAACCAT ATTGATTGGC GTTGTCTGCA  
 300  
 ACAGACTGCA CAGAAGCTTC TTTAGAACT AGATATTCCG GAACATGATA ATTTTACGA  
 360  
 ATGTTATCAA TTAAATGACT TTCTAAAGTC ACAACCGGTT CTATTTGAAT CGGATCACCT  
 420  
 ACAGCTACAA CTTTTTTTGA ACGATATAAT GCTCCACAG CTGCTTGAGG TATTGCTTGT  
 480  
 CCTGCTTCAT CAATAAATAA GTAGTCTATG AAATCTTGTG GTATGCCCCC ATACATAGAT  
 540  
 TTAAAGCTTG CAAACGTCGN ACTAACTACT GGAAATATNA AATGCATCAC ATTCCATGCG  
 600  
 TNGTGTNCTT TATCTGGATG NGCATCAATT AATTCCTTC TATCTNAAA ATCATTAATC  
 660  
 GCATAATAAA TAGTTGGTTT TATTAGCAAT CAATAATAAT TTATGCAATA TCAATNGCTT  
 720  
 CTTAAAAAGA GCATGGACCG TCTT  
 744

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCCTGGATA AGTAGTACCA GTCCACATAA TCTAACCTAA GACAATTAAG ATTAAGATTG  
 60  
 ATCGCATGAT TCAATTTATT TAGCTTTGTA ACCCAATCAT ATTGANTAAA TCTTTAGGGT  
 120  
 GCCAATATGG TGGTGCATAA NCCACNNCAA ACTCAGTTAA CTCATCTACA GTTAGCTGGT  
 180  
 TCATCATTGC CATCGATAGT ACATCAATAC GTTTATCTGC ACCTTCTTTT CCTACTGCAG  
 240  
 CTGCTCTTAA AATCTGACGG TTTGAAGTGT CATAATATAC CCTTAAGTGT AAAGGGGAAT  
 300  
 TTCCTGGGTA ATAATTCGCG TGTGCACCTT GAGTGACTTC CACCATTTTA TAGTCAAATT  
 360  
 GCTTTAGTTC ATTTGGTTTA ACGCCGACAC TCGCAAATGT ATAATCAAAG AACTTCACAA  
 420  
 TATTGTTGCC TAAGAAGCCT TTGAATTCAA TAGTGTCATT TCCAGCAATT TGTTCCGGCAA  
 480  
 CAATACTTGC TGCACGGTGA GCGCCCCAAG CTAAAGGAAC ACTAGCCGGT AGATCGACAT  
 540  
 GTCGATAATG TGATGTTGCA ATATCGCCTA TTGCATAAAT GTTTGGAACA TTTGTTTCAA  
 600  
 ATTTATCGTT TACGGTATGA AACCTTTTCG ATCAAGTTTG ATATTTGAAC TTTCGATAAA  
 660  
 TTTTGAATTG GGGTGAGTAC CGACACCTTC AATAATCATA TCGTAATGTT CAACTTTTCC  
 720  
 TGATTTAAAT GTAATTTTAT TTCCATTGAT AGCATCAATT CCTCATTTAA CGGTATGGAT  
 780  
 CTCCGCTATC TATTCAACAA GTATTGGTTG CTTCATGTCA GCATCCATAT TTATTTATCT  
 840  
 TATCAGATCG ATGATTAA

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGAATGCGAT ATGCCTTTTT ATTCATCGTC ATATAAATTG CATTTTCATT TTTACGTGTC  
60  
ATACGCTGAA AAGGATGCTT CACAAATTGT GGTGTAGTAT AACCAATTCC AATTTCCAAA  
120  
TACAACACTT TATCATCTTG ATGTTGCTCT AGAAAAGCAT TATAACGTTG NNGNTGNGCC  
180  
TGAAATTCAG CATCTTCAAC CATGCCAACT TCCGCTTTAC GTTTATTAC TTCCATTGGA  
240  
GCATCACATT NTGGACATCT TGGAATCATC TCCCAAGGTA TAAGCATATC TTGTTGCGCA  
300  
ACAACCATTT TACGAATTAA ATCATCATTG CGATACGTGT GAGCATGACA ATGCTGACTA  
360  
CACTGNTGNA GTATATACTC CCCNTGTATA TGAAATACAT GAGTCATATC ATATTGAGCA  
420  
GCATCGAAAG CATTGTCTGC ATTCGGAGNT ATGATATGGT ACTGTTTACC CTCCACTAAG  
480  
GATTTTAATG CGAGATAAGA CTGACCTACA GGTGATCT TAATAATTTA NTGTAATAAA  
540  
ACGACTCTCA AATGCCCAAT ACTCTTGCCA ACTGCCATAA GGATGTAAAC TCGCTTGCAA  
600  
CATATCAAAG AAGCGATATT TTTCAATAAA ATCTGGGAAA TTTCCGTAA AACGCTCTCC  
660  
TACATATGTA AATCCGTCAG ATGCAGACAT GCCTGCACCA ATTCCAATCA CTATCGCATC  
720  
TGCTTCATCA ATCGCAGTAC GCAATACTTC AGCCTGCTTT GTCTTTTCAT CCATTAAAAG  
780  
AGACATTGCA TTCCATTTAC TACTCTGCAT CACGGCTCAA TGCCCTCCTTA TACAGTTGGT  
840  
AAATCCTTAT CTTGGAAATA CATTGAACAC GACTTTCAAT GTTGAATTTG GCTCTGCGAG  
900  
ATAGCTTTCT TCTGTTGAC AGCATTCTG CTGCTTCATC TTGAGAAAAG CAATACACTG  
960  
TAGATATACA GCAAAGCGAC ATGATTTAAC TATGTGGGCC AGGC  
1004

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATATTAGCAG CTGTGCTTGÇ TTGTATTTTA GCTGGTGTAC CCTATCAAAG CAATTATTGA  
 60  
 TAGTTTAACT ACATTTTCAG GAATAGAGCA TAGATTGCAA TATGTTGGTA CTAATAGAAC  
 120  
 TAATAAATAT TATAATGATT CCNAAGCAAC AAACACGCTA GCAACACAGT TTGCCTTAAA  
 180  
 TTCATTTAAT CAACCAATCA TTTGGTTATT GTGGTGGTAT TGGATCGAGG GAGATGAATT  
 240  
 TGACGAACTC ATTCCTTATA TGGAAAATGT TNCGCACGAT GGTGTATTTC GGACAAACGA  
 300  
 AAGCTNAGTT TGCTAAACTA GGTAATAGTC AAGGGAAATC GGTCANTGAA GCGAACAATG  
 360  
 TCGAAGACGC TGTTGATAAA GTACAAGATA TTATAGANCC AAATGATGTT GTATTATTGT  
 420  
 CACCTGCTTG TGCGAGTTGG GATCAATATA GTACTTTTGA AGAGCGTGGA GAGAAATTTA  
 480  
 TTGAAAGATT CCGTNCCCAT TTACCATCTT ATTAAAGGGT GTGAGTATTG ATGGATGATG  
 540  
 AAACGAAGAN CGATCAACAA GAATCAAATG AAGATAAAGA TGAATTAGAA TTATTTACGA  
 600  
 GGAATACATC TAAGAAAAGN CGGCAAAGGA GAAAGGTCAA AGGCTACACA TTTTCTACN  
 660  
 TCAAAATAAA GATGATACAT CTCAACAAGC TGATTTTGAT GAAGAAATTT ACTTGAG  
 717

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTCTTCTTCA TCAACATCGA TCATACTTAC TAAATTGTGG ATGTGAAAGC TGTGATGAGT  
 60  
 ATATGTACTT CTCGNNCAAA ACGGTTTAAT GTNTCCTCCT TTTCTCCAGG GTGGTATAAA  
 120  
 AATCGCCTTA ATTGCAACCT TAATGTTAAG TATCGTATCT TCTGCAAGAT AAACGGTACT  
 180  
 CATGCCACCG NCGCCAAGCT TATCTACAAT TTTATATCGC ACATTTATTA TTTTACCTAT  
 240  
 CATACTTTAT CACCTNCAAT AGCCGCGAGT ATGAAAGTAA CGTTATCTTT CGAATGGTTA  
 300  
 TCTAATGCCA ATTGCATTAA TTGATCACCA TGATCTTCTA TTGTACCTTC TTTTACTAAC  
 360  
 AAACGCTTAA TTTTATTGTC TTAAACATAA TCAGTTAATC CATCTGAATT TAATAATAAA  
 420  
 TAATCATAAA AATTTAATCG CTTAATAAAC AAATCTGGAC TCACACGTTT ATCTGTGCCC  
 480  
 ATCACCTTCG TAATAATATT ACGTTGTGGA TGTGTAAATG CTTCTTCCGG CGTAATTTGA  
 540  
 CCCGTTAAAA CAAGATGATT ACAAATGAGT GATCACTAGT AATTTGCACA ATTGTCTACT  
 600  
 ATTAATACAT AGGCTCTAGA ATCACCGACA TTTGGTATCA CAACTGATTT  
 650

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
CACCAAGAAC TTACTTATAT TTTAGACAAC ATAAAAGGGA ATAATAATTA TGGTAAGGAA
60
TTTGTTGCAA CCGNTGAAGA AACATTTCGAC ATTGAATAAA GCGGGGTGAA GCACTATGAA
120
TCAATGGGAT CAGNTCTTAA CACCTTATAA GCAAGCGGTT GATGAGTTGA AAGTGAAACT
180
TAAAGGCATG CGCAAACAAT ATGAAGTTGG TGAACAAGCG TCGCCAATAG AATTTGTTAC
240
TGGTCGTGTT AACCCGCATC GCTAGTATTA TAGATAAGGC AAACAAACGA CAAATACCAT
300
TTGGATAGGT TAAGAGAAGA AATGTACGAT ATCGCTGGGT TTAAGAATGA TGTGCCAATT
360
GGTAGAAGAT ATTGATGTTG GCCGCÇAATA TTTTAAAGGA CAAAGAAAAG ATTTTAAAGN
420
TATTGGAGAC CGAGATTATT TCCCGNACAC TAAAGGAAGG TGGGTACCGT CCGCTTCANG
480
TCAATATTGG ATTTCCCAAC TGGACCAATA CAAGGCCAAA ATTT
524
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
CGTCTATCAT TGTTAACATA TATAGCACCT TCCTTATTTT AATGTTGTTT TAGTTGAATC
60
ACAGTAAAAA GGTGTGTTAAG ATACTCATAC ATTTTATATGT GTAAATATCT ACAAAGTTAC
120
CCANCTACTG ACAATGTTTA TTTNAGATAG TATATGTAAA TTCACAGATA TGCTAATTGC
180
TTAAAAAATG ATTAAAGTGT TGGCTCCAAG CAATGATACT TTAGAAATTT ATTTATCATC
240
TNGACTTTAA AAATTATATT ATAAATGACG TAACTGACAA CAGATATACT TAGTAATGAA
300
GATGTGTAAT GTAATTGTTT AAAATTGATC TCCAAGCAGA TTTTATTTAT CATTTAATTT
360
AAATAGCAAG TGGAGGTACA AGTAATGAAA TTTGGAAAAA CAATCGCAGT AGTATTAGCA
420
TCTAGTGTCT TGCTTGNAGG ATGTACTACG GATAAAAAAG AAATTAAGGC ATATTTAAAG
480
CAAGTGGATA AAATTAAAGA CGATGAAGAA CCAATTAANA CTGTTGGNAA GAAAATTGCT
540
GAATTAGATG AGAAAAAGAA AAAATTAECT GAAGATGTCA ATAGTAAAGA TACAGCAGGT
```

600  
TCGCGGTNAA AGCAGTAAAA GATTTAATTA AAAATGNCGA TGATCCGTCT TAAAGGAATT  
660  
TGAAAAAGAA GAAGACGCAA TTAAGAANGT CTTGAACAAA GACTTTAAGA AAGCAAAANG  
720  
TACGTNGGGA TAACATGATA TGATGTTAAA C  
751

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCTTTGTTTA NCATCCTTAG TCAGTGT CAT AAGGTTGTCC CATCAGAAGG TAGNCCCCAC  
60  
AATAGTTGAA ATCCTCCCAC AATAGGGGTA GNCTCCTGCA TCTGTAAATA CCTACTGGNN  
120  
TGCCANATAC TTTTCTGCT GGTGTGTCAA AGAAATTTGT TGTTCATTT GAGAGAACAC  
180  
TAATAATTTT GACATAATCT GCATATCGCA TATAAATTGT TGC GTTATCA CGATAATCTT  
240  
CATGTAAATC TGCTAAAGCG TTAATAATAG CATCATACAT GTCTGCTCCC NCAACTTCTT  
300  
TAACAGATCC ATTATAAAAT GACATGTGTT CTAATCCAGA TTTAGGACTT ACTGCTAAGG  
360  
CATCTTTACG CTCTTTAGCT GCTAATCCTG ATTGTAGTGC GTTTTCAACC CAGTTTACTA  
420  
AATCTACATC TGATCCATGA ATTACAGTAT CTGAAATTGC AGCAAATACT TTGAANTTAT  
480  
TAAGTAGTGA ACTTGACTGT ATCACCTTGT GCTTTTAATT CTTGTGCTGT NTCTACGTCT  
540  
GTAATGAAAT CATCATCGTC TAAAGTGAT GAAACTCTTG GAATCTCTAA ACCTTTAATG  
600  
TTAGNTAGAC GAGCTTTTAC ACGTAATTGG GTTNNAGCA AATGGCTCTG AAACAATTTT  
660  
TTGTAGAAAAG TGGGTTGGGG AAGAGCTTAT CTCCACCTGA ATCATTTCTT GTTGGTAAAG  
720  
CGTGTAATAA ACGTTGTGCC TCCATTGAAG GTTTTCAAA TTCATTTGGT AAAATCGCTC  
780  
GTGCC  
785

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTTNATAAAN ANCNATCNTA TGCCAATTTG ACCATTGTTT GAATCCATAT ANAAACCGGC  
 60  
 NACGGTTCTT TTCAAATATA ATAGTAAGTG TATAATGAAA ATGTAAATAT TATTAAANAT  
 120  
 GGGGGTTCAC TCAATGAAAA TGAAACGTTT TATAGCTATT GTAATGGCAT TATTTTTAGT  
 180  
 ATTAGNTGGT TGCTCTAATT CTAACGATAA TAATGAAAGT AAAAAAGATG ACGCAGACAA  
 240  
 TGGTAAGAAA CAAGAGATTC AAGTTGCAGC GGCAGCAAGT TTAACAGATG TAACCAAGAA  
 300  
 ACGAGCTTCA GAATTTAAAA AAGAGCATAA AAATGCTGAT ATTAAATTTA ACTATGGTGG  
 360  
 ATCAGGGGCA TNAAGAAAAC AAATTGANTC AGGCGCACCN CTTGTTGACG TATTNATGNC  
 420  
 TNCCNAANTN CTAAAGATGT AGATGCATTN NNAAGACAAG GAATNNAGCG CATTTGATAT  
 480  
 CATATNAATA TGCGNNNNAT AGTCTAGTAT TAATTGGTGA TAAAAGATTC AAATTACACT  
 540  
 TCAGTAAAAA GACTTAAAAG NCAATGATAA ATTAGCATTG GGTGAAGTGA AAAGTGTACC  
 600  
 AGCAGGAAAA TATGCGAAAC AGTATTTAGA TAACAATAAC TTATTTAAAG AAGTCGAAAG  
 660  
 TAAAATCGTT TATGCTAAAG ATGTAAAACA AGTATTAAAT TATGTTTGAA AAGGGTTAAT  
 720  
 GCGAAACAAG GTTTTGTGTA TAAACTGAC TTATATAANC AANN CNAAA AATTGATACT  
 780  
 GTAAAAGTAA TTAAAGAAGT AGAACTTAAG AAACCAATCA CATACGAAGC TGGTGCTACA  
 840  
 TCAGATAGTA AATTANCAAA AGAGTGGATG GATTCTTAAA TCAGATAAGC TAAGAATATT  
 900  
 AAAGATACAC TTTGCAGCAT AAGA  
 924

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCACGAGCT CGTGCCGAAC TTACGGCAGC ACGCGATACN ATAAATACAT TTGTTACAGT  
 60  
 TACGCTACTA ATCGTTTGTG CTACATCTTT AAAATCAACC GCAATACCTT TGTGTTTGTG  
 120  
 AAGTAACGTG TTAACTCTC TCGTTTTAGA TAATAAGCTC ATGAATTTCT CTCCTTGTGT  
 180  
 ATATTTTAT AGAATAAATG CACTTAAATC TTTATNTGTT GAAATTGATT TTAATTTATC  
 240  
 ATCAACATAT TGTGGGGTAA TATCTACAAC TGCATTCGGC ATACTTGGTG CTTCGAATGA  
 300  
 TAAATCTTCT AGCATCTTNT CTAAAATTGT ATGAAGTCGA CGGTGCAACA ATGTNGTCTT  
 360  
 GTATCTTGA TCACTTGA TAAGCAATCT CAAGCTTAAG GCGANTAATT GCTTCCATCG  
 420  
 GGTAAAGTTT ACAGGNAACT TCTTCTTNTT TGGGAGCAAT GCTTCATATT TGGNNTAATT  
 480



AATGACAATG TGGGGTCTGG NCAAAATTCT TACAAAATCT TCCTNCCCGT TANCTA  
536

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTACCTTCAT GTTTTGTAAA GTTGATTAAA GCATTTCATTG CTTGTGTATC ACTTGCATTT  
60  
TCAAAAGTTA CTCTACCAAT GTCGTGGTAA TAAGAATGTT CAGGCCCAAT ACCAGGATAA  
120  
TCAAGTCCTG CTGAAATAGA ATGTGCTAGT TGCACCTTGCC CACCTTCATC TTGAATTAAA  
180  
TACATTTTAG TACCATGTAA TACGCCAGGT GATCCTTTGN CAATTGCAAG TGCATGTTTA  
240  
TCAGTATCCT CGCCTTGACC TCGGGNTTCA ACACCGNATT AATGCAACAT CATCTTTAAT  
300  
AAATGGATAA AAGGCACGAG ACCGATTGCA TTTGAGCCAC CACCGATACA TGCTACAATT  
360  
GCATCCGGAA GTCGACCTTC TTTCTTCAAT ATCTGTGATT TNATTTCTTT ACCAATGACA  
420  
CTCTGAAAAT CTCTAACAAT CGTTGGGAAT GGGTCTGGAC CTAATGCAGA ACCTAATAAA  
480  
TAATGTGTAT CATCTACATG ACTTACCCAA TATTGCAATG CTTTATTAAC TGCATCCGAT  
540  
AAAGTCCCTT GANCTTCTAC AACTGCCACA ACCCTTNGCA CCAAGTAATT CCATTCTAAA  
600  
TACATTAAGT TGGTGTCTTT TAATATCTTC ACTTCCATA AAGACAACAA GTTCCATATC  
660  
AAATAATGGA GGAACCGGAG GACTAGCTAC AACATGTTGA CCCGCACCAG TTTCAGNAAC  
720  
AAGCTTCTTC TTGGCCATTC TTTTGTCAAG CAACGGTGAC TAACGCATAT AATTTATGGC  
780  
GCCGTATGAT TAGATCCTCT CG  
802

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTATTCTTCT ATGTCTTTGA CAAGCGCGAA TATTTTTCGT CGTTGCTTGC CGGTAATTTG  
60  
AAACGGATCT ATGACGCTTA CATCGACTTC CACATCAAAT CCGTTATCAA GTAGTAATGT  
120  
TTCTTTATTG CCTAATTCAA CACCCGAGAT GACAACTGTT GNTGTACCGN CATCTTGAGT

180  
 GATATAACTA GTAATTATTG GCATCTAATC ATTCCAATCA GAACGGGAGG TCTGAAAAAT  
 240  
 CTTCTTCACT ATTGTCAAAC GGATTATTGC CAGTTTGAGC TTGTCCTTGT TGTTGATAAT  
 300  
 TGTTGTTTTG NTGTTGGTTG TTATTCTTCG GTTCTAAGAA TTGAACGCTG TCCGCTACTA  
 360  
 CTTCTGTCAC AAATACACGT CGCCCTTCTT TGTTATCGTA ACTGCGTGAT TGTAACGTC  
 420  
 CATCAACGCC AGCCAATGAC CCTTTGGATA AATAATTATT TACATTTTCT GCTTGTTTTTC  
 480  
 TAAAAGTTAC ACAGTTAATA AAGTCTGCCT CACGTTCTCC TTGAGCGTTA GTAAATGTTC  
 540  
 TGTTAACTGC GATAGTGAAA GTGGTNACAC TCACACCATN TGGGCGCTGT TCTATATTCT  
 600  
 GGATCTTTTT GGGTAAGCGT CCCACTTAAT ACTGTTCTCG TNNTAACATT ATTTGNTTTC  
 660  
 CC  
 662

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGGTAAAC AACATTAACA GCAGCAATCG CTA CTGTATT AGCAAAAAAT GGTGACTCAG  
 60  
 TTGCACAATC ATATGACATG ATTGACAACG CTCCAGAAGA AAAAGAACGT GGTATCACAA  
 120  
 TCAATACTTC TCACATTGAG TACCANACTG ACAAACGTCA CTANGCTCAC GTCGNGCTGCC  
 180  
 CAGNATCCCG CTGACTACGT TAAAAACATG ATCACTGGTG CTGCTCAAAT GGACGGCGGT  
 240  
 ATCTTAGTAG TATCTGCTGC TGACGGTCCA ATGCCACAAA CTCGTGAACA CATTCTTTTA  
 300  
 TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA ACAAAGTTGA CATGGTTGAC  
 360  
 GATGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTCGTG ACTTATTAAG CGAATATGAC  
 420  
 TTCCCAGGTG ACGATGTACC TGTAATCGCT GGTTCAGCAT TAAAAGCTTT AGAAGGCGAT  
 480  
 GCTCAATACG AAGAAAAAAT CTTAGAATTA ATGGAAGCTG TAGATACTTA CATTCCACTC  
 540  
 CAGACGTGAT CCTGACAAAC CATCAAGATG CCAGTGAGAC GTATCTCAAC ACNGTCGGGG  
 600  
 TCTGTTGGTA CAGGCCCGTT GACGTGGGCA ATCAAGTGGT GAGGAGGTGG GATCAC  
 656

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATGCCCCAC ANAATGATGC TGGCAATGAT TTTCACTTAG TTATGAGCGG TAATGAATTT  
60  
TGCGGTAATG CGACGATGTC ATATATACAT CATTTGCAGG AAAGTCATTT GCTTAAAGAC  
120  
CAACAGTTTA AGGTGAAGGT ATCTGGCTGT TCGGATTTAG TGCAATGCGC AATTCATGAT  
180  
TGCCAATACT ATGAAGTTCA AATGCCACAA GCCCATCGTG TTGTGCCAAC AACAATTAAT  
240  
ATGGGTAATC ATTCATGGAA AGCATTAGAA ATTATTTATG AAACATATTG TACATTATGT  
300  
GATTCCNAGC TAAACAAAGT NACAACCTGA AATTCAACAT TTGGNTGGAA GCATTTGTGC  
360  
CGTTGANCAA CAAATGGAGT CACAAATATT  
390

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGNACGAGCG CATNATTAAA AACATATCAG GTTATGTATG CGCATAAAAA ACAGCCTTGA  
60  
AAAACCTTTA TAAATCGGAT TTTCAAAGCG TGTTTTGAAA GGTATTTAAT TAAAACTAAG  
120  
CATGTTGATG TAAATCATCA AAGTTTGTTA AACGTTGTTG CCACTCATT A TACTAATAT  
180  
TATTTGCTTG AACATAACGA TTACGCTCAT GTTTAGCACA TTCATAAGAG CATGCACCTA  
240  
AATATTTAGT TTCGNTTCT TCAGAACTA ATATTTGTTT ATTACATTCT GGGTTAGCGC  
300  
AATTAATATT AACGNTCACA TGGGTTTGGC ATCAAAACCC AATCCTTACC AATAATTGTT  
360  
TTTTCAACTT GGGTTGATAT CAACACTGAT ACGGATCAAC AANTTACAAT ACAATTTNAC  
420  
CCG  
423

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TTGGTGCACC ACCTCAAAAC TTTGGTACCA TTGATGCATT GTACATTAAT TGCGCCAAGT  
 60  
 TTTTGTTAAT GCCACCAATG ATTCAGGTAA TAATTGTCCC AAAAGCAGCA GTTACAATTA  
 120  
 AATCTACATC TAATTGAANC AATTGTTCTA ATTCTTCTGA TCCACTTAAT TTTTCAGGCT  
 180  
 GATATACAGG TAAATCATAT TTCATTNCAA CTTTTTTAAC TGGTGGTGGT GTCATAACAC  
 240  
 GTTTACGTCC AACAGGTCGA TCTGGTTGCG TTACGACTGC AATGACATCA TGTTCGCAA  
 300  
 TAAGCATTTT TAAAACAGTT GTTGAAAAGG CACGAGTACC CATAAATATT ATTTTAGTCA  
 360  
 TTTATAAAAT ATGCCTCCAC TTCTTTATCT GTTAAAATAC GGTCCGCACG TTCNGTAAAA  
 420  
 GGGAGACCGT TCATTTGATC TATAATATGC AAAATCATT CTTGCTACATC TTCATGTGCA  
 480  
 GTTAGTTCAA CTTTGTTCCC ATTGACGTCA TAACTTTTCA CAACTATCAT TTTACTTCTT  
 540  
 GTCACCTTCGC CGTAAACATC TGGCAATGTA ATTGAACCTT CTAAGTCTGT TATTGTTTCA  
 600  
 TTTGATTGAC TAATAATTTT CGGATTAACA AGTTGGTAAT AATCCTTCCA TTTCCATATT  
 660  
 CAATAATTGG CACTTGCAA TGACTTGATT AATTTGAGGG TGCACATAAG CCAGCAGCTT  
 720  
 CTTGGTGCAT ACATTGGTAT CTTCTTAAAT CTTGGTAATA ATCTTTTTTA CGAATCACAA  
 780  
 TTGTTTTAAC TTGCTTGCGC TTTTCCGGT TAAATAGGAT GCGATGCTGG GTACTAACTT  
 840  
 TTTTAATCGC CAATACTCTT ACTCCTCAAT AAATCAATCA ACTATATACC G  
 891

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCACGAGCT ATAAATCCAA TGATGAATTG TAAAAGTGAA TAATTGAGAA AAAGGTTAAT  
 60  
 ATCAAATTTT GGTGTCATCA TTAATGTAAG TTCCTTGGCT AACGTTGAGA AAGTTGTTAA  
 120  
 GCCACCTAAA AAACCGGTGA CAAAGAACGC AGGGAACCAT GAGATTGAAA TTGATAGGCC  
 180  
 TATAGTTAAT CCAATTAAAA AACTACCAAC TAGATTTACT ATCAATGTTG CGATAGGTAA  
 240  
 CTTTGAAGTA AATTTATGAT TAAAATAATC AGTAATGGCA CTTCTAGCAA TTGCGCCAAA  
 300  
 ACCGCCGCCA ATCATGACTA AAATGATTGA TATCATGATA AACCACCACC TAGTTTTATA  
 360  
 CCGACGTAAC ATAACAAAAT CCCAAAGACA TAACTTGTTA CAGCATATAG TAGTAAAGTT  
 420  
 ATAAATTGTT GATGATCAAA CATATGTATT AATTCTTAAT TGAAATGTTG AAAAAGTCGG  
 480  
 CTAAGCACA AGAAAACAGT CGTAATAGCT TTTTITAGGG TCGGATGGTT TGAAAAAATG

540  
CAATCGTTAA GCTGTTAGCA TCCCATTACA AAGGCACCAG TCAATGGTAT CAGTGTCCGA  
600  
TGGAACTCCG CAGTATCAGA AAGATGAGGT ACGTATAAGG CTAAGCACAC CG  
652

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAAACCATCC CCNCGTGCTC GTCACTGATT GTTCCGCCAC CACCTTGTGT TCCACCACTT  
60  
GATTTGATCA GCAGGATTGA AAGTACCTCT NCCACAGTAA TACCCATTAT TAGTCCCACC  
120  
AAACCTGTA CATTACCTGC TGATGCTCCT TTCACCCATG GGCTCGTATT ATNACGACGT  
180  
GTAAATGTCG TNACCACATT TCCATTACGT TTAATAACTA ATTTGTCAGC ATATGTCGTA  
240  
ACATTACCAG CATGAGTATT GACTGTTTGG TTCGCACCAG GTGCAATTGT AATCGCTCCT  
300  
GCCGCTGTTT CAGTGACAGT TGGTTTCGCT GGTTGAACAT CTTTACTAC AAATTTGCT  
360  
GGTAAAGATG TTGCAAATGT ATGTCCATTA TAGATGACAT CATATTTTGC ATTAACGACT  
420  
TGTGCAGTAT TTGGTTTATT CATTGCTGCC CAGTTTGCAT CGTTTGTACC CGTAGTATCA  
480  
CGATTCCATT TATACGTAAA TCCATCTGTT GGTAACCTG AAGCGTTTTG CATATGTGCA  
540  
TATCCTGATG CTTGCGTACC ACTTGCTAAA GTGCCACCAA CTGTTGTTGT ATAAGTAGTT  
600  
TGAGGGAATT CCAAATTGAT ATACGTTTAC AGTTACAGGA ACTCGTTTAG CAGCTGAAAT  
660  
ACCTGGATAT GTGACATCGA CATTAAATG TTGAACGCCT GCTTGCTGGT TATTTGGTTG  
720  
TTGTCTATTT GCCCATGCTG CTGTAATACC ATTCGTATTA GTATTTGGAT CAAATGTAAT  
780  
GTAATCAATA GCGTTTGTAC CATGTGTCAA ATTTTGACCT TTCACATCAC GTGATGGCGC  
840  
CTTAGCATTG GCAACTGGAT AAACCTTGAC TGGAACCTCA ACATTACGCG TACCTTGACC  
900  
ACTAGGTAAT GTTACAACCG CAGTTTTATG TGTGTTGGCG ACTGTATTCT TCCATGTATC  
960  
TGGACTATCA TGCCATGCGA CCGCTGGCCC ATGTGGNGGA TTTTGAATA AATCGTCTTC  
1020  
ATGACCGAAA TCAAACCGN CGCACCTTTA ATAAATACAG CGCTTCAGTA GTTGCTTGTA  
1080  
TTGTGGGGTT ACTGTACAAG AAGCACTATC ATTTGATCAC AGATCAATCT TGGTNNNTGA  
1140  
AC  
1142

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
GGNANTNGAG GAANCAAANC NGCCCTTCNA CNCGGATTAA AACCTGTTNG AANCTGNNGA
60
AGNGTGGGNC NAANNCCTTG ANTGCAAGGT GCGANGGNCG NNTGCAAGNT GTNNAACNGC
120
NNGNGANCGN TTGNCNGTGC ANTGNNAAG ANTGGTGAAA ACCCNTGTGN TANATTGTGC
180
GNCCNNCTTG GTGANGNTGN GTTGNGCNGN NTCTTCAGNA GTCGCANCTG CAGNGTGTCC
240
NATAAGCGCT NTNTGNACGG TTGCTGGTGT TGCNNANTCA TCTATCGCAA CATCGNTAAT
300
TGTTGTATCT CCAGTAATAC CTTGAATATC AGCAACTGCT TGATCATTAA TTTGCGTAAC
360
ATCATTAGTT GNTTGTGCAN TTAAGATATC TTGANACGCT TTTTCTTTAG CTTNTAAAC
420
TAAATCTTTT GCTGCATTTT TCTCTTCAGT TGTAGCGCCA GTTGTATTAT CAATTGCTTG
480
ATTTTGAGTT GTCACAGCTT GATCAACTTC ATTTTTCGCA TTCGATTAA CTGCTGNTGC
540
TGGTTGTGTG CTTTGAATTA NAGAAGACTC AAGCTTGCAT GCCTGCAGTC GACTCTAGAG
600
GATCG
605
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
AAATTCATAA TAAAGNCTTT TGNCATTAAA GTTNNAAGA AGATAAAGAA NCTGCTNNAA
60
ATTGACGTAT CNNAAGAAG TAAAGAAGT TTAAATANTC AAATAATAAA TCNACAACAC
120
AAGANATTTT TGAAGAACA AAAGGTGAAT ATCAAAGAAA GTCAGAGGCA TTAAAAGAAA
180
GATTTATAAA CAGACAAAAA TCTAAAAATG AGTCTGTGGT TTCACTAATC GATGACGAAG
240
ACGACAACGN AAACGACAGG CAACTTGTGG TTTCTGCGCC ATCAAAGAAA CCAACAACAC
300
CGACTACATA TACTGAAACA ACGACTCAGG TANCAATGCC TACAGTTGAG CGTCAAACCT
360
AGCAACAAAT CGTTTACAAA ACACCCAAAA CCATTAGCTG GATTAAATGG TGAAAGTCAT
420
GATTTACAA CAACGCATCA ATCACCAACA ACTTCAAATC ATACGCATAA TAATGTTGTT
480
```

GAATTTGAAG AACGTCTGC TTTACCTGGT AGAAAATCAG GATCACTGGT TGGTATAAGT  
 540  
 CAAATTGATT CTTCTCATCT AACTGAACGT GAGAAGCGTG TAATCAAGCG TGNACACGTT  
 600  
 AAGAGAAGCT CCAAAAGTTA GTTGATAATT TATAAAGATA CACATAGTTA GAAAAGACCG  
 660  
 ATTAAATGCA CAACAAAAAG TAAATACCTT AAGTGAAGGT CATCAAAAAC CGTTTAATAA  
 720  
 CCCAATCAAT AAAGTANCCA TGCCAATAAT ATTAATGCAT GGCTGCAAAG CAAATAATGA  
 780  
 GTTTGTCGTA AAAATACCAA CATTTAACT AGCAATAAAT AATATCCAAG TCATCATTTT  
 840  
 ATTGATGCAA TCTAGTATAG TCCACATTCT AAACAGGTGT GGACTATTAC TTTTTTCACT  
 900  
 TTATATTACC GAAAAAATTA TTATGCTTAA CTATCAATAT CAATAATTAA TTTTAAGCTG  
 960  
 AAAACAATA AAAATGTTAA GACAACGTTT ACTTCAAGTT AATTATTATA CTGAAAATTC  
 1020  
 TGGTATATAA TGCTGTTAGT GAATATAACA GGGAAATTAT ATTGGTTATA ATATTGAGTC  
 1080  
 TATATAAAGG AGAAATAACA GATGAAAAAG AAATTATTAG TTTTAACTAT GAGCACGCTA  
 1140  
 TTTGCTACAC AACTTATCAA TTCAAATCAC GCTAAAGCAT CAGTGACAGA GAGTGTTGAC  
 1200  
 ACAAATTTG TAGTTCCAGA ATCAGGAATT AATAAAATTA TTCCAGCTTA CGATGAATTT  
 1260  
 AAGAATTCGC CAAAAGTAAA TGTTAGTAAT TTAAGTACA ATAAAACTT TGTAGTTTCT  
 1320  
 GAAGACAAAT TGAATAAGAT TGTAGATTCA TCGGCAGCTA GTAAAATTGT AGATAAAAAC  
 1380  
 TTTGCCGTAC CAGAATCAAA GTTAGGAAAC ATTGTACCAG AGTACAAAGA AATCAATAAT  
 1440  
 CGCGTGAATG TAGCAACAAA CAATCCAGCT TCACAACAAG TTGATAAGCA TTTTGTGCT  
 1500  
 AAAGGCCAG AAGTAAATAG ATTTATTACG CAAAACAAAG TAAACCACCA CTTCACTACT  
 1560  
 ACGCAAACCC ACTACAAGAA AGTTATTACT TCATNCAAAA TCAACACATG TNCATTAACA  
 1620  
 TGTNNATCAT GCAAAGGAT TCTTTTAATA NACACTTTAT TGTTACACAT CAGACTCGCC  
 1680  
 TAGATATACA CATCCATCTC AATCTTTATT ATCAAGCATC ATGTGCAGCT CCTGGATATC  
 1740  
 ACGCGCATAA TTTGGTACAC AGGGCATGCT AGCATTA  
 1778

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTGCTTTTGT TCAAGCTTCT GATCAATTTT TTATCGTCTT TTGTAATTC GCGAATGTCT  
 60  
 TCAAACATTG ATAAGACAAT CTGACCCACA TTTTGTAAAT CTTTTTGAGT TTCTTGTAAT  
 120

GCAACACCAG GTGCGTGATA AACAGATCT TTGTGTAAGT GCTGAGGNNT ATAGTCANCA  
 180  
 GCNATATCTT TACCTGGGAC AAGCTTTGTA NCTATCCATG CTAAACCTGC TACANATGGT  
 240  
 AATTGAATCA NAGTATTTGT TATGTTGAAG ATACCATGTG ATACTGCAAT CGTCATCGCT  
 300  
 GGGTTTAAGT GCCATACATC TTGTAACANA CTAATCAAAT GAATCACAAC TGGCAAGAAA  
 360  
 ATTGTGNAGA TAATTACCCC GANTAAATTA AAGATGACGT GTACAAGCGC CGCACGTTTT  
 420  
 GCAGCGATTG ANCCGGCTAA ACTAGCTAAG ATAGCTGGAA TTGTGGGACG AGACAATGTT  
 480  
 ATCACCTAGG AACACAGGGA TTGCTGCGTT TNAGCTGATT AAATCTTGTT GATAAAATTC  
 540  
 TTGTAAAATA CCAATCGNCG GACTTGAANT GTTGANCTAG TGCTGTTACC CCTGCGCCGA  
 600  
 CAATGACACC AAGTATTGGA TGTGATGACA ATATCAAGCA TTAATTGNTT AAAATCCATC  
 660  
 TAATGATGCT AAGGGGTTTA NCGGCATCCA CCCCATAAAT TCTAAGACCG AAGAAAAGAG  
 720  
 ACCCCGAACC CGATAGTATG CGGCCAATGT TATTGATTTT AAGAGCGTTT AAAAGAAAAA  
 780  
 GATTAAAAAT GCACCTAATG CTAAAATTGG CATTTGCATA TTCGCCTAAA TCTAATNCCG  
 840  
 ATAATAAATG CAGTTACCGT TGTTCCGATA TTGGCACCCA TTATCACTCC AATAGCTTGT  
 900  
 TTTAACGTCA TAAATCCAGC TGTTACCAGT CCGATTGTGA TAACGGTCGT ACCTGAACTA  
 960  
 CTTTGTTATTA AAATAGTTAC AACGATACCT GCAATAACAC CTAATACTGG ATTTGATGTA  
 1020  
 AATTTGTTTA AAATATCTCG TAGCCTGTCT CCTGCTGATG CTTGAAGCCC GTCTCCCATG  
 1080  
 ATTTTAAAGC CGTAAAGGAA AATACCTAAA CCACCTAAAA AGGAGAAAAT GACTTCTGTA  
 1140  
 ACCGACATTT CCATTATTTT CACCTCAAAT AAGCTTTATA TTTAGATTAT CGCTTATAAT  
 1200  
 TGTAATTTA ATGTTAAGAT TAGGTAAAAT TATTTAACAA TATATGTTAT TTGTANATGA  
 1260  
 CTTGTAAAAT ATCGTCACTT ATTATGTNAA TTTTCAGTGT GAAATGGCAG GTNTGCAATA  
 1320  
 ACGTGTTTAA CAAAATGATG CAATCAATCA TGTAAATTATG TTTCATCAAA AAAATCATGT  
 1380  
 GAGTGGGATA ACGAAATAAA GTTTGTGAAC ATATCATTTT TATCCCACTC CATGATTTGA  
 1440  
 AATCACCAAA TAAAAATCTA TTAATGGTTT TCGTTATAAC AATTTGTGTT CTTTAAATAA  
 1500  
 TGTCTCAATG TACGTACCTT TTATCTTTTT AAGGAATCCT GCTAATGCGA GTTTCTGCAT  
 1560  
 TTTCGAAT  
 1568

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACCCCATTGA TTCCTGAATC CCCTGAAAGA AGTTGAATCA CCTTGAAGAT CCTGATTCCN  
60  
CCTGTACTTT GTGAACCCAC TGAAACTTAT TGAAGAAGAA TCCCCTGANC CTGTCTGATG  
120  
TTGATAATGA TGCCGACACC GATGTGCTTT GTGATGCCGA TGTACTAGCA CTCATTGACA  
180  
TTGATGTTGA TATCGATGTA CTTAAGGAAC CAGATGCACT TGTACTTGTT GACTGCCTTG  
240  
TGACATTGAA TCACNTAATG ATGTAGATGT GCTTGTTGAG CTCGAGTCAC TTACACTTGT  
300  
TGAACCTGAT ATTGAGTCAC TTAAACTTGT CGATGTTGAA ACTGATACGC TTCCGCTCAT  
360  
TGAGTCAGAT GTTGAAAGTG ATGTACTCGT TGAATTTGAT CCACTGATGT TAGACGAATC  
420  
ACTTGTAGAC ATTGAGTCGC TTTCTGATGC ACTGATGCTC ATAGAGTCAA ATTGACTATT  
480  
ACTTGTTGAG CTTGACTGCG AATCGCTCAC ACTTGTTGAC GTTGATTCTG ATCCACTCAA  
540  
ACTTTGCGAG CTA CTCAATG ATTTTGAATC ACTTAATGAA TCCGAAGTGC TAAGACTTGT  
600  
GGAACCACTT AAAGATATTG ATCCACTTAA TGAGTCGGAG TCACTTGAC TAGTAGAATC  
660  
ACTCATTGAT ATTGAATCAC TTAGCGAGGT AGACTCGCTT ACGCTTTCTG AACCCTTAA  
720  
TGATGTTGAG GTACTCAATG AACCAGATGT ACTTGTTGAA GTCGAACCAC TTGTTGATTT  
780  
TGAATCACTT AATGAATCAG ATTCCTCAC GCTTTCTGAA CTTCTTAGTG ACGTCGATAC  
840  
ACTTAATGAT GACGAATCGC TTGTGCTTAC TGAATCGCTC ATCGATTGTG AGCCACTCAA  
900  
TGAACCTGAC TCGCTTACAC TTTCTGATTT TCTTAATGAC GTTGAGACGC TCAATGAGCC  
960  
AGAATCACTG ACACTTGTTG AGCCACTCAT CGATTTAGAG TCACTTTCAG AATTAGATTC  
1020  
ACTTACACTT TCTGAATCAT TTACAGATTC TGACATACTT TGTGAATCAG ATATGCTTGC  
1080  
GCTCATTACT TCACTAGCCG ATGTTGATGT ACTTGTCGAA TCACTTAACG ATATAGATAC  
1140  
ACTCATCGAA CCAGATGTAC TCGCACTTGT TGAGTCTGAT GTTGAATCAC TCACACTATC  
1200  
AGATAATGAC GTTGAATCAC TCATACTTGT TGATGTACTT GTTGAAAGCG ACATACTTTG  
1260  
TGAATCACTA GTACTTGTAC GCATCGAAGT ACTAGTTGAC AGCTGATGTC TCGTGCC  
1317

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCAAATTGG CGATAGCTAA TATTTGATAA TGATGCGCAT TTCATACAAT TTGTGACTTG  
60

GCAATTATTG AATATTTTATA TAATTTTTTTC TCGTAATAAAA CACAACCTTTG ATAGCGCTAA  
 120  
 AACAGCTGTG TTAAGTTATG AGTTAACGAA TTTAACACAT TTTACTAGGG CGGCATTTAA  
 180  
 GAATATTTAT ACGTTTTTAN CGAATATTTA TTTATTGTAA NACGCTACCA AAAAGTTAGA  
 240  
 CTTCCCTCCC ACTAAAGTNC CACTTTTTTTC TTTCAACTTT TTTAANAAAC GGATATGCAA  
 300  
 CTTTTAGTAT TGGTATCAAA ATGATTGTGA GGTCATATTC TATCAATATA TTTTCTAAA  
 360  
 GAATTGCTTT TATTAACCTT CAATTATGTA CCTAACCTAA AAAGAAGCCA AGGCAACGAA  
 420  
 TGTACCTTG ACTTCTAATA CATATTCAAC TAACTATATA TTCAATCATA CGCGCATGCG  
 480  
 AGAGTGATTG TTGTACATCT ATAATGCGTT GATTTAAAGA ACCTTTATAT GGTAAATCAG  
 540  
 GTTTGAATAA GTGTTGTATA AATAGACCAT CGACTAAAAC GTCAATGTAT GATAATAACT  
 600  
 CTCGACGTTT TGTACAATCA TTTGCTAAAT ATTCATATAA AAATCCAGTC CATACCCAAA  
 660  
 TTGTCTTTGT ATTTCCAAAA CGTGCTCGAA ATGCTTTGAC AAGATTTAAT GTAATATCCA  
 720  
 AATTACAAAA TGTTTCGCCA CCTAATAGAC TTAGCCCAGA TATATAATCA TGATCGCAAT  
 780  
 CATCTAATAT TTCTGCTAAT ATTTTCATCAG TGTATTTCTC GCCATATCTG AACTTTTGTG  
 840  
 AGGCTTTGTT ATAACATCCA ACACAATTAA ATGGACATCC TGATACATAA AACTGTCATC  
 900  
 TTTACTCTTC ACCGTCAACA AAGCTATTTG AATCCTATTT TAGCAATATA ACCTTGTCCT  
 960  
 TGTTTAATGT CCTAAAAGTG TCATCCTTTA GGCGCCTTCA TATGTTTTAC TCGTGCGCAA  
 1020  
 ATTTCTTTAT GACGGCCTTT AATTACTGGA CGTTGAACTG GATTGCCTAA GTAACCCACA  
 1080  
 TGTTTCGTTTA ACGACATCAA CTGTTTTAGG ATTATCATTG NCACAAGTTC GGGCATTTAA  
 1140  
 ATCCTTTTTT AGNTGCTTCA AAATCTCCAT CCGNNATCAC ATTCAATAAC AATGGANCAA  
 1200  
 ATCGGNATAT TTGGNNCCTA AGGTAAACCA ACTTNGGCAA TAAGAGTNGG GCCCAATACC  
 1260  
 CGNTTCTAGG GCTTTCAAAT TGTGTTGCAA TTTCGGATAC TCACAATAGT GAATGAAACC  
 1320  
 ACCACTCGCA TAATAAGGAT AATCTTTTTT AAAATCTAAC TTTTCAAAG GTGTAACATC  
 1380  
 TTTACGTACA TCATAATGGA AAGAGTTTTG ATAATATCCT TTATCTGTAA TGTCTTTAAT  
 1440  
 ATCTCCAAAT CTCTCTTGGT CTAAACGACA AAAACGATCC GTTAGCGANN CACTCGGCGT  
 1500  
 ACTCGTAAAT ACTGANCCAA ATGTCATATA ATTCTGNCCA TNGCGTGTGA TAACGTNTCA  
 1560  
 TTTCTTTAAG AATNACAAGC GTAAATGCTT GNGCTTCTNG AGATGTCTCC CAGTCTGGAC  
 1620  
 CATAGAAAAC AGNAGCTGTN TCATACAACC CTATCTAGCC CATTGAAATC GTTGCACGTT  
 1680  
 TATTTTTAAA TAACTCAGCA ACATCATCTG TTTCTTTTAA TTTATAGTTA AAAGCGCCAC  
 1740  
 TTTTATATAA AATTGGTGCG TTATTCGGTA CAGNATCTTT CAAACGATTT ATACGATAAA  
 1800  
 GTAATGCATC ATGTAACACA TCGATACGTT CATAAAAGAT TTCCCAGAAT TTCGTCATAT  
 1860  
 TACCGGCAGA TTCTAATGCC ATTCTAGGTA AATTAAGTGT NACAACACCA AGATTACAAC

1920  
 GACCATTATT TTCAAATGA CCTTCCGCAT CTTTCCAAC TGGGTAAAA TGAACGACAA  
 1980  
 CCCATTGGNG CTTTGAAATC ACCTAATATT TCTACGAGTT TGGTCAATAA TTTAAAATAT  
 2040  
 CTGGATACAT ACGTTTCGGN GGAACAACCT TAATGCTAGT TGTTTAATGT CATAGGTCGG  
 2100  
 ATCTTGGGGG ACTAAAGTTG GGGTCCCNTC TCTATTGGAA ATCAAA  
 2146

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATTGTCCCAC ACCATTTACT ACAAGANACG AGCGTCCTCC ACATTGTTAC NTTGTGCNAT  
 60  
 CAATNCTTCT NGTTTGTTTT GAANNNAAGA CCGAAGCATT TGTANTCTGC TGTGTTTCGCA  
 120  
 GCCTTGTTTC GCACGTTCTA AGGTATTGAA TACCGTTTAA TGCAGTATTG GCTTGTGTAA  
 180  
 CAGCTTGCAT TGCTCTATCG ACATCTGCNT TAGGTGTATT TCCTCCAGCT GTTTTATNTA  
 240  
 AAATAGTTGC TGCTGCATTT ACTGCTTGAG AATAAGCCGT TCGTTTAGCA TCATCAGCAT  
 300  
 CTTGATAATT TTGACTTTGT AACGTCGTGT CTTTATCACG AATTGATGTT TCTAATTGAC  
 360  
 CCATAGCACC ATCTAATTGT TGCGCTTTGG CTTTAACTGT ATTAACACCT CAACATTTGT  
 420  
 TGCTNGTGTA ATTTCAATTAT CTAACGCATT ACGTTGTGCA TTATTAATGT GTGTTAATGT  
 480  
 ACCTAACGTT TGTTTCGCAG CAGCTTTAGC TTCATTTAAT TTCGCATCAC CGCNCAACGC  
 540  
 CGTCTTCGTA CTGTNCACAT TGTGTAATGC TTGNNAACCT GCTGCTTTGT CTACATTGTG  
 600  
 ACCACTAGCT TTTGTTAAAA TTGCTTTTGC TGCATTTACT GCTTGATCAT AAGCTGATTT  
 660  
 CTTACTTGGC TCAGCATCTA GGTATTTCTG AGTTTGTTTT GGTGTGTCT CATCATTGAT  
 720  
 ACCATTTTGT AACTTGTGC ATTGCGTTAT TTAATTCTTG TTGCTTTNGC AGGTTCTTGG  
 780  
 ATTTACACCA GCTACTGTAG GTGGNACCAT CAATGTTAAG CGTTAACGCA TCTTTTTGTG  
 840  
 CATTGTTAAT TGATGTTAAG TTATTCAAGT TTGTTTTTCG CTGTTGTCTT AGCTTGAGCT  
 900  
 AAGTTTTGGC GCACCATTTA ATGCATGTTT TTTAGTNGGT CACTTGTGAT GTTGCTTGGC  
 960  
 GTAATAGTAT TNGGGNTCCA TCCNNTGGNT TCCACGTTTG GATTAATGAT TGCTT  
 1015

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGCACCAGCT AGAGCGAGTT TTTATATATA CAACACGAAA GAAGACATTG ATCAGTTAAT  
60  
AAATGCCTTG AAACAAACGA AGGAGTTTTT CTCTTATGAA TTTTAATAAT CTAGATCAAT  
120  
TATATAGATC TGTCATTATG GATCATTATA AAAATCCTAC AAATAAAGGT GTATTANATA  
180  
ACGGGTCTAT GACAGTAGAT ATGAATAACC CGACATGCGG TGACCGTATA CGACTAACAT  
240  
TTGATATAGA AGACGGCATT ATAAAAGATG CTAAGTTTGA AGGTGAAGGT TGTTCGATTT  
300  
CAATGGCAAG TGCATCGATG ATGACACAAG CTGTAAAGG GAATCCANTT GGAGAAGCAA  
360  
TCCAAATNGA CCCAAGGAAT TTACCGNAAA TGATGCTTGG TTGGAAGCCT ANTGTGATNC  
420  
AGGGAAGAAT GGGGAGATAT TGAAGCATTC CNGGGTTGAT CTCAATCCCA GCTCGTATTA  
480  
AATTTGTCCA CATACCTTGG AACATTGGA AAAAGGGTCC TTGTTCTTAA AGGAGGGTAA  
540  
AACAGGAGGG TCCGGCTTGA AGAAGAAAAG ATCCTGTAA TCATAAGATG ATTTTGATAT  
600  
TAAGACATAT NNAAGTATNN NAATTTTTAA TAAAGATGTC ATGTCATTGT AATAAATATG  
660  
GTTTACATCA TTGAATTAAA AACTTACGCA CCGCCGTTGT AAATATATTT TTAAGGAGTG  
720  
ATTGAAATGG CTAAAAAGC ACCTGATGTT GGGGATTATA AATATGGATT CCCC GCCGAT  
780  
GATGTATCCA TTTTCAGATC AGAACGTGGT TTAAGTAGA ATATCGTTAG AGAAATTTCT  
840  
AACATGAAAA ATGAGCCGGA ATGGATGTTA GATTTCCGTC TTAAATCATT AAAATTGTTT  
900  
TATAAAATGC CAATGCCTCA ATGGGGTGGC GACTTATCAG AATTGAATTT CGATGACATT  
960  
ACTTACTATG TAAAGCCTTC AGAACAAGCT GAACGTTTAT GGGATGAAGT GCCAGAAGAA  
1020  
ATTAAAAGAA CTTTCGATAA ATTAGGAATT CCTGAAGCTG AACAAAAATA TTTAGCTGGT  
1080  
GTTTCTGCTC AATATGAATC TGAAGTTGTT TACCATAATA TGGAAAAAGA ACTTGAAGAA  
1140  
AAAGGTATTA TCTTTAAAGA TACAGATAGT GCTTTACAAG AAAATGAAGA ATTATTCAAA  
1200  
AAATACTTTG CTTCTGTAGT ACCTGCAGCA GATAACAAAT TTGCGGCGTT AACTCAGCA  
1260  
GTATGGTCAG GTGGNTCGCT CATTTATGTA CCTAAAAATA TCAAACTAGA TACGCCACTA  
1320  
CAAGCTTATT TCCGTATTAA CTCTGAGAAC ATGGGTCAAT TTGAACGTAC ATTAATCATT  
1380  
GCTGATGAAG GTGCTTCTGT ACATTACGTA GAAGGTTGGT ACTGCACCAG TTTATACAAC  
1440  
TAGNTCTTTA CACTCTGCTG TTGGTGGNAA TCATTGGGCA TAAAGATGCG CACNGTCCGC  
1500  
NTTATTCTTA CGAANCAAAA CTGCGGGACA ATGTTTTCAA CTNNAGGTAC  
1550

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

TGATAATACT GCTTAATACA ACATTTATTG CAATTAAAAG TGCAGTAATA GCCAGTTTTT
60
CNTTGANTTC AAAATGANTG TCCTCCNTTT TTGTTTGTA NTAAATCACTA TGCTTGGCTT
120
TATTATGGTC ANNTAAACGT GTTTCATTT GTTGATACTA ACATTTTCAA TAATTGATTC
180
GCTTCATATT GTGAAGTTTG AAAGTGTTC NCTATGGGCA ATGTATTTAT TTCTGCTTCT
240
ATACTTTGAN TGGTATGTTT CGACTGTTCT AGCGCATTTT GTTTCCTGTA ATTTTGAAAG
300
TTTACTGCTT GTTTTTGATG CTTTTTTAAC ATATCCATTT TAGTCTTTAT CGTTTGGTTC
360
TGATGAATCT GTGCTTCAAT TTGTTGATAT GTTTTGATAG AANCCCAAAT TTTAATTTTA
420
NTTGCAATAT AACCCGCTTG TTCCAAANCG TCATCTTTAT AAAACAATTT ATTTGAATCA
480
CCNATTTTCG GCTCCTACTT CCTTTACCAA ACTTGCCATT TAATGGAATA CTGTTTAGCT
540
TCATCTATTC GTACTTCCAC TAGTTTACCC AATCATTTCT TTAGGTGCTT TGAAATTAAC
600
TAGCTTATTT TTATCAGTGT AGCCAGCAAG AACCTGATCA TCTTTTTTAC TACTACCTTC
660
ACAAAGTACT GTTACAGTTT GTCCTTCGTA CTTACTCATA GCTATTTGTG AATAATGACC
720
AACTTTTTTA TTCAAACGTT GCAATCGTTC CTTTTTGACA TTAAAGGTA CATTATCTTT
780
CATTTTAGCA GCAGGCGTAC CATCACGTTG TGAATACAAG TACGTATATG CATGTTCAAA
840
ACCAACTTCA TCATACAGAG TTAAAGTTTC TTCAAATTGT TCCTCTGATT CATTTGGATA
900
CCCTACAATA ATATCTGTAG TTAATGCTAC ATTAGGAAGT CTATCTTTGA TTCGTTTTAC
960
TAAATCCAAA TAACTTTCTC GTGTATATTT TCTACCCATT ATTTTAAATA CTGCATTATT
1020
TCCAGATTGA ACTGGCAAGT GGATATGAGG AACGATATTA CCACCCTCTG AAATAACATC
1080
AATCATGTGA TCTGTAAAGT CCCAAGGATG ACTTGTTGTG AAACGAACTC TTGGAATCGC
1140
TATTTTAGAA ATTGCTTGTA AAAGATCTCC TAAGTCATAT TCTATATCCT GTAAATCTTT
1200
ACCATAAGAA TTTACATTGT GACCTAAAAG CGTTATTTCT TTGTAACCTT CACGAGCAAG
1260
TTCACGTA CTATCTATAA TGTCTTCAGG TCTACGGGTC CGGTCCTTAC TCCTTGTTAA
1320
TGGAACAATA CAATATGTAC AAAACTTATC ACAACCATA ATAATATTGA CCCATGCTTT
1380
ATGTTGCTTC ACGGACTTGT GGNAGATTAC AATAACGTCT NCTTCTTTTA GACATACTCA
1440
CAACAATGT
```

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GAAAGTGT TT CAGAACGTGG AGCAAAAGGC TTCGGAAGTA GCGGAGTGTA AAGACATCTT  
60  
AGATCGAGTT AAGGAGGTTT TGGGGAAGTG ACGCAATACT TAGTCACAAC ATTCAAAGAT  
120  
TCAACAGGAC GACCACATGA ACATATTACT GTGGCTAGAG ATAATCAGAC GTTTACAGTT  
180  
ATTGAGGCAG AGAGTAAAGA AGAAGCTGAG CGCAAATACG AGGCACAAGT TAAGATAAGG  
240  
AGAGATGGAG ATGCCAAAGA AAACGGNAAC GATTGATGTA GATGAAAAC TATTAGTAGT  
300  
AGCTAGTAAT GAAATATCAG AACTATTATA TGAATATGAC AGTGAGTTAA TCNCAGCTGG  
360  
ATGAAGATGG CGATAATAGA GATATCGGAA GGAAAAAAGA GGACGCATTA AAACAAGCTA  
420  
TACAAAATTT CTCGATAAAT TACATGGGGG TGTTTAGTG  
459

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGCACGAGCT CATAATCGC TAGTAAGAAT AATAATCTTA GTATTTGTTT AGTCATTCCC  
60  
CACACTCCCT TATATTTTCA AACAACTGAC TCACTTTAGC ATAATTCCAT CTCTCCTATC  
120  
TTAACCTTGT GCCTCGTANT TGCGCTCAGC TTCTTCTTTA CTCTCTGCCT CAACAACTGT  
180  
AAACGTCTGA TTATCTCTAG CAGTAGTAAA ATGTTTCATGT GGTGTGCCTT GTTGAATCTT  
240  
TGAATGTTGT GACTAAGTAT TGTGTCATTC CTCATAGCTC CCTTGAACCT GTTTGAGCTT  
300  
ACTCATAAAA AACATTACTA AAAATGCTAT TAAGATATGC GTCTTTTGAT GTTTATAAGC  
360  
AAATGTAGAT ATCATAAAGA TAGTAGCAAG CATTAAACATT TCATATATGT TTGTGTGTAT  
420  
AGTCTTTTTA CTCTTAAGAA AAATAATTGC TATGCGATAA AAGAGATAAA CGCCAAACCC  
480  
TATTAAAAAT ATTTCTAACA TGTCGCTCAC TTCCCCAAAA CCTCCTTGAC TCGATCTAAG  
540

ATGTCTTTAT ACTCCGCTAC TTCCGAAGCC TTTTGCTCCA CGTTCTGAAA CACACTCGAA  
 600  
 TTCCTCCACT TGCTTTAGTT CAGGTGTCCA TATAGGCACG ATAACCAATT GAGCTAGTTT  
 660  
 GTCGCCTTCG TTGATTTGAT AAGTTCCATA TTGTCTTATG GCGTCACTCA AATCGATTTC  
 720  
 TCCTTTAATA TCAAAAACAC CTGGTGTGAT ATAACCATTG GATGCAATAG CGTCATTCTT  
 780  
 GATATTAATC CCTAAATTGC CGTGATATCC CGCGTCTATC TTGCCTGTTT CAATCACTAA  
 840  
 ATGCGTTTTA CTACTTACAC CACTACGACT AGTTAATAGT CCGACATAGC CCTCTGGTAT  
 900  
 ACTCACAGCT ACATCTGTTT TGATCACTGC TTTTCTTGT GGTTCGAGTA CGACAGTTTC  
 960  
 AGCTGAGAAT ATGTCATAAC CTGCATCCGT CTTATGATTT CGTTCGGGCA TTCTAGCATT  
 1020  
 TTTTGATAAT AGTTTTACTT GTAATGTGTT AGTCATTTTC CTATTCCTCC TCATATTTAT  
 1080  
 AGACAACCTG ACCTGCCATA ATCCCTACTG CTTTCATCAAG TTCAATACCT CNTTTAACTG  
 1140  
 AATGTTGAAT AGCATTGTGC ATTCCCTCAA GTATTTTCATC AAACGCTTGC GCTTCTTAT  
 1200  
 ACACGTCCTC AATCTCTTTT AGCAACCCCT CTGTGTCATT ACCGTATACG CACTAGCACT  
 1260  
 AATAACGGAC TGTTGATTTT TTTGCGGATT ATTCATTGGT GTCATCCTCC ATAAAAATTT  
 1320  
 TATTGTTTAA TTCCATTCCG AATTTAACTC TTTCATCATC GTTACCGAAT TCGTTTATTA  
 1380  
 AATCTTTTTT AACGCTCTTG CAATACCTAT CCCATGCGCT TGCTTCTTTC TCCAGTTCTT  
 1440  
 TGTTACAATC TCGTAACTTC GCTATATCCC CAATAAGCTC ATCTCGTTGC TTCTTGTAAT  
 1500  
 CTTACAGATC TTTTAATGCT TTGTGAAGTT TATCTAATAA CTTGTTAGAG TTAGTACAAA  
 1560  
 GATTTTTATA TTGTTTCATCT GATAAGGTGA ACGTCATCTC ATAACCTCCA ATAGCATCTC  
 1620  
 ATTTTCAAAA ATATTTCCAA CAATTTCAAT AATATCGGCA TTTTCACTTA GTAATTCAGT  
 1680  
 TACATTGCTA AAAGTTATAT AAAAGGCTCC TTCTTTAAAC TCGATAAAAC TTAATTCTCT  
 1740  
 CGAATTAACA ATCTTGAAC AATATCCCTC TCATAAATCT CCACAACCGG GCACATCTTT  
 1800  
 TAAATCCTGT GTATTGGTAA TAGGTTTTAC TTCAATTGAA ACTTTTATTA ACCTGGTGGA  
 1860  
 AATCAAAATG TACCCACTTA TTAATAATCG GATTTGGGNC AATAATACTC AATAACTTNN  
 1920  
 NNTATCTTNA TCCCAAGCTT TTAATTTCAA CATCAATCTT ACCAACTCCC CATCTTTCCA  
 1980  
 AATCAATGTC AACCGGCAAN GTCAC  
 2005

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGCACGAGCT GTTTTTTTATT TGCTTCGTTA CAAAGCATT A TTGAATTTAT TTTACGTGTT  
60  
CATATTTTGA AACATCAAAG CCGTCTTGCT TAGCTTTGTT GATAATGTCT TTGATTGAAT  
120  
GTAGTCCTTT ATCGGCGAAG TATGATCTTA AGTTGTCTTT TGTAGCTTGG TCAGCATTCT  
180  
TATCTAATAA CACATCGATA TAGCTTAATT CATGTTCTAA GAAGTTTGCG TCATCATGTA  
240  
GTACGAGTCC ATTTTGAGAA TAAACTTTCG CATCTGCTTG ATTACCATAT CCAACAACGC  
300  
CAGTTGCTAA TACACCTACC ATTGCCGTAG CTAATAAAAC CTTTTTAAAT TTCATATCTA  
360  
TCACTCCTCT AAAAATTGTA CTCTATCATA ACACTTGAAT ATTAAGAAAA TTACGGNTTA  
420  
TTAAGTCGGA CTTNANTAAT TCTTAATAAA TAGNTAAACT GACAAATATT NGCTNAAATG  
480  
CAATTANTCT TNAAAACCGG GGTTTATGGA TTTTTCCTAC TAAACCTTG ATTTCAAAAA  
540  
GGGTTTANCT CAAATGAAAC AATAATAAAA AATAATGCAA CATAATAATA AGTACAAATT  
600  
TANTTAAGAA ATTAAATTGA TTGTATATGT ATATTNTGGT AACGTNAAAG AGAAATATNC  
660  
AANATAATTA ATTATTTATT TGAAAAGAGA ATATTAATGA AGTATTAAAC AAAGAGACGT  
720  
GAAACGATGC GATATTTAAA AAGACTTTCA TGGNACATAA GCATCTTAAT TTTAATAGGT  
780  
GGTATTGCTG GGTGGG  
796

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AACTTTGAGT NTTTTGTTN ATATGGAAC TTAAGATTT GGAAATTATN TAGATGGAGA  
60  
TATATCATAT AATCCAGAGG TGCCNAGTTA TTCAGCTAAA TATCAATTAN CTAATGATGA  
120  
TNACAATGTA AAGCAATTAC GTAAAAGATA TGACATNCCA GCAGAATAAA GCACCCAAAG  
180  
TTATTTGTTG AAAGGGTACA GGGTAATTTN AAAGCCTCAT CAGTTGGATA TAAAGACAGT  
240  
GAATTTACTT TCGTAGAGAN NAAAGGTGAA AATATATACT TTAGTGATAG TCTACATCTT  
300  
GANCCAAGTG AGGATAAATA AACGTGACCA ATAAAGAGTA TGAAATCGAA CCCGGAAAAA  
360  
GAGAGTGTGA AATGATGAAA CGATTAAATA AATTAGTGTT AGGCATTAGT TTTCTGTTTT  
420  
TAGTCATTAG TATCACTGCT GGTTGTGGCA TAGGTAAAGA AGCGGAAGTT AAGAAAAGCT  
480  
TTGAAAAAAC ATTGAGTATG TACCCTATTA AAAATCTAGA GGATTTATAC GATAAGGAAG  
540



GCTATCGTGA TGATCAGTTT GATAAAAATG ATAAAGGTAC ATGGATTATA AATTCTGAAA  
 600  
 TGGTTATTCA ACCTAATAAT GAAGATATGG TAGCTAAAGG CATGGTTCTA TATATCGAAT  
 660  
 AGAAATACCA AAACAACAAA TGGTTACTAC TATGTCTGATG TGAATAAGGA CGAGGATGAA  
 720  
 GGAAAACCGC ACGACAATGA AAAAAGATAT CCGGTTAAAA TGGTCCGATA ATAAAATCAT  
 780  
 TCCAACAAAA GAAATTANAG ATAANAACAT AAAAAAAGAA NTCGAAAAC TTAAGTTCTT  
 840  
 TGTTCAATAT GGAAACTTTA AAGATTTGTC GAAGTACAAA GATGGAGATA TTTCATACAA  
 900  
 TCCAGAGGTG CCAAGTTATT CACCAAATA TCAAGTAACT AATGATGACT ATAATGTAAN  
 960  
 ACAATTNCGN AAAAGATATA GATATACCGA CCGAATAAAG CACCANAGCT ATTGTTGANA  
 1020  
 GGTACAGGGA ATTTAAAAGG TTCATCAATT GGCTACACAA AAATTGAATT TACTTTCGTA  
 1080  
 GAGAAAAAGG GAGAAAATAT ATACTTTAGT GATGGGCTAC AG  
 1122

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTGGTCTT CTATTCCCGT TTTGCCATCT CNAATTTCTT ACCATGGCCC ACAAAGTATT  
 60  
 GTNACGTTTG AGCTGATCCT TATTTAATTT TNAAATTGAG AAAAATGTCT CCAAATCCTG  
 120  
 TACCTNCCCC ATATTCCCGC AATACAAATA AAATTTTGTC GTATTTGCTC NCCGTAAGC  
 180  
 TTTAAATGTG GTCATTATAA GANCGGATTG TCTTGTAATT GACCGCATGT CATACCAGTT  
 240  
 AGGAATCACA TGGATATTGT CAGCATTTTT AAGAAATTTG ATGATTTAGT AAGTAGTTTT  
 300  
 TCATTTCCGT ACCCAAGGAC AATGACATTT TCAGCATTTCT TGTAGACATG TCTATTAATG  
 360  
 TAACGCATCA GCTTATCAAT CATGCTACCT GGACGAGTTG CACCTGTCTT AATCGCATTA  
 420  
 TCAGGTGCTA TATCATACAC CACAAAAGAA TATTTTTTCT TAAGCAGTCT GTGTAAAACG  
 480  
 TCTGGTATTA ATGGCAAGAT TGGTGGATTA GAGTAAACAA GAATCTGATC ATATTTCAAC  
 540  
 ATTTTAGGTA TATTAATCAC GAATTTTGAA AATAAACTAA AGAAATTGAT GATCCTTCCA  
 600  
 ACCTTACTTT TGTTATTAAA CCTCGAATAC TTGAGACGTC GAATGCCAAN TC  
 652

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCCTT CAAAAGCACC TTTGATACCG AATAAATTAT GGTTTGGTGA CTTAGATAAA  
60  
GAACTAGCGG GAAGATTTTA ATCGCAAGAC TGGTGCGAAT GTGAAGTATA TTGAAGCACC  
120  
TTATGAACCG CATAAGTTTG TGAAAATGGT GAAGGATAAA GAATTAGCTG ATGAAAAGA  
180  
AGGCGGCTTA CGTNGTACCG CTTGTTTTGA AATGCGTTTG GATATTGTAG CGAAAGCAGC  
240  
TGTAGAACAT GGCTATGATT ATTTTGGCAG TGCAATCACG TTATCACCTA AAAAGAACGC  
300  
ACAATTAATC AATGAACTTG GTATGGATTG TCCAAAAAAT ATACGATGTG AACTTATTTG  
360  
CAAGTGATTT TAAGAAACT AAGGTATTGA GC  
392

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3797 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCAAATGCAG TCAGGGAAGC AATAGGACGA TATGCATAAA GGAGATGGTA AAGTGAACA  
60  
GTGACAGAAG GTAAAGACAC GCTTCAATCA TCGGAGNCAT CAATCAANCA CAAAATAGTA  
120  
AAACAATCAG GAACGCAAAA TGATAATCAA GTAAAGCAAG ATTCTGGAAC GACAAGGTTC  
180  
TAAACAGTCA CACCAAAATA ATGCGACTAA TAATACTGAA CGTCAAAATG ATCAGGTTCA  
240  
AAATACCCAT CATGCTGAAC GTAATGGATC ACAATCGACA ACGTCACAAT CGAATGATGT  
300  
TGATAAATCA CAACCATCCA TTCCGGCACA AAAGGTATTA CCCAATCATG ATAAAGCAGC  
360  
ACCAACTTCA ACTACACCCC CGTCTAATGA TAAAACTGCA CCTAAATCAA CAAAAGCACA  
420  
AGATGCAACC ACGGACAAAC ATCCAAATCA ACAAGATACA CATCAACCCG CGTGCCTCAA  
480  
ATCATAGATG CAAAGCAAGA TGATACTGTT CGCCAAAGTG AACAGAAACC ACAAGTTGGC  
540  
GATTTAAGTA AACATATCGA TGGTCAAAAT TCCCCAGAGA AACCGACAGA TAAAAATACT  
600  
GATAATAAAC AACTAATCAA AGATGCGCTT CAAGCGCCTA AAACACGTTC GACTACAAAT  
660  
GCAGCAGCAG ATGCTAAAAA GGTTCGACCA CTAAAGCGA ATCAAGTACA ACCACTTAAC  
720  
AAATATCCAG TTGTTTTTGT ACATGGATTT TTAGGATTAG TAGGCGATAA TGCACCTGCT  
780  
TTATATCCAA ATTATTGGGG TGGAAATAAA TTAAAGTTA TCGAGGGAAT TGAGAAAGCA

840  
AGGCTATAAT GTACATCAAG CAAGTGTAAG TGCATTTGGT AGTAACTATG ATCGCGCTGT  
900  
AGAACTTTAT TATTACATTA AAGGTGGTCA CGAGCGTAGA TTATGGCGCA GCACATGCAG  
960  
CTAAATACGG ACATGAGCGC TATGGTAAGA CTTATAAAGG AATCATGCCT AATTGGGAAC  
1020  
CTGGTAAAAA GGTACATCTT GTAGGGCATA GTATGGGTGG TCAAACAATT CGTTTAATGG  
1080  
AAGAGTTTTT AAGAAATGGT AACAAAGAAG AAATTGCCTA TCATAAAGCG CATGGTGGAG  
1140  
AAATATCACC ATTATTCACT GGTGGTCATA ACAATATGGT TGCATCAATC ACAACATTAG  
1200  
CAACACCACA TAATGGTTCA CAAGCAGCTG ATAAGTTTGG AAATACAGAA GCTGTTAGAA  
1260  
AAATCATGTT CGCTTTAAAT CGATTTATGG GTAACAAGTA TTCCGAATAT CGATTTAGGA  
1320  
TTAACGCAAT GGGGCTTTAA ACAATTACCA AATGAGAGTT ACATTGACTA TATTAAAACG  
1380  
CGTTAGTAAA AGCAAAATTT GGACATCAGA CGATAATGCT GCCTATGATT TAACGTTAGA  
1440  
TGGCTCTGCA AAATTGAACA ACATGACAAG TATGAATCCT AATATTACGT ATACGACTTA  
1500  
TACAGGTGTG TCTTCACATA CTGGTCCATT AGGGCACGAA AATCCTGCCG AATTAGGCAC  
1560  
GAGACATTTT TCTTAATGGA TACAACGAGT AGAATTATTG GTCATGATGC AAGAGAAGAA  
1620  
TGGCGTAAAA ATGATGGTGT CGTACCAGTG ATTTTCGTCGT TACATCCATC CAATCAACCA  
1680  
TTTATTAATG TTACGAATGA TGAACCTGCC ACACGCAGAG GTATCTGGCA AGTTAAACCA  
1740  
ATCATACAAG GATGGGATCA TGTCGATTTT ATCGGTGTGG ACTTCCTGGA TTTCAACACC  
1800  
GTAAGGTGCA GAACTTGCCA ACTTCTATAC AGGTATAATA AATGACTTGT TGCGTGTGGA  
1860  
AGCGNCTGAA AGTAAAGGAA CACAATTGAA AGCAAGTTAA ATTCATCTTC TGAATTTAAT  
1920  
AGGCTATGTA AATCGTGCTG TTATCATGGC ACATCAGATA TAAGTAGCAT CACAGTGTG  
1980  
AATCTCAAAA TAGTAAAGTG AAATAAAGCG CCTGTCTCAT TAGCGAAAAC TAAAGGGACA  
2040  
GGCGTATCTG TTTATGAGCT TAATAAATTG TATGAATAAT ATGGTTGATC GAATAACTGT  
2100  
TTATCATTGA TGATAAATTT GAGTTTTTTTA AAAATAATTG ATATATTACA CCATTGTTAT  
2160  
AGCGTTTAAA GAAATCAACC CAACTTTACG ATAAATAGTG ATTGCTTCGT CATTAGGTCT  
2220  
ACGATCAAAA TCATGCTCGT TTTTATTAC GCGTTCAAAT GTTGAATGTG GAACATGATT  
2280  
CATGATATGT TCGCTTTCCT CAACGGGAAC ATCATAATCG CCATTACAAT GCGCAATGAA  
2340  
AACAGGTGGA AGTGTTTTAA GNTCATCTGG TGCAATATTA TATTTTGAAT CAGTATAATC  
2400  
ANCAATGTTA ATCATATTTA TCCATTTACC TGTGCCACGT GCATAAACGT AGAGTAAAAA  
2460  
ACGTGTGCGA TTTGATCTTG ANCAACCGGT GTTGGTGAAG TGAGTTGTCC AATCATTGTT  
2520  
TCGTTTATGC TTTGAGCTAT TTTTGCGTAA TACCTATTAG TTGTTTTAAA AGGGTTCAGT  
2580  
GTTGATGCGA CTATAACCAT AAAAATCAAT AACACCATCA ATATCTCTGT CTCGTGCAAT  
2640

TAATAAGACT TAAATATGCA CCTGATGATC TGCCAAAGGT AAAAATAGGG CAATTAGAAT  
 2700  
 ATTGTGATTG AATCGCATCG AATGATGCGT AGACATCCTC AATAATGCAA TCGAGACTTA  
 2760  
 CTTCTGGTAA TAAACGATAA CTTAGTTGAA TTAAATCGTA ATGTTCCGTA AGGATATCGA  
 2820  
 TATACTGTGG GGATAAATCG TTAGCTTTAC CGAACATTAA TCCACCACCG TGGATGTAGA  
 2880  
 CAATAACGCC TTTTGTGGT TGATTTTTTG CTTTAATAAT TGTGTAAGGT AATGCAAATG  
 2940  
 CATCTTTAGT AATTACTTTA TATTTAATTT CAGTCACGAT TTAATAGGCT CCTTAGGAAT  
 3000  
 CCGATATTGA TGTCATTATA ACACTGTCNT NAATTTCCAT GNAAAATAGT CTTAAGACGA  
 3060  
 TGAGTCATGA TAATTCTGTT CCAATTGACG TAAAGCGTCN CGGGTATGCT TCTTTAGACC  
 3120  
 TTCCCCATAA TCCATCATTT TAACAATATC TTTAAAAGCA GCATGTGGNA TGGCTAAATC  
 3180  
 TTCTAAATCT GCCATAGAAA ATTCAAGATT GATATCATGT GGTCGCTGTT CAGCAAGTTT  
 3240  
 ATGCACAAAG TCAGGTTCTG TGACCAAAGG CGAAGACATG CCGACCATAT CTGCATGTTG  
 3300  
 TAAAGCATCT AAAGCAGACT CTGGAGAATT AATCCCGCCA CTTGCAATTA AAGGGATACG  
 3360  
 ACCTGCTAAA TGTTCATAGA CAATTTGGTT AACTGGTCGA CCGAAATGAT CACCTGGTGT  
 3420  
 ACGAGACGTA TTTTGATAAA TATGTCGACC CCAGCTAGCG ATTGCTAAGT ATTGGATGTT  
 3480  
 TGAAACGTCC ATGACCCAAT CGATTAATTG GTTGAACTCG TCAATGGTAT ATCCTAAATC  
 3540  
 ACTGCCTCTG GTTTCTTCTG GCGTTGCTCG AAATCCTAAA ATAAAATTGT CAGGTGCTTC  
 3600  
 TTTATCAATC ACTTCTTGTA CCGCACGCAT AACTTCTAAA CATAATCTTG CACGATTTTT  
 3660  
 TAATGAGTCG GCACCGTAAT GGTCTGTACG TCTATTTGAA AAAGTTGAGA AAAATGTTTG  
 3720  
 AATCAGCAAA CGTTGTGCAA TCGAAATTC CACACCATCA AAACCTGCTT TAATCGCGCG  
 3780  
 TGCATCGAGC TCGTGCC  
 3797

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAAGCCAGTT CAACTNACCG ACCCGGTATA TTTGGGGAAT ATACGAANCN CNNTCAGATG  
 60  
 ATCNAATAT GANTGANACN CGGTNGCGTT CTCNAGNCAN AACAGNGTTA AATAANCGTA  
 120  
 AGTCGGCAGT TATGTCANAT GAGATTACTT CTNCTGATTG GGNAGTTACG NNTCCACACG  
 180  
 AGANNATATC ANNTGGTGAN NCAGNCAGAG TAAAACATAG AGATTTTGAC CCGCCATTGT  
 240

ATGTAGAGGC AGAAGTTATT GCCGAAGAAT ATAACATAAT TTCAGAAAAAT AGCACATATA  
 300  
 CATTTCGGTCA ACCTAAAGAG TTCAAAGAAT CAGAATTACG AGAAGAGTTT AACAAAGCGAT  
 360  
 TGAACATAAT ACATCAAAAAG TTAAACGATA ATATTAGCAA TATCAACACT ATAGTAAAAG  
 420  
 ATGTTGTAGA TAGTGAATTA GAATACTTTG AACGCAAAAT ACACAAAAGT GATACACCGC  
 480  
 CAGAAAATCC AGTCAATGAT ATGCTTTGGT ATGATACAAG TAACCCTGAT GTTGCTGTCT  
 540  
 TGCGTAGATA TTGGAATGGT CGATGGATTG AAGAAACACC AAATGATGTT GNAAAATTAG  
 600  
 GTGGTATAAC AAGAGAGGAA AGCGCTATTC AGTGAATTAA ACAATATATT TATTAATTTA  
 660  
 TCTATACAAC ACGCTAGTCT TTTGTCAAGA AGCTACAGAA TTAAGTGAAT AGCGAGTACT  
 720  
 TAGTAGATAA TGATTTGAAA GCGGACTTAC AAGCAAGTTT AGACGCTGTG ATTGATGTTT  
 780  
 ATAATCAAAT TAAAAATAAT TTAGAATCTA TGACACCCGA AACTGCAACG ATTGGTCGGT  
 840  
 TGGTAGATAC AAAAAGCTTTA TTTCTTGAGT ATAGAAAGAA ATTACAAGAT GTTTATACAG  
 900  
 ATGTAGAAGA TGTCAAAATC GCCATTTTCAG ATAGATTTAA ATTATTACAG TCACAATACA  
 960  
 CTGATGAAAA ATATAAAGAA GCGTTGGAAA TAATAGCAAC AAAATTTGGT TTAACGGTGA  
 1020  
 ATGAAGATTT GCAGTTAGTC GGAGAACCTA ATGTTGTTAA ATCAGCTATT GAAGCAGCTA  
 1080  
 GAGAATCCAC AAAAGAACAA TTACGTGACT ATGTNAAAAC ATCGGACTAT NAAACAGACA  
 1140  
 ANGACGGGAT TGTTGAACGT NTAGATACTG CTGAAGCTGA GAGAACGACT TTNNAAGGGG  
 1200  
 AAATCAAAGA TAAAGNTACG GTTANACGAA TATCGAAACG GATTGGAAGA ACAAACAA  
 1260  
 TATACTGATG ACCAGTTAAG TGATTTGTCC AATAATCCTG AGATTAAAGC AAGTATTGAA  
 1320  
 CAAGCAAATC AAGAAGCGCA AGAAGCTTTA AAATCATACA TTGATGCTCA AGATGATCTT  
 1380  
 AAAGAGAAGG AATCCCAAGC GTATGCTGAT GGTAAAATTT CGGAGAGAAG AGCAACGCGC  
 1440  
 TATACAAGAT GCTCAAGCTA AACTTGNAGA GGCAAAACAA AACGCAGGAN CTTAAAGGCT  
 1500  
 TAGANACGCT GAAAAGANAG CTAATGTTTA TACAGACAAC AAGGTCAAAG AAAGCACAGA  
 1560  
 TGCACAGAGG AAAACATTGA CTCGCTATGG TTCTCAAATT ATACACAATG GTAAGGAAAT  
 1620  
 CANATTAAGA ACTACTAAAG AAGAGTTTAA TGCTTCTAAA AGAACACTAT CAAGAGTGTT  
 1680  
 AGCAGACATC ACTGTAAATG CTATGAAAGG CATCTATTTA AGGTATGACG AAAATGGGGC  
 1740  
 GATTACTTCA CATACTATTG ATAAAGATGG CGTGAAAATT AGTGGCGATA AAGTTGATAT  
 1800  
 AACAGCGAAT AGAGAATTTA ATGTATTCGC AAATAATATT AATAACAAAG TTGGTAAAAA  
 1860  
 TGACATTGTT AATAGCCTAA ACTTATCAAA TGAAGGTCTT GACATCAATG TGAATAGAAT  
 1920  
 TGGTATTAAA GCGGGAATG CTAACCGTTA TGTACAAGTT CAAAATGATT TTATTGAACT  
 1980  
 TGGCGGAATC GTACAACGAA CTTGGAAAGG CAAACGATCA ACCGATGATA TATTCACACG  
 2040  
 TCTTAAAGAT GGACATCTAA GGTTTAGAAA TAATACCGCA GGCGGGTCAC TTTATATGTC

2100  
 ACATTTTGGT ATTTCAACAT ATATTGATGG AGAAGGCGAA GACGGAGGTT CATCCGGTAC  
 2160  
 TATTCAATGG TGGGATAAAA CTTACAGTGA TAGCGGTATG AATGGCATAA CAATCAATTC  
 2220  
 TTATGGCGGT GTAGTCGCTT TAACATCTGA CTACAATCGA ATTATTATCG ATTCATATGC  
 2280  
 TTCAGCTAAT ATTGAAAGTA GAGAAGCGCC GATATATTTA TCTCCGAACA CCCAAAAATT  
 2340  
 AAACCTGGNT TTAANCCGAT TCGCATTAC ATTATCAAAC GCTGATAGGT NCATTACGAA  
 2400  
 ACTGGCGGTT ATATCATGTT GGGTTCAAGA TGNAANCTAT AAGTNCGGTG CTGGATTAAG  
 2460  
 ATTTTCTAAA CGTACCAATA AAGGATTGGT TCAAGTCGTT AATGGTGACT ATGCTACAGG  
 2520  
 CGGAGACACT ACAATTGAAT CAGGTATGGC CAAATTCAAC TTAGTTAANC GGAAGAGATG  
 2580  
 GAAATAGTTA CGTTAGCATT CAAAGTTATG ATTTATTGGC GGTAGGTTCT GATAATGCTG  
 2640  
 GCGATAGAGT CGCTTCTAAT TCTATTTATA AGCGTACTTA TTCAGCACCT GCTAACTTAC  
 2700  
 ACATTACTTC TGCTGGAACA ATTGGGCGTG CTAATTCTGC CAAAAAGTAT AAAATTTCAA  
 2760  
 TCGAAACCA ATACATCAAT GAAGACGATC AGTTCAGTCA TTCAAAGAG ATTTTAAAGC  
 2820  
 TTCCAATTCG TACATGGTTT GACAAATATG AATCGGAAAT AATGGCTAAA GAATTGGAAA  
 2880  
 GTGGTAAAAA GTTATCTGAT GATACTTTTA AACTTAGTCG ACATACTGGC TTAATAGCGG  
 2940  
 AAGAGTTGA AGAATTAGGA TTTAATGAAT TTGTTATTTA TGATGACAAC GGAGAAATCG  
 3000  
 AAGGTATCGC ATACGATAGA CTTTGGGTTT ATCTANNACC TATTATTACC CNAAAACCAN  
 3060  
 CANTCAAANA NCGNAAAACN TANTGGNGGN NTTAACNTCT NATNGACNGC AACCAGGGTC  
 3120  
 CNCATNCCAC CTCCACATTA TACAANTCAC TTTCTCNCGT CACTA  
 3165

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAAACAAGCG ATTATCACAG CAATTATTTT AATAGCACTG AGCTTGATTT TACCTGCATT  
 60  
 TGCAGTAGGT AATCACATTT CAATCTTCGT CATTTCTATG ATATTCTTTG CAGGTAGCTT  
 120  
 TGCTTTAATG TATGCACCTT TACTTAACGA AGCCATTAAA ACAATAGATC TTAATATGAC  
 180  
 AGGTGTGGCT ATTGGTTTTT ATAATTTAAT TATTAATGTG GCGGTATCTG TAGGTATTGC  
 240  
 GATTGCTGCG GCTCTAATCG ATTTTAAAGC ATTAAATTTT CCAGGCAATG ATGCATTAAG  
 300  
 TTCACATTTT GGTATTATTT TAATTATTTT AGGTTTAATG AGTATTGGTC CGGATTAGTT

360  
 TTATTCCGNC ATCTTTAAAT CCGGTGGGAC AACAACTCTG AAAAAATAAT AGATATTAAA  
 420  
 TCGCGAGATA TATCCGTATT TTATTGGTAA AATTAAATTA AAGAGATTAT ATTACACGAG  
 480  
 GAGTAGTAAG TATTGAAATT GGAGAAATAT ATAGATCACA CTTTATTGAA GCCTGAGTCA  
 540  
 ACACGTACGC AAATCGATCA AATCATCGAT GAAGCGAAAG CATACCATTT TAAATCTGTA  
 600  
 TGTGTGAATC CAACGCATGT TAAATATGCA GCAGAGCGAC TAGCTGATTC AGAGGTGCTC  
 660  
 GTTTGTACGG TAATAGGATT CCCATTAGGT GCGTCGACAA CTGCAACGAA AGCATTTGAA  
 720  
 ACAGAAGATG CAATTCAAAA TGGTGCAGAT GAAATTGACA TGGTCATCAA CATCGGCGCA  
 780  
 TTAAAAGATG GACGTTTTGA TGATGTACAA CAAGACATTG AAGCAGTGGT TAAAGCTGCG  
 840  
 AAAGGTCACA CAGTAAAAGT GATTATTGAG ACGGTATTGT TGGAACCATG ACGAAATTGT  
 900  
 AAAAGCGAGT GAATTAACAA AAGCGGCTGG TGCGGACTTC GTTAAACTT CAACAGGTTT  
 960  
 TGCAGGTGGC GGTGCGACTG CAGAAGACGT TAAATTAATG AAAGATACAA GTAGGTGCTG  
 1020  
 ATGTAGAAGT AAAAGCATCA GGTGGCGTAC GTAATTTAGA AGGATTTCAA TAAAATGGTT  
 1080  
 GAAGCAGGTG CGACACGTAT TGGGCGCGAG CGCAGGCGTT CCAAATTATG CAAGGTTTAG  
 1140  
 AAGCAGATTC AAGATTACTA ATATATATAA AATTTGGGAG TGATAGCTAT GACAAAGACC  
 1200  
 ATTTAATCGN GTTCATTTTA TCCGTATGG  
 1229

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGCACGAGAC GTAAATGNAA AGAAAACCGG CCTNCNTGAT TAAGANATTT AGAAAAGTGT  
 60  
 TTGTCATNAC GGTGTGCCA GTGNTNAGTA TGTCCAAATA NAGGAAGTGA NAACGATGGN  
 120  
 ACCGTATTTT TAAAANAGGC AGNACATANC ATTTTAGATA GGAAGTGATA ATATGAATTT  
 180  
 GGCTAAACGC ANATTACAAG GGGAACNATT AACAANAGAG ACTGTAGTGA AAATTTATGA  
 240  
 GGATACTAAT ATTGATACCT TAGNTTTATT AAATGAGGCG NACATCTTTA AGNANACATT  
 300  
 ATTTTGGTGC NATNAGTCAA ATTAAACATG ATTTTAAATG CTAAAAGTGG NATATGTCCT  
 360  
 GAGAATTGTG GGCNCGAGAC TGTGGACAAT CACGAGATAT TAAACAANAA CAGCGATATG  
 420  
 CTTTAATTCC AGAGGAACAA ATTATCGATN GANCANAGGT GGCACATGAT AATCATATTG  
 480  
 GAACATATTG TATTGTTATG AGTGGTAGAG GACCGAGCGA TAAAGAAGTT GATCATATTA

540  
 GTAATCCTGT AAGAACGATT AAATCTCAAC ACCCGCAACT AAAAATCTGT GCATGTTTAG  
 600  
 GATTAACGGA TTGCCGACCA AGCTAAGAAA CTTAAGTCAG CTGTTGTAGA CAGATATANC  
 660  
 CACAATATTA ATACCAAGTG AAAATTACCC ATTGATAACC GTCGTGCCAA CGCATAGTTA  
 720  
 TNAAGATAGA ACAGATACGA TAGAACTAAT GAAAGCGAAT AATATATCAC CATGTTCTGG  
 780  
 CGTGATTTGT GGTATGGGAG AATCTAATCA AGATATTGTT GATATGGCAT TTGCTTTAAA  
 840  
 AGAAATGGAT GCCGACAGTA TTCCGATTAA TTTTTTGCAT CCAATCAAAG GCACAAAGTT  
 900  
 TGAAGCATG GATGATTTAA CACCAATGAA ATGTTTAAGA ATCGTAGCAT TATTCCGATT  
 960  
 AATCAATCCT ACGAAAGAAA TTCGTATTGC TGGAGGAAGA GAGGTCAACT TACGTTCGTT  
 1020  
 ACAGCCATTA GCATTAAAAG CGGCGAANTN CAATATTTGG GCGGGG  
 1066

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CCAAGTAAGT ATAGAAGCAG CATCCTTAGA AAAGAAAAAT GTAGATTTGA ACGAATTATT  
 60  
 ACAGCGTCTC AATGACGTTG AACAAACGGA ATACACCAGG TTCGCTTNAC CCTAAATTTT  
 120  
 TAAATGTTTC GTCACCTTATT CAATATATTC AAGCAGCATA TCATGAACCT CTTAGAGAAG  
 180  
 AATTTAAAAA TTTAACACCT TATGTGACGA AATTATCGAA AGTACATGGA CCTAACCATC  
 240  
 CATATTTAGT CGAGTTAAAA GAAACATATG ATACATTTAA AAGTGGCATG TTAGAGCATA  
 300  
 TCCAAAAAGA AGATGATGTT GATTTTCAAA ACTAATTAAA TATGAACAAG GTGAAGTAGT  
 360  
 AAACGATATT AATACAGTGA TTGATGATTT AGTATCTGAT CACATTGCAA CGGGACAATT  
 420  
 GTTAGTGAAA ATGAGCGATT TAACATCTAG CTATGAACCA CCGATAGAGG CATGTGGTAC  
 480  
 GTGGCGACTC GTTTATCAGA GATTAAAAGC ACTTGAAGTG TTAACACATG AGCATGTTCA  
 540  
 TTTAGAGAAT CATGTTTTAT TTAAAAAAGT ATCATAAATA ACGCGATTAG AACTGTTGG  
 600  
 CAAAGTAATG TCAGCAGTTT TTCGCTATAC TTAACAGAAA TTTAGTGATA TGAACAGCAT  
 660  
 TATTTGAAAA GAAAAATGGT CAACTTAGCA TAAAAATTGA TATGAAAATT TAATGGTATA  
 720  
 GATAATTAAA TAGTAGCGTG TTTTTTTAAT AATTTATTCA TGAATTTTAC ATGCACTATT  
 780  
 ATGATAAAAT AAACATAATT ATAATTCAC T GAGGTGCTAT CGTGCTATCG CTAACAATGT  
 840  
 TATTACTTGA GCGTGTAGGT TTAATTATTA TTNTGGGCCT ATGTGTTGAT GAATTATTCC



900  
 ATATTTTTTAA AAACCTTTAAT GAATCCGTCG ACGCTACATG GAAAGCACGT TGGCAATTAT  
 960  
 GTATTATTTT CAGTTTGTTT GCCTTAATGT TCTAATTTAA CTGGTATCGT CATCGATCAT  
 1020  
 CAACATAGTT TGTGAGGAAG TGTGTACTTC CGTTTAGATG ATGATGTATC TTTAGCTAAC  
 1080  
 ACACGTGTAT TAACGATAGG TGTGCGAGGA TTAGTTGGTG GCCCTTTTGT AGGTCTATTT  
 1140  
 GTTGGCGTTA TTTCAGGTAT TTTCAGAGTG TATATGGGTG GGGCGGATGC ACAAGTTTAT  
 1200  
 CTTATCTCAT CTATATTTAT CGGNATTAAT TGCTGGTTAT TTNGGGCTTA CAAAGCTCAA  
 1260  
 AGGACGCAAA GCGGTTACCC GAGGTATTTG GCGAAAAAGT GGCCAATGAA TTGGGANTTG  
 1320  
 GTTATTGGGA AATGAATCAA ATGTNGGAGC AATTTTAAACA TTTTTCCTCA CGACAAAGCA  
 1380  
 TATTGCGGTT GACTCATATC ATTAATTGCA CTACCAATGA TTATTGTTAA TAGCGTTGGT  
 1440  
 ACGGCGATTT TTATGTCTAT TATCATTTCC AACATTAAAA GCAAGAAGAG CAAATGAAGC  
 1500  
 CTGTTCCAAA CACATGACGT ACTGCAATTG ATGAACCAGA CATTGCCGTA TTTTAAAGAA  
 1560  
 GGATTGAATA GAGAATCGGC ACAGCAAATT GCGATGATTA TTAATAATTT AATGAAAGTA  
 1620  
 TCTGCCGTAG CAATTACAAG CAAAAATGAA ATCTTATCGC ATGTAGGTGC AGGTAGTGAT  
 1680  
 CATCACATAC CAACAAATGA AATATTAACA AGTCTGTCTA AAGATGTATT GAAATCAGGA  
 1740  
 AAGTTGAAAG AAGTGCATAC TAAAGAAGAG ATTGGTTGTA GTCATCCGAA TTGCCCGCTT  
 1800  
 AGAGCAGCTA TCGTGACACC ACTTGAGATG CATGGTTCTA TCGTCGGTAC ATTGAAGATG  
 1860  
 TATTTTACAA ACCCTAATGA TTTAACTTTT GTGGAACGTC AACTTGCAGA AGGATTGGCA  
 1920  
 AATATTTTTA GTAGCCAAAT TGAAC TTGGT GAAGCCGAAA CGCAAAGTAA GTTATTGAAA  
 1980  
 GATGCTGAGA TTAAGTCATT ACAGGCACAA GTGAGTCCAC ATTTTTTCTT CAATTCAATT  
 2040  
 AACACGATTT CAGCTTTAGT TAGAATAAAT AGCGAAAAGG CACGAGAGTT ACTATTAGAA  
 2100  
 TTGAGTTATT TTTTCAGAGC GAATTTACAA GGCTCAAAGC AACATACGGA TTACTTTAGA  
 2160  
 TAAAGAGTTA AGTCAAGTGC GTGCATACTT ATCACTCGAA CAAGCACNGT TATCCAGGAA  
 2220  
 GATTTAATAT CAATATTAAT GTTGAAGACA AATATCGCGA TGTGCTTGTA CCACCATTTT  
 2280  
 TAATTCAAAT TTTAGTTGAA AATGCCATCA AACATGCGTT TACGAATCGA AAGCAAGGTA  
 2340  
 ACGATATTGA CGTGTGAGTG ATTAAAGAAA CTGCAACACA TGTACGTATT ATTGTACAAG  
 2400  
 ATAATGGTCA GGGTATTTCT AAAGATAAAA TGCATTTGTT GGGAGAAACA TCTGTAGAAT  
 2460  
 CAGAATCTGG AACTGGTAGT GCTTTAGAAA ATTTAACTT ACGCCTAAAN GGATTATTTG  
 2520  
 GAAATCCGC AGCATTACCA ATGTGAATCC GACATCGAGN GGTACCACTT TTTGGTGTGT  
 2580  
 ACCTTCCTTA TGAAAGACAA GAGGAGGAAT AAATATGAAA GCATTAATCA TAGATGATGA  
 2640  
 GCCATTAGCA CGCTAATGAA TTAACATATT TATTAAATGA AATTGGTGGT TTTGAAGAAA  
 2700

TTAATGAGGC AGAAAATGTA AAAGAAACAT TGGAAGCACC TACTTGATCA ATCAATATGA  
2760  
CATTATATTT TTAGATGTCA ATTTAATGGA TGAAAATGGG ATCGAATTAG GAGCTAAGAT  
2820  
TCAAAAGATG AAAGAGCCAC CTGCGATTAT TTTTGCAACT GCACATGACC AATACGCAGT  
2880  
ACAGGCATTT GAATTAAATG CGACAGACTA TATTTTGAAA CCGTTTGGTC AAAAACGTAT  
2940  
TGAACAAGCA GTCAATAAAG TGCGTGCGAC TAAAGCCAAA GATGATAATA ACGCAAGTGC  
3000  
AATTGCGAAT GATATGTCCG CGAATTTTGA TCAAAGCTTA CCTGTTGAAA TTGACGATAA  
3060  
AATTCACATG TTAAAGCAAC ANAATATTAT TGGGATTGGC ACACATAATG GTATTACAAC  
3120  
CATACATACA ACGAATCATA AATACGAAAC AACAGAGCCA TTGAATCGTT ATGAAAAACG  
3180  
ATTGAATCCC ACTTATTTTA TACGTATTCA TCGTTCATAT AG  
3222

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATCAATGTAA CCTAATAGTT TATGTCTATC TTGTGTACCA ACTACTACAT CGACACCAGG  
60  
AATTTCCATA ATTTTCAGCTG ATGAAGTTTG CGCATAACAA CCTGTTACAC AGATTACAGC  
120  
ATCAGGATTG TGTCTTATTG CACGTCTAAT TATTTGACGA CTTTTTTTAT CACCTGTATT  
180  
CGTTACTGTA CAAGTATTAA TAACAAATAC ATCAGCATTG GCTTCAAAGT CAACGCGCTC  
240  
ATAGTTTGCT TCTTTAAATA ATTGCCAGAT TGCTTCAGTT TCATAATGGT TTAATTTTACA  
300  
ACCTAATGTG TGAAACGCAA CTGTTGACAT AAATATTCAC CCCATTAATT CTTTTTCATA  
360  
ACTTATTGCA CTTAACGCAT ACAATGGCGC AGTTTCTGCC CGTAAAATTC TCGGTCCAAG  
420  
ACCAACAACGT GTACTAGTAT TACTAAATAA TGAAATTTCA ATTTCTGACA AACCACCCTC  
480  
AGGACCAAAA ATCATCAACA CTTTATCCTG AGCCTTGAAT TGTTGTAAAG TNTGCTTGAA  
540  
ATTGCTTAAC TCACCATCTT TTGCTTCCTC TTCATATGCA ATAAGAATAT AGTCNTAATT  
600  
ATCAATAGTA TCACAAATTA ATTTTAAATT CCGACTCCGA ATTGAATAGA TGGAAATCCAC  
660  
TAAACGAATA GCTTTGTTCA GCAGCTTCTT TAATTATTTT TTGCCAACGC TCTATCTTTT  
720  
TGACAACCTT CGCCTCCGTT TAATTTAACA ATTGAGCGTT CCATGCTCAC AGCTATAAAT  
780  
GATGAAGCAC CCAATTCATA GCTTT  
805

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
GGCACGAGCG TAGATTTAGC ATTTTCAAGA GACCAAGAAC ACAAAGAAAT ATGTACAGCA
60
TCGTATAATG GAAGAAAGTG AACGTTTCAA TGAATGGATT GAGCAAGGCG CAGCAATCTA
120
TATTTGTGGC GATGAAAAAT GTATGGCGAA AGATGTCCAT CAAGCCATTA AAGATGTATT
180
GGTAAAAGAA CGTCATATTT CTCAAGAAGA AGCAGAGTTA TTATTGCGAC AAATGAAACA
240
ACAACAACGC TATCAACGTG ATGTTTATTA GCGATTGGTG TTAAATATTT TAAGGTGTAA
300
TGATGTAAAA AGATATAAAG GATGTTGCTC AACATGAATA TGCCATTAAT GATAGATTTA
360
ACAAATAAAA ATGTCGTCAT AGTTGGNTGG AGGCGTCGTT GCAAGTCGTC CGGGCACCAA
420
ACATTAAATC AATACGTTGA ACATATGGAC GGTCAATCAGT CCGACAATCA CTGAAAAACT
480
TCAAAATATG GTAGATAACG GTGTCGTCAA TATGGAAAGA AAAAGAATTT GAACCAAGCG
540
ATATTGTAGA CGCGTATCTA GTTATTGCAG CAACCAATGA GCCACGTGTC AATGAAGCGG
600
TAAACAAGC CTTACCTGAG CATGCCCTTT TTAATAATGT TGGAGATGCA TCAAATGCCA
660
ATGTTGTATT TCCAAGTGCA CTACACCGCG ACAAGCTAAC TATCAGTGTA TCAACTGATG
720
GTGCGAGTCC TAAGTTGACA AAATCAATTA TGGCAGAGCT TGAGGCGTTA TATCCACCAT
780
CATACAGTTC GTATATCGAC TTTTATATA CTTGCCGACA GAAAATAAAA GTACTTGATA
840
TAACATATAT ACGAAAAGCA ACAGTTACTG TCACAAATTG TGTCACAAGA ATATTTAAAT
900
CATGACAAAC AAGCTCAATT TTTAGCGTGG TTGGATGTAA GATAATAATA GCGGACCGTC
960
TAACCGTCTA AGGTAAGTCT TCTTATTTTA ACTTTAACGC TTAATCATTG AAATTAAGAC
1020
ATGGGTGGCT TTGTGAATAG TCTAATAATG AAGGATTTAA GCGATAATGA TATGCGTTTT
1080
AAATATGAAT ATTACAATAG AGAAAAAGAT ACGTAGAACA AACTTAATAA AATAGATGGA
1140
TAAATTGAAA TCTGGTTGAA GTCGTTACTA TCATAGCGAC CTTTAGCCAG ATTTTTTGTG
1200
CAATAGAAAG CAATAATAAA AATGATAGAT CAANATGAAA TACAGGACAG GATATACAAG
1260
GATTAGTCAT GCCATGTTAT CAAGTAGGAA AATCAAACCT CACTATTGAT AGTTACGCAN
1320
AAAGATTTTT TTGATAAAAT GAGATAACTT AAAGATAAAA AATTATATTA ATTATAATAT
1380
TTAAGTTAAA GAGGGGGATT ATGTAAATTG TATTTAAAGT GGAGGGAGAA AATAATATGA
1440
ATAGTGAG
1448
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
CGACATGGAA GAACNTANAC CCTCGTNNAG GAGGCCCAAGA AAGGNAGCNT NAAGNNAAT
60
TAAGNNAAGC GAAAAGCACC AACAATAAAA CCTGATGGCA GCATCATTCA ATGCGTGCCA
120
CCAGGTTTTT ATGTTTTGTC AAGAAAATTA AATAAATCAT TAAATGATTC GGCCCATCGT
180
AGGATGTGAA TAAATACTAT CTCGTAATAC GGTATATGGA ATGTTTTGAT CAATCGCAAG
240
TTTAATTATA TTAATTAATT CTTCAGATTG CTTACCATAT AATGTAGCAC CTAAAATCAT
300
ATTATTTTCA TTATTAATGA CTACTTTAAA TAAACCTCTT GGATCATTGT TAATTTTGTG
360
ACGAGGTATA GCACTTACTA AAAGTTGATG TTCAGTGTA TCATAATGTT GAGCGGCAGC
420
TTCTTTACTA GTTAATCCAA CACGTGATAA TGGTGGATCT ATAAATACTG TATAAGGCAC
480
GCTACCTCTA TTGTCAGTCG TACGTGACTG ATTACCATAT AACGCTGATT TGATAATTCTG
540
ATAATCATCT AAAGATATAT ACGTAAATTG AAGTCCGCCT TTAACATCAC CTGCAGCATA
600
AATATGTGGC ACAGATGTTT GAAGTTGAGC ATTGACTTTA ATTTTCGCCTC TATCACCTAA
660
TTCGATATCA GTATTTTCTA AAGCTAAGGC TGTATTCGGT TTGCGCCCGA TAGCCAAAAG
720
TACTGCATCA GCCTCANAGT TGCCAACATT AGNACGGACT GTTGTATGAT GATCGTCAGA
780
TGACAATTCA GTCGTTTCAA CATTTGTATG CAATGCAATG CCTTTATTTT CTAAGTCAGT
840
AATAGCATGT GCANCGACAT CTTGATCTTC GCCGTGGCAT AAATGATTCA CCACGTTCTA
900
ATACNGTTAC CTTACTACCT AAATTCGCAA ACATTGAAGC AAATCTAAG GCAATATAAC
960
CGCCACCTAC AATAACGAGA TGCTTAGGTT GATAGCTAAT GTTTAATAAA CCTGTTGAAT
1020
CGAAGACATG TTTAGCTTGA TCAAGGCCTT TTATGTTAGG AATGATAGAG GTAGCACCGG
1080
TATTAATAAT GATATGAGGT GCAGTAATAC TAGCGACGAT ATCGCCG
1127
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAAGANATAN CGTGGTNTTG AAGATTTGGG ANGTTAATAG ATNAAGGGGA ATATGCANTT  
60  
ATTACCGGGA GNNNAGTATC CAAGNAAATC TAGAGTCAAT AGGTTAATAA TCTTATGCCT  
120  
TTTTAATTTT GAATAAAAGT GGGGTGGTGT AATGTTTGA TTTACCCANC CGACCCGAAC  
180  
AAGATTGNCG TTTNACGCGA TTAGAAGNAA ATGATAAGCC TATGTTTGNN AAATTCGACA  
240  
GAATAGAAGA CAGTCTGAGA ACGCAAGAAA AAATTTATGA CAAGTTAGAT AGAAATTTTCG  
300  
AAGAACTAAG GCACGAGCGA CAAGGTAGAA GATGAAAAGA ATAAAGAAAA GAATGCCAAA  
360  
AATATTAGAG ACATAAAAAT GTGGATTCTA GGATTAATAG GGACGATCTT CTAAGTACGA  
420  
TTTGTCATAG CCTTACTAAG AACTATTTTTT GGTATTTAAA GGAGGTGATT ACCATGCTTA  
480  
AAGGGATTTT AGGATATAGC TTCTGGGCGT GCTTCTGGTT TGGTAAATGT AAATAACAGT  
540  
TAAGAGTCAG TGCTTCGGCA CTGGCTTTTTT ATTTTGATTG AAATGAGGTG CATACTGGG  
600  
ATTACCTAAT CCGAAAAATA GAAAGCCAC AGCTAGTGAA GTGGTTGAAT GGGCGTTATA  
660  
TATCGCTAAA AACAAAATAG CTATTGATGT ACCTGGTTCT GGAATGGGAG CACAATGCTG  
720  
GGAATTTACC TAATTATTTA CTCCGATAAA TATTGGGGAT TTAGAACATG GGGAAATGCT  
780  
GATGCTATGG CTCAGAAATC CAATTAATAG AGGTAGAGAT TTCAAGATAA TTAGAATCAA  
840  
AAGACTTGGT ACACAACCAG GCGACTGGGT TTTTGG  
876

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCACGAGCG GCACGAGCGT GTTGATCAAA GATTTTGTAG GCAGTTTTAC AACGTCCGAT  
60  
TCAGCAAGTT ATGCACAAGA TTTTAAATCT GAGGAAAACG CTAAAAAGAT TGCTGAAACT  
120  
TTAAATCTTT TATATCAATT AACAGGCAAT CAAAACGGTG TGAAAGTTGT GAAAGAAGTT  
180  
GTGGATAGAA CTGACTTGTC ATCTGATAAA TCAGTTGATA GCGAAACAAT GTAACATAC  
240  
TAAGTTATGA GCATTACGCT CATAGCTTTC TTAGAAAAGTA GGTGTAGTTT TGGATGATAT  
300  
TCAGAAAATA AAAAAAGAGC TTTCTGAATT AGTTGAACGT GTTGATGATG TTGAAATACT  
360  
AGCAAACGAA ACAGCTGATC ATGTGCTTGA ACTTAGAGAG GAACATAAGC AACATCATAA  
420  
TGAACATAAGA GAATCTCATA AAGAACTTAA AGATAAGCAA GATAAAGTTG TAGATGAGAA

480  
 TTTAGAGCAA ACAAAGATAT TAAACAGAAT TGAAGAAAGA TATCANACGC AAGTAGNTGT  
 540  
 TGNGCAAAAA AATGAAGAAA AGACACTCGC CCAAAATAAA TGGCTCGTAG GTGCCATATG  
 600  
 GGCGCTTGTA ACAATTGTTA TGATTGCAGT CATTACTGCA TCAATTNCTG CGTTATTACC  
 660  
 TTAAGGGAGG TGGACATAAT GAGTTGGGCA AGATGGTTAT CATGTTATTT GTNTGGTCGT  
 720  
 AAATGTAAAT AATGTTTTTG GTCAGTGCAT CGGCACTGGC TTTTTATTTT GATTGAAAAG  
 780  
 AGGTACGTAC ATGGTATTAC ACAGCTCACA AGACAGGAAG CATACTCCAA GTGAAGTTGG  
 840  
 GAAGTGTTGT TAATACCAAG TAAGTAGGAT ATCTGANATG TATAATAGAG TAAAAATGAA  
 900  
 ATCTTTTTTAT TATAGACACA TATAAAAAGT GTATAGTAAT ATATGTATGT ATAATTAAAT  
 960  
 GATAATCATT TCATAATTAT TGTATATAAC TAAATAACTA CTTAACANAA ATAATTATGC  
 1020  
 TTTAGAGNTG ACCANNATGA NNNANNCCAG CATTTACATT ACTTTTATTC ATTGCCCTNA  
 1080  
 CGTTGACNAC AAGTCCCANT TGTAATGGT AGCGAGAAAA GCGNAGNAAT AAATGCGAAA  
 1140  
 GATTTGCGAA AAAAGTCTGA ATTCCAGGN ACAGCTTTAG NCAATCTTAN NCANATCTAT  
 1200  
 TATTACNATG NNANAGCTAN AACTGAAAAT AAAGAGAGTC CNCGACCACA TTTTACAGC  
 1260  
 ATACTATATT GTTTANAGGC TTTTTTACAG ATCATTCGTG GTATANCGAT TTATTAGTAG  
 1320  
 ATTNTGATTC NNAGGATATT GTTNATAAAA ATAAAGGGNA AANAGTAGAC TTGTATGGTG  
 1380  
 CTTATTATGG TTATCAATGT GCGGGTGGTA CACCACACAA AACAGCTTGT ATGTATGGTG  
 1440  
 GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA AAAAGTGCCG ATCAATTTAT  
 1500  
 GGCTAGACGG TAAACANAAT ACAGTACCTT TGGAACGGT TAAAACGAAT AAGAAAAATG  
 1560  
 TAACTGTTCA GGAGTTGGAT CTTCAAGCAA GACGTTATTT ACAGGAAAAA TATAATTTAT  
 1620  
 ATAACTCTGA TGTTTTTGAT GGGAAGGTTT AGAGGGGATT AATCGTGTTT CATACTTCTA  
 1680  
 CAGAACCTTC GGTTAATTAC GATTAATTTG GTGCTCAAGG ACAGTATTCA NATACACTAT  
 1740  
 TAAGAATNTA TAGAGATAAT AAAACGATTA ACTCTGAAAA CNTGCGTAG  
 1789

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGATCTACAT TCGCTGCGCC AATACACACA ATAGGATAAT CTTCAATTTAA AACATATGCC  
 60  
 TTTCCCATAA CATATTCCTT TTGTATTAAT CCTGAAATAA TGTTTGCTAC GCTGGGTCTA

120  
 GATAATCCAA TTGCCTCAGC AAGTTCACGT TGTGAAATAA NCGGATTATC TTTAATTCTT  
 180  
 TTTAAAATTT CTTTCTCAGN ATCGCTCATA ACCATCCCTC CTCATATTGA CTTAAAATAC  
 240  
 TTGAATCAGT GAATTCACCA AAAATATCGT AGCATGCTGT TATTTCTGTT GTAAACGCTT  
 300  
 ACATTTTNCC GTTATATCAA TGATATTTGT TTATAAAATA CGCATAATTT CGTAAAAAGT  
 360  
 AAGTTCATTG CCATCGTGTA AAAGNTACTC GAGCAAATGA TAAATGTTTA TACAGTATGA  
 420  
 TATTTGTCGA CAATAAATTA TGACATTTTT ATGTCTTATA TTTTCTATA AAAAAACGTG  
 480  
 ACTCATTATC GATTTTTTCA TCGACTGAAT CACGTTACGA TGTTTTATTT GTTTTNCTA  
 540  
 TTCAATATGA TGATGCTATG CGTCCAACGT CACCTCGATT AATCATGTCT TGCTTAGTAA  
 600  
 CAATTGGATA TTTTTTAAAT ACGGATTGAA CCAAGATAA CCCTGCAAGC GCACCCTACA  
 660  
 ATCGCCATTA CTACACCATA AATTACAATA GTCATTGGAT GATTAAATCC ANACATTACT  
 720  
 AAAAATCCTN CAATCGGTGT AGCTGTACCT GTCGCATCGT TAATTAAACC TGACATAGCA  
 780  
 ATAATTAAAC CAGCAATCGC ACCACCAAAG AAATTTGTAA TATAGATTGG AATTGGATTG  
 840  
 GCTGATACAA TATCTGCTTG TGATAAAGGT TCAATACTTA CTGCAATCGT AGACTTACGA  
 900  
 TCACCTAATT TTAAGCGATG GAATAGCGTC CCATTCATAA ATGCCGAAC TAAATGCTGCC  
 960  
 ATGGCACCAA TAGCCATAGG TACACCCGTT AAACCTAATA ATGCTGTCAA TGCCATTGAA  
 1020  
 CTCAATGGCG CTGTGCCGAC AACCGTGATA ATACCACCTA AAATGATACC CATGATAATT  
 1080  
 GGATTCGTAT TCGTACTACT TTGGATAATA TCACCAATTC GAATCAATGT ACTATTCACT  
 1140  
 ACTGGCGTTA ATAATACTGC AATAAGACGA GCTAATGGCG CTAAGATGAC AATCGGATCC  
 1200  
 AATTAAAGTCG ACAACCATCC GGGCACATAT TTCTCTTGTA TATTTTCATCA CATATCCAAT  
 1260  
 CAATATTTAA CCCGNAAGG AAACCTGGGT AATAAATCCA TACCACCGCA ACGCTCGGGC  
 1320  
 CGGTTATTAA CTTAATGGAT ATTCTGGGGG ATACAACCGA TTAGGTTAAT GCTTGTTGAA  
 1380  
 TCCCAGGCGG GAGGGGACAA CAACCTAGGA  
 1410

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AATTATCCG GTTTCGCCGT CTTTGTGTTGT GGCTATGTTA CATTCAACAA TAGATTTGCC  
 60  
 AGTGATACTG TCATCTTCGT CACGGTTATA ATAATCATCA CGGTAAAGTA GCATTGCTAA

120  
 ACTTGCATCG GCTTCTATTC CGCCTGATTC TTTCATGTCT GATAGCATTG GTCGTTTATC  
 180  
 CTGCCCTAGAT TCAACACCAC GATTTCAGTTG TGAAAGTAGT ACGATGATTG CGCCTGTCTC  
 240  
 GTTAGCGATT ATCTTTAAGT CACGTGATAT CTTTTCTACT GCTACACGTC TATCAACTTT  
 300  
 CGCATCAGTA TCCATCAGTT GAAGATAATC TATAAAAATA ACTTGGTTGC TCGGTCTGAA  
 360  
 TGCCTCATTG GTTTGAGCTC GCACATCTTG CGGTGGTAAT ATTTACTTTT GGTCAAGAAA  
 420  
 TATCAAATAC CTAAC TTCAA TGATTTGGAT CCCATTGCAT TTGT TAACTT CGTTAAGTCA  
 480  
 TCCGGTGTTA AGTTCCTGAT TTCTTTTATC TTGGTTAACT CAATACCAGT AATTGTTGAT  
 540  
 AACATACGTT TCAATACTGA TGTGCCAGTT GTTTC AAGAC TAAAGAAAGA TGTTTTATAT  
 600  
 CCATTTTCGTG CTATGTTCAA CATCATGTTT AATGCAAAAC CTGTTTTTACC CACTGAGGGA  
 660  
 CGCGCGTGCC ATGACGATTA ATTGCGACGG CTCTAATCCC CCTATTTTGT AATCCATGAG  
 720  
 CTTATAACCC GTCTTAATTT GCTTCTTAGG GCTATCGCTG TATAACTCAT CAACAACTC  
 780  
 CTCAACAAAC TTCTTG GTTC CATCTTCTTT TTTGT TAGTA ATCGTTTTTA AATCCTTGAG  
 840  
 TTCATCAATC AAGTTGT TAA AGTTTTGGTT CGTAGGTTGT TGTTTAACT CAGTTACCAA  
 900  
 TTCGTTAGCT TTGTTGAGCT CGTGCC  
 926

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCAATAATCC ATTNCAAGGC TTTTTCGTTG CCCCAATNAA GAAGCACGAG ACCCATCCCC  
 60  
 GCTATTAAAT ACCTGCAATT TGAAATTTGC CAAGGGCACC ATGGTGTGAC CGACAAGTAT  
 120  
 TAAAATCCTG CACCAGCGAA AAGCATTACC TAATGAATTA TTATCATTAA TCGATATTAT  
 180  
 TGTGCCAAAC GAAACAGAAG CCGAATTGTT ATCTGGGATT AAAGTAACTA ATGAACAATC  
 240  
 TATGAAAGAC AATGCCAATT ACTTTTTATC TTTAGGCATT AAGACTGTTT TGATTACGCT  
 300  
 AGGTAAGCAA GGTACATATT TTGCTACTAA AAATCAAAGC CAACACATCG AAGCTTATAA  
 360  
 AGTAAATGCG ATTGATACAA CTGCTGCAGG CGACACATTT ATTGGTGCAT TTGTCAGTCG  
 420  
 CTTAAACAAG TCGCAAGATA ACTTAGCAGA TGCTATTGAT TTTGGTAATA AAGCGAGCTC  
 480  
 ACTCACTGTA CAAAAACAC GGCGCGCAAG CATCTATTCC TCTACTAGAA GAAGTAAATC  
 540  
 AAGTTTAAAT GAATCAAACA CAGCTATGAT ATGAAGGTTT AGCATATAAC ATGCAACATT



600  
 CGTATATCAT GGCTGTGCTT TTTTATCTTT ATAAACATC ATCTATTAGA AATAATTTTC  
 660  
 CACTAAACCT ATGCTTGTTG ACTCATGTTT AGTTATAAAT GAAGTGACAA TTTTTTGTAA  
 720  
 TCTTTTAAAC TTCCAAATTA TTGCATATAA ATATGCTATA TTAATGATAA TAATTATCAA  
 780  
 TTAAAAGGAG GTTATGCTAT GTCTAAAGAA GCTGGTCATA CATTTTTAGC TAAATTAGGA  
 840  
 AAAACTCGTC TACGCCCCGG TGGGTAAAGA AGCAACAGAT TGGNTTAATA CANCAAGGGG  
 900  
 CATTTTCACA AGATAAACAA GTGTTAGAAG TGGCATTGTA ATATTGTGCA CAACATCTAT  
 960  
 TTATCTAGCT CATACATATG GCTGTCACAT TCAAGGCGTT GGATATAAAT AAGAAAGCAT  
 1020  
 TAGAAAAAGC ACAGGAAAAT TTCCAGCAGC AGGTCTTGAA TCATATATTC AAGTTCAACA  
 1080  
 AGCGAATTGC TGTTAAATTG CCCTTTGATG ACAATCAATT CNATGTCGTT TTAAATGAAG  
 1140  
 CAATGTTAAC AATGTTACCC ATCGCCATAA AGGAAAAAGC ATTACGCGAG TNCTACCGAG  
 1200  
 TCATAAGCC NGGGGGTNTN TTGTTAACCA CATGATNTTG TCATCGTTAA TGAATCANAT  
 1260  
 NCCACANATG TTGTAAATC ATTATCTGCA GCAATTAATG TCNATGTCTC ACCGCAGACG  
 1320  
 AAACCTGGCT GGTTAGATTT ATATCATCAA AGCTGGTTTT AATCAGGTGC ATTATCCATA  
 1380  
 CTGGTCCATG AGTTTAATGA CACCAA  
 1406

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGACGTAATN ATACGCCTTT TCTGATTATT TCTTTACTAT TCTAAAACT GTTGTCTAC  
 60  
 TAATACCTAC CATTTTGAAA TTTCATTTGG CGTGTACATT CTACTTGCGA ATAATTGTTT  
 120  
 AATATATTTA CGTTTATCTT CAGAAAGTTG AGGTCGTCCT CCATACCTAC CACGTTCTTT  
 180  
 TGCAGATTCT AGACCATTTG TTGTTCTTTC TTTTAATAAT ATATTTTCTG AATCTGCTAA  
 240  
 CATTTTAAAT ACTTCAATAA ATGATTGTCC TTCTTCACTA TTAGTATTTA TGCCTAAATC  
 300  
 AAGCACTTCT AAATGGATAT CATATGGTAA TATTCTACTT TCAAAAAATT CCATGAGTTT  
 360  
 TTTTGGTGTG AATCCTAGTA CTTTAAATTT TTCTATCACT AATGTATCAT CTGTTTTCAA  
 420  
 CTCGTCTAAA CAATGCTCAA GTTCTAGTTG TTCTTTATAA TAAACATTTA CTGCTCAGA  
 480  
 ATAAACTAAG TCACAACCAT TTATTAAGAG TTTCGTTAAT TGAGTATCTA GATTTTGATC  
 540  
 AGGATATGCT ACACGTGCGT AACCAATTTT CCTCATTTTA TACACCCTTC CAGCTTATTC

600  
ATTTTCTCCG ATTAATAAAC CTTGCTCGT GCCGTTTCAA CAAGTCGGGC CCTG  
654

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCAAAGGCTT TGAAGATATG AGTGGTAAAG AATGTACCTA AGGATGACAT TGAATAGAGG  
60  
GAGTAAAGAA AGCGACAGCT GATGCATCCT CGCTAGTTTG GACGGCATGA ATAGAATGAC  
120  
GTTAGGAAAT GAAGTTCTGA CTAACAAAAA GATTGAAACT GAAATCAAGA TGCTTGAGAA  
180  
AAAAATTGAC CAAATGGATA AATCAGAAAA TAATTCACAA GAAGCAGAAG TTGCTAAAGC  
240  
ACTTATTAAG TTAGCGGGTG TTAATAATGA TTAATGAAAT GTTAAACCCG AAACAACAAG  
300  
AAGTCTGGAC CTGCTTTATA AACGATAAAC CCAAAGTATT AATAGCGAGT GGTGCCAAAA  
360  
GGGCAGGTAA AACATATGTG TTCATCCTGC TTTTTTTAAT GCATATAGCT ACTTATAAAG  
420  
ACAAGGGGCT TAACTTCATT ATTGGAGGAG CAACACAAGC ATCTATAAGA CGTAACATAC  
480  
TAGATGATAT GGAGTTAATA CTAGGTAGAG AGTTAACACT CGACAAATCT AACGCAGTCA  
540  
AAATATTCGG TAATAAAGTG TATGTATTCG ACGGACAAAA CTCGGATGCA TGGAAAAAAG  
600  
CGCGTGGTTT TACTTCAGCA GGTGCTTTTT TAAATGAGGG AACAGCATTA CACAATATGT  
660  
TTATTAAAGA AGTGTCTCA CGTTGTAGTT ACAAAGGCGC GAGAATATTA ATTGATACCA  
720  
ACCCCGAAAA CCCGATGCAT CCAGTTAAAA AAGATTACAT TGATAAGAGT GGTCAACGGT  
780  
TATCGAATGG AAGACTAAAT ATCAAAGCAT TCCAATTTAC TTTGTTTGAC AATACATTTT  
840  
TAGATGAAGA ATATATTGAA TCGATTATCG CAAGTACACC AACAGGAATG TTCACAGATC  
900  
GTGATATTTA TGGTAAGTGG GTTTCTGCTG AAGGTGTTGT ATATAAAGAT TTCAAAGAAA  
960  
AAGTTCATTA CATCACAGAA GAAGAATTTA AACTAAACA AATAAAAAGG AAATATGCAG  
1020  
GCGTCGACTG GGGATATGAG CATTATGGTT CTATTATGGT TGTAGCGGAA GACTTCGACG  
1080  
GAAACAAGTA CGTTATTGAA GAACACGCAC ACAGACATAA AGAAATAGAT GACTGGGTAG  
1140  
CTATTGCAA AGAGTTATAA AAGCATGGCG ATATCCTTTT TATGTGATAC GCTAGACCTG  
1200  
ACATATTGAC ATT  
1213

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
CATTATTATT TGTCGTTAAA TACAATAGAA AATACTATAC CTGTATATGC AATTCGACAA
60
TAGATAAATT ATTAAATATG CTTACAACAA TCTTAATATC CTTTAACGCA CTACAATAGT
120
GCTCTGATAA TAGGTTATAA ATGTACGTAA AACCATTGTC TCAATAAAAA TGAAAACGTA
180
TACTTCAAGA AGGATGGGTT ACTTAATATA AACAAGGGGG TAACATATAT GACTTTATAT
240
TTAGATGGTG ANACACTAAC AATTGAGGAT ATTAACATCAT TTTCACAACA ACACTCAAAG
300
ATTGANATTA TTGATGATGC GTTAGAACGT NTCAAAAAAA GTAGAGCGGG AGGTGAACGT
360
ATTATTGAAA ATGANGAAC GGGNTTGACG GGTATCACTA CAGGGTTGNG GGGTTTATTT
420
AGTGATGTAC GTATTAGCAC CCGACGCAAT ATNATGAATN ACAAGTGAAT CTGATACGCT
480
CACATGCCTG TGGACTAGGT GAGCCATTTT CAAAAGAAGT AGCATTAGTC ATGATGATTT
540
NACGATTGAA TACATTATTA AAAGGTCATT CAGGTGCCAC TTTAGTAATT AGTGAGACAA
600
TTACAATTTT TTATAAATGA ACGTATTATA CCGATAATCC CACAACAAGG CTCTCTCGGT
660
GCATCAGGAG ATTTAGCGCC ATTATCATAT TTAGCATTAG CATTAATTGG TGAAGGGAAG
720
TATTGTACAG AGGGGAAGAA AAGGATAGTG ACGATGTATT AAGAGAATTA AATAGACAAC
780
CTTTGAACCT TCAGGCTAAA GAGGGTTTAG CATTGATTAA TGGTACGCAA GCTATGACAG
840
CTCAAGGTGT CATTAGTTAT ATAGAAGCAG AAGATTTAGG TTACCAATCT GAATGGATTG
900
CTGCATTAA C GATCAGTCT CTTAATGGCA TTATAGATGC ATATCGACAT GATGTGCACT
960
CTGTTCTGTA TTTTCAAGAA CAGATTAATG TGGCAGCGCG TATGCGTGAT TGGTTAGAAG
1020
GATCAACATT AACGACGCGA CAAGCAGAAA TACGTGTACA AGATGCATAT ACGTTGCGTT
1080
GTATACCACA AATCCATGGC GCTGGTGCCC AAGTATTCAA TTATGTTAAA CAGCAATTAG
1140
A
1141
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TTTGTGCTTC GTCAATCTTG TCACCANCTA ACTCTAAACG CTTTCCTTTT GTCGTTTTTCG  
 60  
 GGNTCCCACC ACAATTAATC TGTTTTGATT TCTGACATAT CAATCTTCCT AGTTAACCCA  
 120  
 AGCCAAATCT TTACCATACT CAATTTCTTT ACCTTGGAAC AAGCTGTTTT TCTTGTTGAG  
 180  
 TACCACATAT CTACCTTTGA CGGTATTAGA ACTAAGCTCT ATATAAAAAT CCAATGCCAT  
 240  
 TTTATAGGTT GTACATAATT GCTTTAAAC TTCATATCTA GTNTGATAAG AAGTCCATGA  
 300  
 CGTAGTACGT AAGCCATCGT ATTCGGTNTG TTCAGAACT TCCCAACCTG TATCGCTCAA  
 360  
 CACATCTTTC AATGCTTCTG AAGTTGTCTT TTTCTCAAAT TTGCCTGGTG CATACGGTTT  
 420  
 AGCTGTTGTT ATATCAGCAA GATAAGACGC TATACATTCT ATCTCTGTGT AGCCGTCCT  
 480  
 CGTATCTTGA ACCCAGTTAA TAATAAATTC ACGCCATTGT TTGTTTGAAT CCCTTATAAT  
 540  
 AACACGATGT CGTTCACGGA ACNTTTCAGC TCTTCTGAT GATATGAGCA GTTCAAGCAT  
 600  
 TTCTGAATTG TCATTAACAT TACGTTTATG AATCGCTCTA ACTAAGGAAG GATCATCAGT  
 660  
 AGAAAGGAAA TCTATAATCT TGTCGTTAAA ATCTAAAACA TGTATCACAC TCTCATCTCC  
 720  
 TTTCTATAAA TATCTATCTT GCCATTTAAC CGTCGTATCA AAGACGTTTT CAGGTTGTAT  
 780  
 GATTAATTCA CTGTACCCAG AATCAACATT GAAATAATTA CTTCCAAACG ATTTCTCGCT  
 840  
 CCAACATTGG TTCCTCATTT GATGACAACA CTTNNNGCTT GNATATCTAT TTTCACTAAA  
 900  
 TCACCTTTTT GTATAATGAC ATCCCTTGCG CCTTTCGGNT TCGGTAGAAT CTCCGTATTG  
 960  
 AATGAACCTA ATCCATTCAT CTCCATCCAC TTATAACCGT NATACTTCGC ACTATAGATA  
 1020  
 GCTATGATAG AAGCTGGACG CTGATAAAAC TTACCGCCAT CTATCCACTC TTTCTCATCC  
 1080  
 ATATCAATAG GTTTACGTCT ATCTGGGTCT TTAATGTGAT CAAATTTCCA AGTTTTAATA  
 1140  
 GAAATTTTAT TACCTACTCT TCTGAGCCGC ATATAAACAN CGATTCTGTC CAAGTTATAC  
 1200  
 ATTATCGGTT TATTCTGATA GTCGTATATC TTTTGGGGT CTCCTTTTTG GTTATACG  
 1258

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TCGAATTTGG TGTTGNCCGT TCCTGTATNA CATTCTGNCT TATCTAATGG GGGACGTTAT  
 60  
 GATGAGTGCC CACNNATTAG GGATGATCGT NCGAGAGTAA GTGTTGGTGC AAGGTCAAGT  
 120  
 GTGTTGCGCAC CTTTCCACAA ANTTAGGGTT AATCATCATT GATGAAGAAC ATGAATCTAC

180  
 ATATAAACAA GAAGATTATC CGAGATATCA CGCTAGAGAA ATTGCCCAAT GGCGAAGTGA  
 240  
 ATATCATCAC TGTCCAGTCA TTTTAGGAAG TGCAACACCA TGTCTTGAAA GTTATGCACG  
 300  
 AGCTGAAAAA GACGTTTATC ATTTGCTATC ATTACCAAAC AGAGTGAACC AACAAAGCTTT  
 360  
 ACCTGAAATT GATATAGTAG ACATGCGTGA AGAATTGAGT GAAGGTAATC GGTCAATGTT  
 420  
 TTCAAAAGAT TTACGTGAAG CCATACAATT AAGATNAAGA TCGACAGGAA CAAGTTGTTT  
 480  
 TATTTTTTAA TCCGACGTGG TTATGCATCG TTTATGTTAT GTCGGGATTG TGGATATGTA  
 540  
 CCGCAATGTC CAANCTGTGA TATTTTCATTA ACGTATCATA AAACGACAGA CTTATTAAAA  
 600  
 TGTCACTATT GTGGTTACCA AGAGACGCCA CCGAATCAAT GTCCAAATTG TGAGAGTGAA  
 660  
 CACATTCGAC AAGTAGGTAC TGGTACTCAG AAAGTTGAAG AACTATTGCA ACAAGAATTT  
 720  
 GAAGATGCGC GCATAATTAG GATGGATGTA GATACAACCT CAAAGAAAGG TGCACATGAA  
 780  
 AAGTTATTGA CTGAATTCTGA AAAAGGTAAC GGTGACATTT TACTAGGTAC TCAGATGATT  
 840  
 GCGAAAGGAT TAGATTATCC AAATATTACT TTAGTTGGTG TGCTGAATGC NGATACAATG  
 900  
 TTAAATTTAC CTGATTTTCG GGCGAGCGAA CGTACTTATC AACTATTAAC GCAAGTGGCT  
 960  
 GGTAGAGCTG GTCGTCATGA AAAGGCAGGT CAAGTCATCA TTCAAACGTA TAATCCAGAT  
 1020  
 CATTATTCAA TATTGGATTG TTCAAAAAAA TGATTATTTA ACATTTTATC GTCAGGAAAT  
 1080  
 GGAATATCGT CAAATTAGGA AAGTATCCAC CGTATTTATT ATTTGGTTAN TTTCACAATC  
 1140  
 TCACATAAAG AAATGAAGAA GGTTATGGAA GCATCGCAGC ATGTTTCATAA AATTTTATTA  
 1200  
 CAGCATTTAC AAGAAAAAGC GCTTGGTACT AGGTCCATCC TCCGGCAGCA CTTGCGAGAA  
 1260  
 TCAACAATGA ATTTAGATTC CCAAATTTTA GTGAAATATA AAAGTGAACC TGGATTATTA  
 1320  
 CAAGCCANTC AGTTTTTTAGA TGACTATTAC CATGAAAAAT TTATAAAAGA AAAATTAGCA  
 1380  
 TTGAAGATTG ATATTGGANC CACAGATGAT GATGTAACAT TACTAATTAT TAGAAACAAG  
 1440  
 NNCAAGTATT GTACGAGTAT TTGAACCCAG TGTGTGAATA TTTACTTNAN GNACAAGAAA  
 1500  
 AAGGGCAGAA TATACAACTG TTAACATTTT AAATTAGCAG TTTATATTCT GTCTTTTTAT  
 1560  
 ATGGCTTTAT AACTTACGTG ATTTTGGTTT GATAAGGAAT TTATTAGTAT TTTCATTTAC  
 1620

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

AATTGGGCAC GGGTANACAG TTGTAGCGTT ATTAAGNATT TTAAC TTTTG CGAAGTTAGC  
 60  
 AACAA TTTNC CAATGATGTT ATTTTATCAA TGTTACCTCA AGCAGCAACT ACAANCGATT  
 120  
 GCGTTACCAG TATCAGCTGG TATCGGTGGT ATAAAAGAAT TAACATCATT AGCAGNTATT  
 180  
 TTAAATGGTG TCATTATTTA TGCCCTAGGT AATAAATTCN TGAAGCTTTT CCGAATTACT  
 240  
 AACCC TATTG CCCGAGGATT AGCACTTGGA ACNAGTGGTC ACACATTAGG TGTAGCACCA  
 300  
 GCCAAAGAAT TAGGACCTGT AGAAGAATCA ATGGCAAGTA TAGCTTTAGT GTTAGTTGGT  
 360  
 GTAGTTGTTG TAGCAGTTGT GCCTGTCTTT GTAGCAATAT TCTTCTAAAA CGAAAAACCT  
 420  
 AAGCAAGATA ATAGCAATTT GAGCCATTGT TATTATCGTA AAAAAACGTC TATACTCCAG  
 480  
 TTTATAACTG GGATATAGAC GTTTTTATGT ATTTATTACT TTTTACTAGG AATATAAAAC  
 540  
 TGTGCATGNC GATAATGAAA TACGATGTCA GACGAATCAA AGGGTTTGCC AGTCATTGTA  
 600  
 TAAAAAGTCT GGTGGTAACG TAAACATGGT TCACCTGTAG ACAATTGTAG TAATGAAGCT  
 660  
 TCACTTGAAG TGAGTTTATC TACATTAAAG AAAATATCTG AAAAACCAAT ACGAAGTTTC  
 720  
 ATGTTTGATT CTAAATAATC GAAGATAGAG CCCTTAGCAA TATCATCATT TAAATATTTT  
 780  
 ACGATTTCTT TATGATAATA AGAATATTCG ATACATAAAA CATCATCGTC CACGAATCTT  
 840  
 AATCGCTCTA AATAGTAGAC GGTATCACTC GTGCC  
 875

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAACTAGTGA TTCAGGATAT AGGAATTGTA TTGTCGGAAT TCANACAGGT GGATATGGTC  
 60  
 AAGATTTAAA AAGATTATAA CTTGGCCCAA TTATNACGGN GATCTTGAAA ACGATTANTG  
 120  
 GATTAGAACG AATTCGAATT TCTTCAATTG AAGCAAGTCA ACTTACAGAT GAAGTAATTG  
 180  
 ACGTTTTAGA ACGTTCAACA AAAGTTGTGC GTCATTTGCA TATTCCATTA CAATCTGGTT  
 240  
 CAGATACAGT ATTAAAACGT ATGAGACGTA AGTATACAAT GGATAGATTT TCAGAACGAT  
 300  
 TAACAAAATT GCATAAAGCT TTACCAGACT TGGCAGTTAC GAGTGATGTA ATTGTTGGTT  
 360  
 TCCCAGGTGA AACTGAAGCA GAGTTCCAAG AAACATATGA TTTTATCGTA AAGCATAAGT  
 420  
 TCTCTGAAC TGCATGTTTTT CCTTATTCTC CTAGAATTGG CACGCCAGCT GCAAGAATGG  
 480  
 ATGACCAAAT TGATGAAGAA ATTAAAAATG AACGCGTGCA TAAGGTTAAT TACGCTTAAG

540  
CAATCAACTC GGAAAGTTAT ATGCGTCTTA AATTGGATCA AAGATGTGCT TGGANGGTNA  
600  
TTCCCTGAGG GAACAAGGGT GGACACAAGA AGGGTACAAT TAGGTGGRRD CTNS  
654

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTANCNAANG GAANTTCAGC ATCCTTAAAA ATACCTATTT GACTGTAGAA ACCTTTTGNT  
60  
GCGTACAATA TCTAAACCTT GTCGTGCTGC TGGAACTGCA CCTGAACATT CAACAACAAC  
120  
ATCTGCACCG TAACCGTCTG TAATTCCATT GATATACGTT TTTAAGTCTG TGTGTTGTAA  
180  
ATTGACTACA TAATCCATGT GCAATGCTTC TGCTTTATCT AATCTGACTT NGTGGCANTG  
240  
TCCAATCCAG TTACCACAAC AGGTGCGCCT TTACTTTTCA ACACTTGTGC TACAAGTAAT  
300  
CCGATTGGCC CAGGTCCCAT TACAACTGCT ACATCGCCAG AGTTCACCTG AATCTTAGAA  
360  
ACGCCATGAT GTGCACATGC TAATGGTTCT TGTCATAGCT GCAGACTGAT ACGATACTTC  
420  
CGCTTCTGGA ATATGATNCA AACTTTCTTC ACGTGCAATG ACATAATTAG TAAATGCGCC  
480  
ATCAACTTGT GTTCCAATAC CTTTTCGATG GTTGCATAAA TGATAGTTTT TTGATTTACA  
540  
GGAATCACAC TCATTACANA CCATAGAATG TAGTTTCAGA AGTGACNCGG TCACCAACTT  
600  
TAAATCNTT AACGTCTGCT CCCAACTTCA ACGATNTCAC CAGAAAATTC ATGACCTAAT  
660  
GTCACTGGAA AATTAACCTN ATAATGCCCT TCATAAGTAT GAAGGTCTGT GCCACAAATT  
720  
CCTGCATAAT GTACTTTAAT CTTTACTTTA TCATCTAGCG GTGTTGCAAC TTCTTTATCA  
780  
AGAAGTTCTA AGTTGCCATG TCCTTCTCTT GTTTTTACTA AAGCTTCCAC CACAAACACN  
840  
TCGANTTTTT ANTTGNAATA GACTNNATAG NTTNAAGATA AGATAGTTAN CGATATTNCC  
900  
ACCTTGATCA ATACTTGANA TTTCAGATGA ACCTTTTGNC ATTTGTACAT TCGTACCTTT  
960  
CGCCATATCT GTGAAAATGG GTGCTACGTC TGTTGCAATA TATAATGAAA TTGCAATCAT  
1020  
AATCGTACCC ACAATGACAG AATGAATAAT GTTTCCTCTT GCTGCACCAA CAATAAACGC  
1080  
GACAACAAAT GGTATAGTTG CTAAGTCACC AAAAGGTAGT ACTTGTTTTT CTGGTAAAAAT  
1140  
AACGGCTAAT AAAACAGTGA TAGGTACTAA AATTAATGCT GTCGAAATAA CCGCTGGATG  
1200  
ACCTAATGCT ACAGCCGCAT CCAATCCAAT ATAAATTTCA CGTTCGCCAA AACGTTTATT  
1260  
TAGCCATGTT CTTGCAGACT CTGAACTGG CATTAAACCT TCCATTAAGA TTTTACCAT

1320  
TCTAGGCATT AAGACCATTA CTGCAGCCAT TGACATTCCT AAATTAATGA TGTCTCCAGG  
1380  
TTTGTAACCT GCTAACACAC CAATACCTAA ACCTAAAATT AAGCCGACAA ATATAGACTC  
1440  
TCC  
1443

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTAGCAACT CAAGAAAACG TTAATTTATC AATTCGCGGA ATTCCTAAAG AAGTAGTAGC  
60  
ACGTGGTGCA CATCCATGTA TTATTTCTAT GGAGGGTCTT GAAAAAGAAG GCGACACTTA  
120  
TGTCATTCCT CATGTACATG AATTATTGAC ACCATTAGTT TCAGTAGTTG CATTACAATT  
180  
GATTTTCATAT TATGCAGCAT TACACAGAGA TTTAGATGTG GATAAACCAC GTAACCTTGC  
240  
TAAATCAGTT ACTGTAGAAT AATTCACTTT TTTAGAATCA ATCATGTATT AAAATTAAAG  
300  
TATATGGCAC CCTTTTAGAT TAATCGACTA GAAGGGTGCT TTTTLAGGTC GACTTAGCTT  
360  
TTACTTCATC TTAATTTGGC AGAAATGCGT NAAAAGGAAG TGTTTTATTT ATTTAAATAG  
420  
TCTGACAATT AAGGGTGTTA TGTTAATATG ATTTTATGAG AAGTATGGAG TAGCNATAGA  
480  
GGGGTGACCT CGCATGTTAA TTCAATTAAG ATCCACATTG GGCGANTGAA GCAAGGAAAA  
540  
ACAATTTTAA AAAATATTTT TGCCACATT CCTAAAGGTG ATAAATGGAT ATTATATGGG  
600  
TTGANTGGTG CTGGTAAGAC AACGCTATTA AATATATTAA ATGCATATGA GCCTGCGACA  
660  
ACTGGCGGTG TTAATCTATT TGGTAAAATG CCAGGCAAGG TAGGGTATTC TGCAGAGACT  
720  
GTNCGACAAC ATATAGGTTT TGTATCTCAT AGTTTACTGG AAAAGTNTCC AAGAGGGTGA  
780  
AAGAGTAATC GATGTGGTGA TAAGCGGTGC TTTTAAATCA ACTGGTGTTT ATCAAGATAT  
840  
TGATGATGAG GTACGTAATG AAGCACATCA TTTACTTAAA TTAGTTGGAA TATCTGCTAA  
900  
AGCGCAACAA TATATTGGTT ATTTATCTAC AGGTGAAAAA CAACGAGTGA TGATTGCACG  
960  
AGCTTTAATG GGGCAACCTC AGGTTTTTAA TTTTAGATGA GCCAGCAGCT GGTTTAGACT  
1020  
TTATTGCTCG TGAGTCACTA TTGAATATAC TTGACTCATT GTCAGATTCA TATCCAACGC  
1080  
CTTGCGATGA TTATGTGACG CAC  
1103

(2) INFORMATION FOR SEQ ID NO:129:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1095 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
CTGACATATT TAATGTTTAC ATCTAGTGCA TCAGGTTACG CCGTNTGTAT AGCGATGTTG
60
AGACGTTTAA CTGGATTAACTAATATCATT GGTAATTTTT ANCCAAAANA TATTGNTNGG
120
GTTTAATTGG CCCGAGTACT TTTACCANTA TCATGGTTAA NTAATTTTTT GNTGTGACTC
180
NAGGTGTACC NCCCAAACCG TTGCATGCTA ATTTAATGAT TCGGACTTTA AGCGGACATA
240
TCCAACATAT TGCATTTGGA CCTATTGCAT CACTTGAATC AATAAAACAT CTTGGTACGA
300
ATGGTGGAGG ATTTTGTAGCA GGAAATTCTG CAACACCTTT TGAAAATCCA AATATTTGGA
360
GCAATTTTAT AGAAATGGGC AGTATGATGT TACTTCCTAT GTCAATGTTG TTCTTATTTG
420
GTCGCATGTT AAGTAGACAT GTTAAACGAG TACATCGTCA TCGGTTGATA TTATTTGTCTG
480
CAATGTTTTT CATTTTTATA GCAATTCTTA CATTAACTAT GTGGAGTGAG TATCGTGGTA
540
ATCCAATACT AGCGAATTTA GGCATTTATG GACCGAATAT GGAAGGTAAA GAGGTACGGT
600
TTGGAGCAGG TTTGTCAGCA CTATTTACAG TTATTACGAC GGCATTTACA ACGGGTTCTG
660
TTAATAACAT GCATGATAGC TTAACGCCTA TAGGTGGATT AGGACCAATG GTATTAATGA
720
TGCTAAATGT TGTATTTGGT GGCGAAGGCG TAGGACTCAT GAATTTATTG ATATTNNTCT
780
TACTGACGGT GTTTATATGC AGTTTGATGG TTGGTAAAAC ACCAGAATAT TTAAATATGC
840
CAATTGGCGC CCGTGAAATG AAATGTATTG TCTTAGTCTT TCTCATACAC CCAATTTTAA
900
TTTTAGTATT TTCAGCACTT GCTTTTATGA TTCCTGGAGC AAGTGAAAGT ATAACGAATC
960
CGTCTTTTCA TGGTATTTCA CAAGTTATGT TATGAAATGA CATCAGCTGC TGGCGAACAA
1020
TGGATCAGGG TTTGAAGGAC TGAAANGAAT GAATNCAACA TTTCTGGGAA ATATCTCTAC
1080
AGGAATCATT AATGT
1095
```

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 913 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GGTGTTGTTT TCCTCCAATT TTTGGATCTT TTTTGCTCTA AAATCTCATC TTTTTTAATC  
 60  
 TAAATAGATC AAGAGTGGCG TCTAAGTTTT CTTCCTTTTG AAGAAGTCGG GTTTCCTTGT  
 120  
 CTNTGAAGAT CNCAACGTCT TTCTCGNAGT TCTGCTTCAG TNTGTTCTCT TNGGAGTTGG  
 180  
 TNTTCTTCTT TTGCNTCAAG TAATTTCTCT TTTTGTGATAN TGTCAGCTTC TTTATGTGCT  
 240  
 TGATNAACAA TATCNTCGGC AGTTTGTCTA GCTTGTGATT GCTTTTGAAG CANCANATTT  
 300  
 CGGGCNACAA CATACCCTCC AACAACTCCT AGAATGATCC CCANCACATG AGTAGGAGGC  
 360  
 TTAATAAATT CACACACACA CCTCCTTTTC TAGGGGTTTG CTCCTTTAAT ATGAAATCCA  
 420  
 ATATGACTTT ATGAAATTAA AAATAAATCA AACCAAATTA ATTTGTGCGG TTTAATAGGA  
 480  
 GATAAGTGTC AAGTTATCAA TTTGCACTTT TGCATATAT TGAATGCTAT TTCTACTATT  
 540  
 TTCTAAAGTT TTGAAGCTCG ATTATAAAAC TATTGATAAT GTAATAATAA ATAAAATAAA  
 600  
 AACCTTATA GTCTCGATTT GTAGTGTATC CCATAAAGTT AGATATTATT CTAGCTTTAT  
 660  
 GAGATGAATA TCACTTTCAA TCAATCCTAT AAGGATATTT GCTAAGTTTA ACTATAGATA  
 720  
 TAAATTTGTG TACTATTCTT CGTCAAATAA TGACTTTGGT GCATCTTCTG TTTCTTCAAC  
 780  
 ATCACCATCA GATATACCTA ATTTTCTCT CAATTTACGA TCAATTTCTT CTTTAATTTG  
 840  
 TGGATTTTCT TTCAAGTACA TTTTAACATT TTCCTTACCT NGACCCATTC GTTCGCCATN  
 900  
 GCAAGAATAC CAG  
 913

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TGANGTAAAT TTGGTTGTGG CTCANTCGCA TCTGCGAAAG NGNAGTGCCC NGAGACCGCC  
 60  
 TGTAATGTTT ATGACGACCC TAGAATAATA ATAACTAAA AGCGCCGCCT NATGAAANTG  
 120  
 AGCGCCTTGG ATGNAATCAC TCCAAACGGA CACCNTCGAA NCCACCTNGA GATGTANANG  
 180  
 AAATACATAG TAAACCTACG AGTGATCCAN CGATATAAGG GTTCATGTCT GATACAGATG  
 240  
 TGATTGCTAA TGTTGGTAAG TAGATAACAA TTGCAACACG CCCTAAATGG TAAACGACAA  
 300  
 ATAATAATGA GCCANTGACA CGTATGCTAG GGCCAAATCT AGCTTCTAAA TATTCATATG  
 360  
 CAGATGTTAC CTTTAACTTT TTAAAGAAAG GGACATAGAA ATAAATAAGT AATGGAATAA  
 420  
 TTGCGACGAT AGCAATGTGA CCAGCGATAT ATGACCAATC TGTTAAAAAT GCTTTCCTCT  
 480

GGTGTAGACA TAAATGTAAT CGCACTTAAC GTAGTAGCAT AAATTGAAAA GCCAACTACC  
 540  
 CAAGATGGCA AGCGACCACT TGCGGTAAAG AACTATTGG TACTTTGGCT CGCGCGCTTG  
 600  
 GTAAAATAAA CGCCAATGAA CAACATAGCT AGTAGATAAA TGATAACGGC AACCCAGTTT  
 660  
 AGTGTGCCAA ATCCAACCTC TTTCATGGGC AACATCCCCT TTACAATGTA TTGATTCTTT  
 720  
 GATGTCTATA AATCGTATTT TGCAATGAGT TGATCTACAT GTTCGTCGAT GTGCTTCGTT  
 780  
 AAAAGGTTTG AAAGGTCTTT TCGGTAATCC TGCATCAATG TCACGATGAC GTAATATTTT  
 840  
 TTTCAATGTT GGATAAATCC CCATNGATNA CAACTGTTTC GATAATGTCT TTTGAATCAT  
 900  
 GTTGTAGTTG GTAAGCTTCT TGAATTTGAC CTTGTCGTGC TAAGTCGAAG ANTTCTCTAG  
 960  
 CGCTCGTGCC  
 970

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAAGACATGA ACGCATACGA AGATAGTTAT GAAAACCGAA CTAAAAAAC AACTGCTGGC  
 60  
 AGTAGCGATT TAAGTATGTA ATTAACGAGG GCATTAGCCC TCTATTTTGT TGTACAAAAT  
 120  
 AACGATAAAC GAGGTATTTA ATATGACTGA AACAACTTTT AATCCAATTA CATCATTAAC  
 180  
 AATTAACAAT GAAGAAGTGA AAGCAAAAGC AACATTTATG TTCGATAAAA CCGCTAAAAA  
 240  
 ATTTGCAACT GAACAAGAAG ATAACAAAGG TAGAAAACAA ACGATTTTCAG GATTTACTAA  
 300  
 TGTTTATNAC GCTTTATTAG AACGTGACAC AGTGGCAATC GTAGACTTTT GGGAAATGTGC  
 360  
 AACAGCTTAT CTAGGTAAAA GCGCGCCTAA AAGAGAAGAT ATTGAAGCGG AAATCATGGA  
 420  
 AATCATCGAA AGAGAAAACG ACACGTTGAT CTTTACAAG GTGCGTTGGA CGTAATGAAT  
 480  
 AATAGCGGTT TTTTCAAGCA GAAATCACGT CTATTCTGGA CACAGATGAA CCAAGCGCCA  
 540  
 TCGTTAGCCA AAGAAGACGA GAAAGAGGGC GCGAAAGCTG GTATCGAGAT GATGAAGAAC  
 600  
 AACTACAAAG AAATCATGAC CGTAGCACCT TATTAGACTA TTCGGAAATA AGGCAGATGA  
 660  
 CAAGTCGTTA CATAGGTTAT ATGAGTAATG ACGAGCTAAT GAGCATGCTA CCTGCCGAAT  
 720  
 GGAATGACTG GATTATTGGC GCTAGACAAG CATTGATTGA CCAAAGGGAC NTCGCTCGTC  
 780  
 CCGCTCGTGC C  
 791

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
GGCACGAGCT AAAATATATG AAGCTAAAGG CCGTCCATCT GACAATCCGC TTATTGTTCA
60
TATACACAGT AAAGTTCAAT TAAAAGATTT TACATATACT TTGGCACGAG CGTAGAAAAG
120
TTAATGCAGG CATTCTGGCC GGGCCCTATT TCGTTTATAT TGCCGCTAAA GCCAGGCTAT
180
CTATGTCGAA AAGTTTCTGG AGGTTTATCA TCAGTTGCTG TTAGAATGCC AAGCCATTCT
240
GTAGGTAGAC AATTATTACA AATCATAAAT GAACCTCTAG CTGCTCCAAG TGCTAATTTA
300
AGTGGTAGAC CTTACCAAC AACTTTCAAT CATGTATATC AAGATTTGAA TGCCCGTATA
360
GATGGTATTG TTCAAGCTGA ACAAAGTGAA GAAGGATTAG AAAGTACGGT TTTAGATTGC
420
ACATCTTTTC CTTATAAAAT TGCAAGACCT GGTTCCTATA CAGCAGCAAT GATTACAGAA
480
ATACTCCGA ATAGTATCGC CCATGCTGAT TATAATGATA CTGAACAGGC AATTGCACCA
540
GGTATGAAGT ATTAAGCATT ACTCACCCAA TACAACACTT ACAATTATTA CAGATATTGA
600
GAGCAAAATT GGAAATGACG GTAAAGATTG GTCTTCTATA GCTTTTATTG TGCCGAGTAA
660
TAAGGTGGCG TTTATACCAA GTGAAGCGCA ATTCATTCAA TTATGTCAGG ATGACAATGA
720
TGTTAAACAA GCAAGTCATA ATCTTTATGA TGGTGTTACA TTCACTTGAT GAAAATGAAA
780
ATATTTGAGC GGCATATATA TACGGCTTTG AGCTCGTGCC
820
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
GTGACTTGAA AGATATAGTA TATCGGATTT GTAATGCGCC GTTAATCAAT TATGATGCCA
60
TTAAGATGAC CCGACTTAAA ATACNCAGTC CGACACAAGA TTGCTATGAG TTTTTTGGGT
120
GGAGATATTG AATTATATAA TTATCACTAT TAATACCTAC ATCAAAGGTA TGCTATTGAT
180
TTAGTTATTA AAGNAAATCA TAAAACATAT AAGAATCAAG GAAAAGTAAA TACTGATTAT
240
TTTTGTTTTG GAAAAGATAT CATTGCGCCA GCAAATGGTA CAGTTGAAAA AGTAGTGAAT
```

300  
 GGGGTTCAAG ACAACAGTAT TGGAAGTACG AATGAATCAC AGTTTTTAGG AAATTATATT  
 360  
 GTAATTAAGC ACGCAGAAAA TGAGTATAGC TTAATAGCTC ATTTACAACA ATATTCAATC  
 420  
 ATTGTGAATG AGGGGCAAAA TGTTAAATAT GGTGACTTCC TTGGGAAGGT TGGGAATTCT  
 480  
 GGCAATTCTA CTGAACCTCA TATACATTTT CAAGTAATGA ATGATAAGAA TATTGAAGCA  
 540  
 TGTACGTCTT TGAAAATTCG ATTTTTTAAAT AATCTAGAAC TTATCAAAGG GGATGTGGTC  
 600  
 TGCGGATTAC AAGGTGAATG ATGGCGATAC TTATAAAATC TCGACACTAT AAAAATGGTA  
 660  
 TAGTGTGCGAG ATTTTCTTGC TTATTTAGTT AATTCAAAGT GTACGCCGGA TTCATTAGAA  
 720  
 GTTGATGTAT TTGTGTTTGT AATAGAGTAT CCAGTTATTG AAATTTTAGA TTCAATATCT  
 780  
 GAAGCGGTAT TTGTAGATTC GGGATTATAG AAGCTACATT CATAAGTGTT ATCATCTNTG  
 840  
 GTNTTCNAAG AATTAAACAT TCCCTTTGGC TTTTAACTTC CGACTTTAGT GGTGGGNTAA  
 900  
 TGNCAAAAAG TNTGGAGNTG CTTATTACTA TTAATTAACA ACCCAGCCCA ATTGGGNCAC  
 960  
 CCCCCAACGG ATTTGGACCA ATCCTCAACT TACCTGCTTA TGAATCCCTG GCTCCCAACC  
 1020  
 CCCGCAAATT TGCTAAACCC AAAATCCACT TCCAANGTTT CCAAACCTAC TTTCTTCCAA  
 1080  
 GNTAATTTCT TCAAGGATTT TTTTTGG  
 1107

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

AAGTTTGATC CACCCACCNT AAACCCATCG CCTAACAATA AANCCGAANN TCACCTCCTG  
 60  
 CCTGTTGATC CAATTGTTCC CATTCCAATA ACCGCCACCT CTTTTTCTAG AACACCCACA  
 120  
 CCTATCGTTC TATGGTTAAT ATGTTGACA TCTGTATGCG GTATAGCGAC CGAACATAGA  
 180  
 TGTGTTGGTA AACCAGTANC NAATTCTTTT TCTCTGTCGA TGAATGCATC TTAAACGTT  
 240  
 GACTTCACGA ACCCATTTTG AAATAACACA TCTGACATTT GNGACAATAC GGATTCTTTA  
 300  
 TCAGTTGCCG ACNAATTGAG CATTATATTT TCTTTATGCA CCTAATTGCT TGTCCCATCC  
 360  
 ATTTTCCCTC GCTTCTTTAT TTGAATAATT TTTTAAATC TCATTTACAT CAGAATTTTT  
 420  
 GCGACTTTGT ATGATGCGCT TAATTGCGTC ATTGTCTTGC GCCACATCTC TCAATTGTAG  
 480  
 TAACGCTCTT AAGTGTGTCA CTTTATCAAC AGCAGCAATA GGTACAATAA TATGGATTGC  
 540  
 TGTGCCATCT GACATGTATA TTGGTTCTTG TAATATCAAC ATACTCATCG CTGTTTTATG

600  
 TACATGCTTT TCAGAGTATG CATGTGGAAT AGCAATATTT TGCATGATAA CCATATACGA  
 660  
 ATCANCANAT ACCNNGGAAT TCCATCTCAT GAATATATTT AATATCAATA AAATGATTAG  
 720  
 CAACTAACAC AGCACGNGCT TTAGCAATAG CTTTCATCAAT ATTTTCAACA GGAGGCNTNC  
 780  
 TTTNCACGGG CCTGGCCGGT ATCAAGGCAG CTAAATCTAA TGTCTTATTT TGTGTGACAA  
 840  
 TCGATCCATT AATGGTTGAA ATTGAATTAT AATTGGCAAT AAAATCTTCT AAACCATCAC  
 900  
 GTAGTTCTGT AATGTCATTA ACTGTCGTTG TCGGTTCAAT TAATGCCATT AACTTGTTTA  
 960  
 TTTCTTATC AATGTCAGCC GATTCCTTAT TAATGTACTT CATCACTTCT TTACGTAAC  
 1020  
 TTCGTTGCTC ATTTTCAGAT AAAGCTACTT TTGTGATAAA TAATTTTTTA TGTGTTAGGA  
 1080  
 CAAACATTGG TGAAAAGACG AAGTCATAAT CTAATGTGTA ATTTTCAAAT GTTCT  
 1135

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CGTGCGAGCT GCTTTTGGTA AAAACGGCGG TAATATGGGT GTATCTGGAT CAGTTGCTTA  
 60  
 TATGTTTGAT CATGTGGCAA CATTGTTGAT TGAAGGAAAG TCTGTTGACG AAATACTTGA  
 120  
 AACATTAATG GAACCAAGAT GTAAGATGNA AATGATGTGA TTGACGATAA TGGATTGACA  
 180  
 ATAGTCTATG CTTGAACCAA GATCCAATTT CCAGTCGTTT CAAGATGCGC TTCGTNCACC  
 240  
 AGGTTGTTGG AAGAATTTAA AAGTTGCTTG AATTTGAAAT TGTTACCCTC CAAACAAGAT  
 300  
 ATTGAACTTT CTGAAGCGGA CCNAAGTAAC ATTTGAAAAA TTAATCGATG CATTAGAAGA  
 360  
 TTTAGAAGAT GTACAAAACG TATTCCATAA TGTGGATTG AAATAATGAA ATCAGCAGAA  
 420  
 CAATGGATTG ATGAATTGCA ACTTGAATCA CATCCTGAAG GTGGTTTCTA TAGAGAGACA  
 480  
 ATTCGAGAAG TATTGAAAGA TGGACGCAGA GCGCCGTTTA GNAGTATTTA TTTTTTACTT  
 540  
 ACAGATGACA ATATTTTCGCA TTTTCATCGA ATTGATGCTG ATGAAGTATG GTACTATCAT  
 600  
 GCTGGTGATT CTCTAACAAAT TCATATGATA AATCCGGATG GGAATATAC GACTGCAACA  
 660  
 TTGGGTACTG ATATCCAAAA TGGAGATGTA TTGCAATATG TAGTGCCTAA AGGAACAATT  
 720  
 TTTGCTTCTT CAATCGAAAT TTCAAATACT TATAGTTTAG TAGGTTGTAT GTGTCAACCG  
 780  
 GCATNTGAGT TTAAGCAGTT TGAATTGTTT AAGCAATCTG AATTAATTAC ACAATATCCG  
 840  
 CATCTTAAAT CAGTGATTGA NAAATATGCT TTAAATAAAA AATGATCAAT GAAGTGGTTT

900  
GAAGGTTGTT AATAAACCTT TGAGTCACTT CATTTTTATA TGTATTCTTG ATTGAATCAG  
960  
AATAGATTTG ATG  
973

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1701 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GGCACGAGCT GGTTGCATAT CTAAACTTTG GTAATCTACA CCTTCTTTAG ATTTACCGAA  
60  
TGCGATAGCT GGAGACTTAA CTGCGGCTAC TTTCGCATGT GGAATAGCAA TACCTCGCCG  
120  
ATACCAGTTG TACTTTGTGA TTCTCGATTG TGAATCGCTT CCTTAAATGA CGCGACATCA  
180  
CTTAATTTAC CTGCCTTGNC TAATTGGAAT TACCTAACTC ATCAATAACA CCATTTTTGT  
240  
CATTTGCCAN TAAATCCATT GCTATCGTAT CTTTTGTTAA TAACTCTGTT ACTCTCATTA  
300  
TTTTCACTCC CCATCAAGTA CGCTAATCGN AACTTGGTGA TTCTATTTTT TCTTATAGCG  
360  
GTCCCGTGTT TGCTAAGTCC TCAATCAAAA TGCCGGGGCA AGTACCGCAA TGCGACTGCT  
420  
TGGTTGGGAA TGCTTTTTCA ATCGTTAAAC CTGGAAGCAA TTCCAGCCAC CATGCCTGCA  
480  
ACTGTACTAT CACCAGAGCC AACTGTATTA ACCACTTTCC CTTGTGGATT AACTGCTTTA  
540  
ATACTGATTT CTTTATCAAT ATAAATAGCA CCATCACCGC CAAGCGAGAC AATAACAGAT  
600  
TGCGCACCTT TATCAACTAA CAAACGACCA TATTTAATAA CATCTGTGTC TGAGTTCACT  
660  
GTTGTATTAA ACATCACTTC TAATTCATCT TTATTAGGTT TAATAAATAG TGGNTGAAAT  
720  
GGTAAACGC TTTCAAGCCA ATTCTTTTTT AGCGTCGACC GACTAATTTA GCACCTGTCT  
780  
GTGCTGTAAT TTGTGCAAGT TTGCGCATAC GCATCGCTTG GAATACNACT TGGTACACTT  
840  
CCAGCAACAA TAACGATATC NTCGCTTGTT GTATTTTTTAA TGTGTTGTAA CAGTTGTTCA  
900  
AATTGTGTTG ACGTTATATG AGGACCCGGT GCATTGATTT CTGTTTCTTG TCCTGTTTTT  
960  
AATTTACAT TAATACGTGT ATCTTCATCN ACNNCAATAA AATTCGATTG AATTGCNCTG  
1020  
TTANTTAATG TATCTATAAT GAATTTCCCA GGAAATCCAC CTGCANATCC CAAGGCAGTT  
1080  
GACTCAACAT CTAATGTCTT TAAGACGGCG CGAGACGATT AATACCCTTT CCCCCCAGC  
1140  
GAAGTAATAT GTTGCTGTTG CTCTGTCCAA NNCCATCAAG GTTNAGAATC ATTCGTAAAA  
1200  
ATGACATAAG TCAATTGTAG GAGTGNGAGT CNCCTGTATA AATCATAAAG TCCCTCCTAT  
1260  
AAAGTGAGAC TTTTGTGGT ATTCTTTTAN CGAGTCTTGA GTTAATGCTT TTTCAGATGT

1320  
 GATGANTGTC GTACTTTCTA GCACAGGGAC ACGAGCACAA TATACTTTAT TAAACTTAGA  
 1380  
 NTGATCCTAT AAGNACANAT GANTGAGTGG CTAATGACAT TGCTGTTTGT GTAACATAATN  
 1440  
 CCTCTTGCTC ATCGGGAGTA GTTAATCCAA GTTCAATATC TAATCCATTC ATCCCGATAA  
 1500  
 AAGCTTTATC GNAACAATAT CGTCTTAATA TCTCCATAGC ACTAGANCCA ATCGTAGCNA  
 1560  
 GTGTATTTTC TTAACTTGA CCACCTAGCA TAATTGTTTT AATACCTTTT GGAAGTAAAG  
 1620  
 CTTCTACATG TGTTAAACCA TTGGTTACCA CAATGATATC TTTGCTTGA ATATATTTAA  
 1680  
 TTAGCGGCAC GAGCTCGTCC C  
 1701

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CCCGGTGTA ACCGTATGGA TGGATGCTAG CACCAANTTA ATAATCCTCC ACAATANCAT  
 60  
 TAAGGGTATT CATGTAGGTG NCACAACATG GTAAAGGCTC TACCAGTTGC TTACCTTAGA  
 120  
 ACAGCTTTAA GTTGNAATG GTTATGAAGT AGGTACATTT ACGTCGCCGT TTATTGAAAC  
 180  
 ATTTAATGAN CGAATTAGTC TAAATGGTGT GCCAATATCA AATGACGCTA TTGTAGAATT  
 240  
 AGTATCACGT ATTAAACCAG TAAGTGAAAT GATGGAACGT GAAACAGATT TAGGTGTTGC  
 300  
 AACTGAATTC GAAATAATCA CAGCGATGAT GTTTTTATAT TTTGGTGAAA TACATCCTGT  
 360  
 TGATTTTGTC ATTGTTGAGG CTGGATTGGG TATAAAGAAC GATTTCGACAA ATGTCTTTAC  
 420  
 ACCGGTTTTA TCAATCTTAA CTAGTATCGG TCTAGACCAT ACAGATATTT TAGGTGGTAC  
 480  
 TTATCTAGAT ATTGCTAGGG ATAAAGGCGC GATTATAAAG CCTAACGTTC CAGTGATATA  
 540  
 TGCTGTAA AATGAAGATG CATTAAAATA TGTTGCTGA ACGCGCAATT GAACAACATG  
 600  
 CAAAGCCAAT TGAATTAGAT AGAGAAATTG TTGTTGTATC GCAAAAATGA TGAATTTACT  
 660  
 TACCCGNTAT TAAAGATTAT GAATNAGAAA CAATCAATNT NAAGCATTGT TAGGGTNGAA  
 720  
 CATCAAGAAA CAANATGCTG CATTAGCCAT AACAANTCTT ATTGGANTCA AATTGAACAA  
 780  
 GGATTAATTG AATNCAGATT TNCAANAAGA TGATAGACGG GTTTGATCAA GTCCGTGGAC  
 840  
 NTGNCGTTTT GGGCAGGT  
 858

(2) INFORMATION FOR SEQ ID NO:139:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GAATTCNAAG TCACTTTCTT TTTTAAGCTT TAAATTTCTC CCCATTTTTT TAGCCCCCTA
60
TAAGGATTGA ATATCAATGC CTTCTNTCAT TAAAATTTCT CTAATTTGCG AAACAAATAA
120
TAATGCATGT TCTCCATCAC CATGCACACA AATTGTATCT GCTTGTAAAG TTACTTCCTT
180
ATTGTTTTGT GAAATAACTT TATTTTCCNN CACCATCTTT AAAACCTGCT TAAGTGCTTC
240
GTCAGTATCA GTAATCACAG CATCACTTTC TTTTCTGATT GATAAAATCA TATATGTTCC
300
TATAAACACT AAAAATCCTA TAACTAGGTA ATAATATTAA ATTCAAGGAT CGANCCTCCG
360
CTAAGCGACA ACAACAATGG TGACAATAAC AACAACAAC GAGAATTNAA ATACCTAATT
420
CAAAAAGGGG TNATNGGNCT TACAATGAAT GTGGCCNAAA ATTGGGGAGG NTCCAAGGNG
480
GGNTCAAATT RRDCTNS
497
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
CCCTGGTTGA TTGGAAAATG TAATTGAATG AAACGGGTAA AACCTTCCCC AAAGCACCAT
60
AATTGTTGCA AGTAGGTTGC CACCCCAATC CTGGTTTACC CTGATTTGAA AGGCTTTGGG
120
CAAGCCGAAA TATAGATATC TCTAACCGAC GAGATTTATA ATTTGATGAT TTATCAATTA
180
GGTGCATTAC AAGGGTTTTG TCGCATTCAT CAACTTAAAA TTAATCATGT TAAACCCGCA
240
TGGTGCATTG TATCAGATGG GTGCAAAAGA CAGAGAAATA GCAAACCCCC GTNATANCAC
300
NACCTGTTNA TGNCNTTGAT CCATCACTAG TGTTAGTAGG ATTAGCAATC ATATCTAATT
360
TCAGAAGCAA AGAATGTCGG ATATAATCCA GCTTCTGAAG TGTTTGCTGA TAGACGATAC
420
GAAGATGATG GGCAGCTCGT TAGTAGAAAA GAAAGTGATG CTGTGATTAC TGATACTGAC
480
GAAGCACTTA AGCAGGTTTT AAAGATGGTG NAGGAAAATA AAGTTATTTT AAAAAACAAT
540
AAGGAAGTAA CGTTACAAGC AGATACAATT TGTGTGCATG GTGATGGAGA ACATGCATTA
600
```

TTATTTGTTT CGCAAATTAG AGAAATTTTA ATGAAAGAAG GCATTGATAT TCAATCCTTA  
 660  
 TAGGGGGCTA AAAAAATGGG GAGAAATTTA AAGCTTAAAA AAGAAAGTGA CTTTGAATTC  
 720  
 ACAAAAAATC ATAAAAGGTT ATTATTAGGT TCTGTATTTC ACGATGGCAA CTTCTGCAAT  
 780  
 TGGCCCAGCA TTTTAAACGC AAACAGNAGT ATCAACATCA CAATCGTTTG NAAGTCNCGN  
 840  
 ATCTGCCATA TNACTGTCTA TCATCATTGA CATTGGTGCA CAAATTAATA TATGGCGCAT  
 900  
 ATNAGTTGTA ACTGGTTTAA GAGGTCAAGA AATATCAAAT AAAGTTGTTC CTGGGCTTGG  
 960  
 TCTCGTGCC  
 969

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGNACGAGCG GCACGAGCGC ACTTATTTTA TCAGAACATT CTAAAAAGAA TATATTCAAT  
 60  
 ATAAAAAAGG CTGTGTAGGG GTGTCTTATG AATAATAGAA ATGTGTATGA TATCGAAGTA  
 120  
 AGTGATTATA AAGGCTTAAC TTATAAATTA GAAGCATTTA GAGGTAAAGT GATTTTAGTT  
 180  
 GTTAATACTG CAACAGAATG TATATATAGC GAACAATTGA AAAAAGTAGA GACTTTGTNT  
 240  
 CAAAAATATA AGGATCGTGG GTTTGTAGTG TTGAGTCCC CGAATAATAA TTGTGACAAT  
 300  
 CGACAACCAG GNTCTAATGA AGAAATCTTG AAAATTAGNC GGNGAGAAAT TTGGGTGTTA  
 360  
 CATTTCCAGT GCTAGCTTAA AATATCTTGT GAACGGGAAC GAATGAACAT CCCCNTATT  
 420  
 TACGCATTTN ANAGGAATGA ACAAACCAGG AATCTTNGGG CCCCCAATAA AATGGAATTT  
 480  
 CACAAAAATT TATAATCGAT CGACAAGGCA ATGTTGTAAA TCGATTCTTG CCAATGGAAG  
 540  
 ATCCAATGGA TATATCGACA AATATAGAAA TATTATTGGA AGAATCTTCA ATCTTAAATT  
 600  
 TAANATTGAG CGCTTAGTNT GCAAATACAC AA  
 632

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCCCACNAAG TACNCGAAAC GCAAACAAAC ATCTTAAAAG GAGGAACGAA CAATGCAAGC  
 60  
 ATTACAAACA TTTAATTGGA AAGAGCTACC AGTAAGAACA GTGGAAATTG AAAACGAACC  
 120  
 TTATTTTGTG GGAAAAGATA TTGCTGAAAT TTTAGGATAT GCAAGGGCAG ACAATGCCAT  
 180  
 CAGAAATCAT GTTGATAGCG AGGACAAGCT GACGCACCAA TTTAGCGACA GCAGGTCAAA  
 240  
 ACAGAAATGT AACGATCAAT CAACGAATCA GGATTATACA GTTTAATCTT TTCTAGCAAA  
 300  
 TTAGAAAATG CGAAGCGGTT CAAACGTTGG GTAACCTCGG AAGTTTACC AACATTAAGA  
 360  
 AAAACTGGTG CTTACCAAGT ACCTAGCGAC CCAATGCAAG CATTGAGATT AATGTTTGAA  
 420  
 GCTACAGAAG AAACAAAACA AGAAATTAAA AACGTAAAAG ATGATGTTGA TNGATTTGAA  
 480  
 AGAAAATCAA AAAGTGGATG CGGGAGACTA CAATTTCTTA ACTAGAACTA TCAATCAAAG  
 540  
 AGTAGCTCAC ATNCAAAGAC TACATGCGAT AACAAATCAA AAACAACGTA GCGAATTATT  
 600  
 CNGGGATATT AATTCAGAAG TGAAAAAGAT GACTGGTGCA AGTTCAAGAA CGAATGTTAG  
 660  
 AC  
 662

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TAATTCGCAA TAGGAGTGAT GAATATCATA AATTTTACCC TCCAAATGAA GCTAATGAAG  
 60  
 TCCTGGACCC GAGTAAGACG CATGTAGCCA AGCTAAAATA ATCCACTCTA CCTTATCTTT  
 120  
 AGTTAATAAT GTTACTAAAT GTTGTTTATA CGCTGCTTTT GAATCAAATT GTTTTGGTTC  
 180  
 ATTAATATAA ACAGGAATAT CGTGCTTGTT TGCTCTATCT ATACAAAACG CATTTTGATG  
 240  
 ATCCGTATAT AGCNCCGTAA CTTCAATATT TTCAAGTTTT CTGATTCAA CATGCTCAAC  
 300  
 TATATTTTCA AAGTTACTTC CTGAACCTGA TGCAAAAATC GCAATTTTAA CCATTGTTAT  
 360  
 ACCCCCAACA ATTCAATTGC AGTTGACTCA TTTTTCACAA TATGACCAAT TTGATAAGCT  
 420  
 TCCACATTTT GTTCTGCTAA AATCTTCAAA GCGCGTCGAT GCATCTTTTT CATCAACGAT  
 480  
 AACCGTATAG CCAATACCCA TGTTAAAAAT GTTATACATT TCATTTGTGT CTATATTGCC  
 540  
 TTGTTGTTGT AACCAATCAA ATATTTTTGG CGTTGGAAAT GATGTAGTAT CAATTCTAGC  
 600  
 AGCATATCCG GCTGGCAATG CACGTGGAAT ATTTTCATAA AAACCTCCAC CAGTAATATG  
 660  
 ATTCATTGCC TTAATAGAAA CTTCTTTTTT TAAAGCAAGT ACAGGTNTGA CATATAATTT

720  
 AGTTGGCTCT AAAAAGACAT CTATAAATGG ACGATTATCG NAGGGTGATG CCAAATCAAT  
 780  
 GNCTGATTCA NTAATTAATN TGCGCACTAA ACTGTNTCCA TTNGANTGAA TGNCACTTGG  
 840  
 ACGCAAGTCC TATAACAAC TGGCCCTCTT NCAATTCTTG AACCATCTTA CAATAGNCAA  
 900  
 CCTTTTTCAA CTGCTCCAAC AGCAAATCCG GCTACATCAT ATTACCTTC GTGATACATT  
 960

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATNAATTT GGCGANTCAC TTGTCGCTAA GTGGCTCCAC CTTGTCATCT ATTATTGCAT  
 60  
 CACTCATGGG NCGNACATCA TAGTGTGAT TTGATTCAGC CATATCNACG TTTTGATTTT  
 120  
 TCTAATAGAA GATCAGCAAC AACATCAACA TTTGAATGAT TCATATATGA TGCAGGTACG  
 180  
 TCTTTTAATG TTTTAATGTT ATCAATATAA AGATTGATGT AGTGTTGCGG GATATTGTAG  
 240  
 TGATGTTCAA GTAACATATC AGTAACAAGT TGATTAAAGA CACTTTCATC TAATTCACCA  
 300  
 CGTGCCACAG CGCTTTCTAT TAATGCTTTA TTTGGGAAAA TAGGCACGAG CGAACGTCAC  
 360  
 GTAACCATTT NGCGACATCT TCAAACGTAT CCGCTTCTAA TCCTTCCCAG GGGTTACGTG  
 420  
 CTGCAAAAAT CGAAATCGGT GATAATGGTG TAATAACACG TTTCGCATTT TCAATGACTG  
 480  
 AATTGATATT TAACTGTGTT GTCATACCTT TCACCTCCTA TAAATACTTC TTCAAATAAT  
 540  
 TCGGATGACT TTCTATCGCT TTCGAGCGTG CTTACCTAG ATTAACAAAC CACACGTACA  
 600  
 ATACCGCAAA ACCCTTAGAG TATCGATGAC GCGCCACCCA AATACTTAAT AAATGCCAA  
 660  
 AGATTAAAT GACAACACTA ATGATGACAC TCACTGTAGG CGGTGTTGTC GCATGTGTTG  
 720  
 TTATATTTTG GTAATACATC GTAAAAATAA TTGTGTGTGA TGACGTAGAT AAATGTCACA  
 780  
 ATTGCAATCA AAATCATGCC AACCAGACGT GCCATGCGCC CTTTACTAAA GGCTACCATC  
 840  
 TGATTCCAAG ATACAAGTTA ATGACCATGC TAGAATGAGT GCACTTAACA CTTCATATGC  
 900  
 ACTTCTGTCA CTACCATCCA AATAGAATGC ACGATAATAG CTAATACACG TCCATGACAT  
 960  
 CCAGCATAAG CTCTTACAAT GCTGTTTTGA ATATGATCGC TCCCAARRDC TNS  
 1013

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
ATCCACCCAT NACGNTACTC ATANCATTGT CAACAGTAAG TAATGTCCAT ATGCATATCN
60
ATNCCGCTCG GCANTATANC ACCCAACCGG ATTTCATAAG TGGGCGGATA AAGTGATNAG
120
AGTGATCTCA ACACTATCGA NTAGNTACCA GCGTTCTTTA TCGGTNTTAT TTTATNATTT
180
ATTGTCACAN ATTTANTGAA TATAGATAGC GTTATACTAA GTCAGNTTAT ATTACCTGTA
240
ATCACGCTAT CTTTAGGTAT GTGTGCATAC ATCATTCGTT TAGTGCGTTC TAATTTATTG
300
ATGTTATTGC AAAGTAATAT CGTACAANCA GCAAGATTAC GCGGTATGAA TGANCGTTAT
360
ATTTTAATTC ATGATTTACT AAAACCAACA ATTTTGCCGA TTATCCCATT ACTAGGGATT
420
TCACTTGGCA GTCTAATAGG TGGTACTGTA GTGATTGAAA ATTTATTTGA TAATACCTGG
480
TATTGGTTAT CTATTAATGG GATAGTATTA AATCTCGAGA TTATCCTGTT ATTCANGGAT
540
GCGTGTTATT TATTGGCTTC TTCGTTGTTA TTATCAATAC GATTGCTGAT TTATTAACGT
600
TATTACTTGA TCCGAAGCAG CGTTTACAAT TAGGAAATCC CACAAAACAC AACCAATACA
660
CCATTGATAT CAGAAAGTAG TGNCCGTCAT GCATAAAATA TTTTCANAGA ATAACCTGAT
720
ATTTTTTTGTA TTCGTTGCAT TTATTTTTGT GGTAATTGTA CTGCAATTCT TTGTCAGTAG
780
TGAAAATGCA ACCACAGTCA ATTTATCACA AACTTTTGAA CCGATTAGTT GGTTCGATTT
840
ATTAGGAACT GATGATTATG GGAGAGATTT ATTTACCCGA ATTATTATCG GTGCACGTTT
900
AACATTGTTT GTTACTGTTT TAACATTAAT AGCTATCGTT GTCATAGGTG TTACACTAGG
960
TCTATTTGCC GGATATAAAA AAGGGTGGAT TGAACGATTA GTGTTAAGGT TTATTGATGT
1020
TGGTCTAAGT AG
1032
```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
GGCAGGAGAC TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACAACAA AAACAACATT
60
ACCCGTATTA TCCAAAGACT TTATAATAAG ACCCCCCCA ANTTGATGTT CCTAAACNA
120
```

GCTGGTGCAT CTATGATTTT ATTGATCGTT AACATCTTAT CGGATANACA ATTGAAAGAT  
180  
TNAATATACC CTACGCAATA TCCCAAAATC NAGAAGTGTT AATTGAAGTA CATGATCCCC  
240  
ATGAATTAGA ACGTGCCNAT ANGGTTAATG CTAAATTGAT TGGTGTAAT AACAGGGACT  
300  
TAAAACGATT TGTCACAAAT GTGGAACATN CAAATACTAT TTTAGAAAAT AAAAAACCAA  
360  
ATCATCATTA TATTTCTGAA AGTGGTATTC ACGATGCATC TGATGTAAGA AAAATCTTGC  
420  
ATAGTGGTAT CGATGGCTTA CTAATAGGTG AGGCGCTTAT GCGTTGTGAC AATCTATCTG  
480  
AATTTTTACG ACAACTGAAA ATNCNAAAGG TGAAGTCATG ATGAAATTGA AATTTTGTGG  
540  
CTTTACATCA ATAAAGGATG TTACAGCGGC CAGTCAATTA CCTATTGATT CGATAGGTTT  
600  
CATCCATTAT GAAAAAGTA AAAGGCATCA AACAATACCC AAATAA  
646

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGCACGAGCG TCAGTCCAAA TCACGCCTTG TGGTTTCTCT GGAATTGTCA TCTATTACTC  
60  
ACCCCCAAAT ACATCATTA TGTTAATATT GTGAATTGCT TCAATTGGAT TTATTGTTTC  
120  
ATCTACAGNN CGATATCGCT TACTATCAAT CATGNCATCT ACATGACATA CCGATTGATA  
180  
ACTACAAAAA GCACATGGCA ATTTGTGTGT GTNCTTTAAT GGTGCAACTN CAGTATGTCC  
240  
ATCCATAATA TNTGAAGCTG TNTCTATAAA ATTCTCTNTG TTATGCTGAA TGAATTTATA  
300  
AATTGNTGGT TCATCTGACA CTTGGCTGGC TCGTTTACTC AAAGAGACAT CTTTTATTCA  
360  
ANCCAACTGG GTACAAATAT CTGAAGGTGA ANTTAGGGTT CTTNAACGAA TTTCCAATGC  
420  
ATCAAATAGC AGGGGGGTCT TGCATTCAAC TAAACCCTCA GGTTAANCTT NNNAATTAAT  
480  
CTTGNTCTTG GNTNTCTTTC ANCAATATCA AGACCATGAT TTAATTTACT CTTGGGCCAA  
540  
GTCATGGAGT TTTATATCCA CCGGG  
565

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CTTGAAGTAG TAGGGTTACA AGGCTCAACT TACCTTTTAA AAGGACCAAA CGGTGAAAAC  
60  
GTAAAGTTAA ACCAATCAGA AATGAACGAT GATGATGAAT TAGAAGTAGG TGAAGAATAT  
120  
AGTTTCTTCA TTTATCCAAA CCGTTCAGGT GAATTATTTG GAACTCAAAA TATGCCTGAT  
180  
ATTACGAAAG ATAAATATGA TTTTGGTAAA GTACTTAAAA CGGATCGCGA TGGGGNACGT  
240  
ATAGATGTTG GGTTTACCCC GNGAAGTGTT AGTACCATGG GAAGATTTAC CAAAAGTGAA  
300  
ATCACTATGG CCACAACCTG GTGGATCATT TGNTAGTTAC ATTACGAATT GACCGTGAGA  
360  
ATCATATGTA TGGACGTTTA GCGAGTGAAT CTGTTGTAGA AAATATGTTT ACACCTGTAC  
420  
ACGATGATAA TTTAAAAAAC GAAGTCATTG AAGCCAAACC TTGGCNCGAG CGTATTACGA  
480  
ATTGGTAGCT TCTTATTAAG CGAATCAGGT TACAAAATTT TCGTACATGA ATCAGAACGT  
540  
AAAGCTGAAC CAAGATTAGG TGAATCTGTT CAAGTTAGAA TTATCGGGCA TAATGATAAA  
600  
GGTGAGTTAA ATGGTTCATT TTTACCACTT GCACATGAAC GNTTTAGACG ATGACGGCCA  
660  
AGTCATCTGT GATTTACTAG GTGAATATGA TGGGGAATTA CCATTCTGGG ACAAATCAA  
720  
GCCCTGAAGC GATTAAAGAA GTATTCAAAT ATGAGTAAAG GTTCATTCAA AACGTGCAAA  
780  
TCGGNCACTT ATATTAAACA GAAGGATTAT TAATATTAGG AAACAGGGTA AAAATCACTT  
840  
TTAACTTAAA AAAGGGTTGG CGGGTCGNNT TTGGNCTCAA AAAGAATTAA TCATTNTNAC  
900  
AACGNNNTCG GNGGATGCG  
919

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTGCATCTGG TGAAGGAAAT CAANTANNTN TTATNNCTGA AGTGATTGCA TGGTGCAACN  
60  
TCAATATCA CATATGGCTC AGTGGANTAT ATGGATAAAG GCTTAACAGG TCATATCATG  
120  
CGGCGTGGTA TTACTGAAGC GGATGCCTCA ATTAATTGGG CACTAGGTTT AATGAATGAG  
180  
GGTAGCCAAA TTATTGATAA TACAACAAAT TTATGTGGTG ATCGCACAAAC AAGNNCACTT  
240  
AAATCAGGAG GTGNAGGTAC AGGAGAACAA AAAATTAATC TAACATCTAA ANTCGCACAA  
300  
ATATGGTAAA GAAACAGATG GTTATNTCCT TAAACATGGT GTTATGAAAG AACATGCATC  
360  
ATCTTGTATT TTAATGGGTA TCCGGCTACA TTANGCATGG GGGGAACATA ATCAAGTGCT

420  
AATCAGGAAT CACGTGTTAT TNATGTTATC TTGAACATGC TCGGGGGNGA CGCGAATCCT  
480  
ATTTTATTTA ATTGANGAAG ATGATGTACA AGCTGGTCAT GCTGCATCAG TAGGCCGTGT  
540  
TGGATCCCAG ATCAACTTTT ACTATTTAAT GAGTCGTGGT ATTTCTCAA A GAGAAGCGGA  
600  
ACGTCTTGTT ATACAGGGTT TCTTAGATCC AGTAGTACGT GAATTACCTA TCGAAGACGT  
660  
TAAACGTCAA TTGAGAGAAG TAATTGAACG CAAAGTTTCT AAATAATATT TTGAAAATAA  
720  
AAGTTTGTA TAGATATAGA CTGTCGATAT TGGTATAAGA CTAATACAAC GTCAGTATTT  
780  
AAATGATTAG GATTTTTATT TAAGAAAGGT CGTGAATGAA GTGGCCGAAC ACTCATTGTA  
840  
CGTTNATGAA GTAATCAAGG ATTTTCCGAT ATTAGATCAA AAAGTCCATG GCAAACGTTT  
900  
AGCATATCTT GATTCAACAG CGACAAGTCC AACGCCTATG CCAGTGTTAA ATGTT  
955

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

NAAATTCCT ATACGTTATA CTTTAATTGT TAATAAGCCA CATAAATAAG AGGGGGAAAT  
60  
GCTGTGTACA AGCAAGGTGA ACCAAATTTA TGGACTGGAA GGTTAGATAG TGAAACAGAC  
120  
CCGAAAAAAT TTAGACATTT TCAAACAGTA ACATTTGAAG ATTTGTCTAA GCTGGAAAAG  
180  
AGTAGTATGC CATCAGGGGT CGGTATATTA GGCTATGCTG TTGGACAAAG GTGTTGCTTT  
240  
ANACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG  
300  
TTTGGCGGAT TTGGATCACT GTGAACTNT AGTCGATTAC GGAAATGTTT NTCATGATCA  
360  
TGAGGAATTA NCTNGATACN CAACCANGAA TTTGGTACTG TNTTGGCAAA TTGAGCTCTN  
420  
TCTTTAGAGC TTGGNNCATT GATAGGTTCT CTCGCAGGTG GT  
462

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:



GGCACGAGCG TAAGATTAAC CATTGACCAT AATATATATT GTGTTTTTCC AAAATCGGCT  
60  
CTGCTAATTT TAAATAGGGG CGATATATTG TTATAAACT ATTGAAAAAT TCTTGTGATA  
120  
GCATAGTGAC ATCTCCTAAG ACAAATAGT TAGCTTAGCT AACCTTTTCA CAACAATAGT  
180  
AATTATAAAA CGGGAGCAAT TAGAAATCAA TATATAATTA TTAAGAGCAA AAATAATTAT  
240  
ACTTTGTAA AATAAGCGTA ATTACATGTA AATAGGGGGA TACTAATGAT ATTGAAATGT  
300  
GCATCACATC ACTCATTATA TAGATCAGTT AGATCGGTTT AGTTCTCCAG GAGATGTTAT  
360  
AAAATNACAT TCAGGTGGGT ATCATCATAA ATATGGAACA TTCAATAAAT TAGGTTATAT  
420  
CAATGAAAAT TATATTGAGC TACTGGATGT AGAAAATAAT GAAAAGTTGA AAAAGATGGC  
480  
AAANACGATA GAAGGTGGAG TCGCTTGCGC TACTCAAATT GCACAAGAGA AGTATGAGCA  
540  
AGGCTTTAAA AATATGTGTG TGCGNACAAA TGATATAGAG GCAGTTAAAA ATAATCTACA  
600  
ANGTGAGCAG GTTGANGTAG TAGCGCCGAC TCAAATGGAA AGAGATACAC ATAAAGATGG  
660  
TAAGGTAAAG TGGCAATTGC TTATATTATG AATCAGGATG ATGATGAAAT TACGCACCAT  
720  
TTTTTATTCA ATGGGAGAAA GTGCCTCCAT GC  
752

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CAAATGTTTA TCATGATATG ATGAATATAA TAATCGGGTA TATAACTGTA TGATTAATTA  
60  
CACAATAAAG AGAGGGAATA TAATATGNGN NAAGTGTCOA TTAAAGATGT TGCTAGAGAA  
120  
GCTGGTGTAT CAGTTNCANC TGTGTCACAT ATTTTAAATC ATAATGATAG TCGTTTTTCC  
180  
GCANCACCGA TAAAAACGT ACATGCTGTT CCAGAACGTT TAGGCTATGC CCCTAATAAA  
240  
CATGCAAAAC AAGCTCGTGC GCGGCAGTAA AATTCAAAT ATTGGCGTCA TTTTACCTAG  
300  
CTTAACAAAT CCGTTTTTCT CAGCACTGAT GCAAAGTATT CATGAACATA AACCATCTGA  
360  
TGTTGATTTA TGCTTTTTAA CATCTACAGC AACTGATNTG TATGACAATA TTAAACATTT  
420  
AATTGATCGA GGTATTGACG GATTAATTAT CGCACAATAC ATATCATCCC CGGACGCCCT  
480  
AAATAACTAT CTAAAGAAAC ATCATGTACC TTATGTCGTA CTGGATCAAA AATGACCATC  
540  
AAAGGCTATA CAGATTGTGN TCCGGACAAA ATTGAATATC AAGGGTGGGA CAACTTTGGC  
600  
AGCACAACAA TTTAATAGAA CTCGGGTCAC AAACCATATT GATAATTGGT TGCAACCATA  
660

TTGACAATGA TGGNGAATAT TGTCGACTCC TGTCGCTGGA TTTGTCGATA CTTTGC GCGC  
720  
GAATCAATTG CCAGAACCCAC AAATCGTCCC TACTGAATTA TCTAAACGCC GTGGCTAACC  
780  
ATGTTGAATG A  
791

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TTTGTCTTTG GAATGGGCTC GTTTTTTTTA ACCTAATAAG AAATGATAGG GCATTTGAGA  
60  
TTGGAAGGNC ATTTTGGCTT TGTGCAAATA ATACAATAAG CTAAATGTCT NTTTTTGT  
120  
TTGTGAAAAT ATGATGGATG GCTTGTGTGG GCAAGTTTGC TAATTTAATA AGATATGCAT  
180  
TTTTC AATTT AGGAGTTGGC CATGCATCTA CACTTTATAA TGGTGAGAGC GTGGTGAGGT  
240  
ATTGTTAATC ACGCAATTGT AGCGAGGAGT TATTGCTACA TATGTCGTTA TGGCCTATTG  
300  
ATTTTCTAAA ATAGCTGTAT CAGATCATGT GACNAAATAA AAATAATTTG TTGAAAGCCT  
360  
TTACATAACT TGTCTAGACA AGTTATACTC GTTTTAAGAC ATTAAGGGAG TGAAATATAT  
420  
GGCTGTAAAA AGAGAAGATG TAAAAGCCAT CGTAAGNCGC TATTGGGGGA NAAGAAAATC  
480  
NTGAAGCTGC ANCGCATTGT GTAACNCGAT TACGTTTNGT GCTTAANGAT GAAANCANAG  
540  
TTGATAAAGA CGCATT AAGG AACACGCGT TGGTCAAGGG GCAGTTCAAA GCAGACCATC  
600  
AATATCAAAT TGTCATTGGT CCAGGAN CAG TCGATGAAGT GTATAAGCAG TTTATTGATG  
660  
AAACAGGTGC TCAAGAAGCT TCGAAAGATG AAGCGAAACA AGCAGCTGCG AAAAAAGGGA  
720  
ATCCAGTACA ACGTTTGATC AAATTGTTAG GGGAGATTTT TATACCAATA TTACCTGCGA  
780  
TTGTGACAAC TGGTTTGTTA ATGGGGATTC AATAATTTAC TTACAATGAA AGGTTTATTT  
840  
GGTCCCAAAA GCACTTATTG AGATGTATCC CGCAAATTGC TGATATTTCA AACATCCATT  
900  
AATGTGATTG CGAGTTACCG CATTTATTTT CTTACCANCA TTAATTGGTT GGAGTAATAT  
960  
GCTGTGTATT TGGTGGTAGT CCGATCCTAG GCATAGTCTT AGGTTTGATT TTAATGCATC  
1020  
CGCAATTAGT ATCTCAGTAT GATTTGGCAA AAGGGAATAT TCCGACGTGG AACTTATTTG  
1080  
GCTTAGAGAT TAAGCAGTTG AATTACCAAG GTCAAGTGTT GCCTGTTTTA ATTGCAGCTT  
1140  
ATGTTCTAGC TAAAATTTGA AAAAGGATTA AATAAAGTCG TTCACGATTC GATAAAAATG  
1200  
TTGGTCGTTG GACCGTAACG CTTTTAGTTA CTGGATTTTT AGCATTTATT ATCATTGGAC  
1260

CAGTTGCATT ATTGATTGGT ACAGGTATTA CTTCTGGTGT TACATTTATA TTCC  
1314

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATAATTATTG NTGGAAAATA ACATTGAGCC CAATTCCCAA CAGTGGCCGA CATTTTCCAT  
60  
CCATTTACCC CCCCCTGACT TTGTATCCGA ATTCNACCN TCCACCNAAG TTGNCATCAA  
120  
TATGTTAATA ACCCAAATCC CAAATTGGAA ATATTTTGCC AAGCCAAGTT TTGATGATGC  
180  
GCATTTGTCC TAATATTTTC CACTTAACAA GATCCGACCC CCAGCCAAGA AAATACATCA  
240  
ACTGAGAAAT ATAATGNCCA AGACTGGTTT CCAACACACA TTCGACATAA TGAGTTGTCT  
300  
AAATTGACTG AGCAACAAC TGTGATTGAG TTGCTTATGC ATATGATTCA TTATGGCAGC  
360  
AGCGTACATA TCATTGGAAC CCAAAGTATC TTAAATGATG ATAAAGTGAA TCAAGTATGC  
420  
GACTATATCG AGTTACATTT TCATGAAGAT TTAAGCCTTT CAGAATTAAG CGAATACGTT  
480  
GGGTGGTCAG AGAGCCATCT GTCTAAAAAG TTTACAGAAT CGCTAGGTGT AGGATTCCAA  
540  
CATTTCTTAA ATACGACGCG AATTGAGCAT GCGAACTCG ATTTAACATA CACAGATGAA  
600  
ACGATTACTG ATATTGCATT GCAAATGGC TTTTCAAGTG CAGCGAGCTT TGCGAGAACA  
660  
TTTAAACACT TTACGCATCA AACGCCTAAA CAATATCGAG GTGATCGTCC AGCAATCACT  
720  
GAAAATCAAC AATCGGCACA ACATAATTAT CACGACCGTG AATTGATATT ACTTTTAAAT  
780  
GACTACATTG AAGAAATGAA TCAATTCAAT TGAAGATATT GAAAAGNTGA ACTTATAAAG  
840  
AGATTGCCTT NAAACCAACT AATCAACAAC TAAATCCAAT TATAATCCAT ATTATTCAAG  
900  
TTGGGCTATT TGAGGAATTT GCTCCAATAC ACAGTATCAA TCCACAGTTG CTTACATGTT  
960  
CATCCCATGA TT  
972

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

AAACCATTTT CCAAAAACCAA GCTGGGCATC CAAGTTTTCC TATTGTAATC TGCAGGTAAC  
 60  
 CAAGGGAATG CTTCCGTGAA TTTAGGTGGT AGCGTAACAT CTATTCAACC ATTACGTATT  
 120  
 AATTTAACAA GTAATGAGAA TTTTACAGAT AAAGATTGGC AAATTACAGG TATTCCGCGT  
 180  
 ACATTACACA TTGAAAACCTC GACAAATAGA ACTAATAATG CTAGAGAACG TAACATTGAA  
 240  
 CTTGTTGGTA ATTTATTACC AGGGGATTAC TTTGGTACGA TACGTTTTGG ACGTAAAGAA  
 300  
 CAATTATTTG AAATTCGTGT TANNCCACAT NCACCACAAT TACAACGACA GCTGAGCAAT  
 360  
 TANGAGGTCA GGAATTACAA AAGTGCCTGT TAATATTTTCG GGAATACCGT TGGATCCATC  
 420  
 GGCATTGGTT TATTTANTTG CACCAACTAA TCAACTACGA ATGGTGGTAG TGAGGCAGAT  
 480  
 CAAATACCAT CTGGTTATAC CAT  
 503

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1118 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCACGAGAC TCAAANCACT GAAGCATTAA CAAAATAATA CTATATTACT GTCTAATCAT  
 60  
 AGACATGTTG TATTTAACTA ACAGTTCATT AAAGTAGAAT TTATTTCACT TTCAATGAAC  
 120  
 TGTTTTTTTAT TTACGTTTGA CTAATTTACA ACCTTTTCAA TAGTAGTTTT CATGCCACGA  
 180  
 GCTATCCTAA CCCACAGATT AGTGATTTCT ATACAATTCC TCTTTTGTCT TTACATTTTC  
 240  
 TTAAAATATT TGCGATGTTG AGTATAAATT TTTGTTTTCT TCCTACCTTT TTCGTTATGA  
 300  
 TTAAAGTTAT AAATATTATT ATGTACAACG ATTCAATCGC TCTATTTTTTC AACTTTCAAC  
 360  
 ATATTATTAA TTCGGAAAGG ACCACTTTAA AATTTAACNG GCCACAACAA ATCAAATCAA  
 420  
 TTAATCACTT TTTCCAAAAT AATCATATAA GGAGGTTCTT TTCATTATGA ATATCATTGA  
 480  
 GCAAAAATTT TATGACAGTA AAGCTTTTTT CAATACACAA CAAACTAAAG TTATTAGTTT  
 540  
 TAGAAAAGAT CAATTAAAGA AGTTAAGCAA AGCTATTAAA TCATACGAGA GCGATATTTT  
 600  
 AGAAGCACTA TATACAGATT TAGGAAAAAA TAAAGGCACG AAGCTTATGC TACTGAAATT  
 660  
 GGCATAACTT TGAAAAGTAT CAAAATGCC CGNAAGGAAC TTAAAACTG GACTAAAACA  
 720  
 AAAAATGTAG ACACACCTTT ATATTTATTT CCAACAAAAA GCTATATCAA AAAAGAACCT  
 780  
 TATGGAACAG TTTTGATCAT TGCACCATTT AACTATCCTT TTCAACTAGT ATTGGAACCT  
 840  
 TTAATCGGTG CTATTGCAGC AGGTAATACA GCAATTATTA AACCATCTGA GTTGACACCA

900  
AATGTTGCAC GAGTGATTAA ACGATTAATC AATGAAACAT TTGATGCAAA TTACATTGAA  
960  
GTTATTGAGG GAGGAATTGA AGAAACGCAA ACGTTAATTC ACTTACCTTT TGACTATGTC  
1020  
TCTTACAGGA GTGAAATTGT AGGCAAATCG TTTATCAAGC TGCAGCGAAA TTTAGTCCTG  
1080  
TGACATAGAA TGGTGGGGAA ATCTCCAGTC ATCGNGGG  
1118

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CCANTTGCCG TTTCTCCTA AACACCAGCG GNACGAGCTC ATGATGGCAT ACATTGTAAA  
60  
TCCGATAATT GACAGTCCAG TTGCTAATCC ATCTAAACCA TCTGTTAAAT TTACCGCATT  
120  
AGAAAAACCT ACTTGCCAAA AAACAATGAA AATAACATAT GCAAATGATA GTGGGATTGC  
180  
TACATTGCGTA AATGGAATAT GTATGCTCGT AGAAAAATTC ACCAAATGAA ACACATTACT  
240  
TAAAACAAAG AAAATAATCG CAATACCAAT TTGCGCCAAA AACTTCTGTT TACTTGTTAA  
300  
ACCTTGTTA TTCTTTTAA CAACAATAAT ATAATCATCT ATAAAACCAA TTAACCCAAA  
360  
ACCAATCGGT CACAAATAAT AACAGGTATG ATTGGATTAG CTTGATCTTA CAAATATAAT  
420  
AGCCACCAA GACGGTTATC ACAAATACTT TAATAGAAAT GGTTAGGCCA CCCATCGTTG  
480  
GTGTACCAGT CTTCTTCATA TGGCTTTGTG GACCTTCTTC TCGAATACTT TGACCAAATT  
540  
TCATCCTTTT TAATGTAGGT ATTAAACAG GTACCAAAC AAATGTAATC ACTAGCGCTA  
600  
ATAACGCATA TACAAAATC ATAACATCT CCTCTTCTTA ATCCAGACTT TTTTAACCAC  
660  
TAATATATTA TCAAG  
675

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTAGATACA ATTACTCAAT ATGATGTACT GGAAGCANTT ATAGATACTA AAAAACACAT  
60

TGNCTGTNCG ATGANTNTCA TCTTCACATG ANNTANCGGG TTGATTAACN AAGATTGCAG  
 120  
 ACCGTGNTGT TGTGATGANA AATGGTCANC TGATAGAGCA TGGTACACGT GAATCAGTCT  
 180  
 TGCATCATCC AGAACATGTT TATACGAAGT ATTTATTATC ANCGNAGAAG AAGANTAATG  
 240  
 ATCATTTTAA ACATGTGATG AGGGGTGATG TACATGANTA AAGTTACAGA TGTTGAAAAA  
 300  
 TCATATCAAA GCNCACATGT TTTTAAGCGT CGTCGAACAC CTATCGTGAA AGGTGTGTCA  
 360  
 TTTGAGTGTC CAATCGGTGC GACGATTGCG ATTATCGGAG AAAGTGGTAG CGGTAAATCG  
 420  
 ACGTTGAGTC GTATGATATT AGGTATTGAG AAACCGGATA AAGGCTGTGT AACCTTAAAT  
 480  
 GATCTACCGA TGCATAAGAA GAAAGTCAGA CGTCATCAAA TTGGTGCTGT ATTTCAAGAT  
 540  
 TATACGTCAT CATTACACCC ATTTCAGACT GTTAGAGAAA TCTTATTTGA AGTGATGTGT  
 600  
 CAATGTGATG GACAACCTAA AGAAGTTATG GAAGTCCAAG CAATTACATT GTTGGAAGAA  
 660  
 GTCGGTCTAT CTAAGGCATA CATGGATAAA TATCCTAATA TGTTATCAGG TGGAGAAGCG  
 720  
 CAGCGTGTTG CGATTGCGCT CGTGCC  
 746

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AATGTCAGAC AGATACTGCC ACAAGATGCG TGCNTATGAG ATTTGCTGT GTATGAATAG  
 60  
 CGACACGAGC GGCACGAGCG CTCACNTCAT TTCCAATTAA AACTAATGCC TAAATCTGAT  
 120  
 GCAGTAAAT CTATCATGAT TCACTCTTAA CATCCGTATT TCGTGCTACT AATTGATGTC  
 180  
 TTGCATTGAA AAATTGACCA TAGCTTAAAT ATGTCGCAAT CAAAGCAGAC ATAATGNTCG  
 240  
 CAGTTGTATG AATAACACG ACTAACAATT GAAATTTAAT CGCTTGTAAG GGTGGTACGC  
 300  
 CACCAATAAT TAAGCCTGTC ATCATACCAG GAATCGACAC AAGCCCATAT GTTTTAACCG  
 360  
 AATCAATTGT TGGCACCTAT AGCTAAACGA ATACTTTCAC GTATTGCACC TTTAGAAGCC  
 420  
 AATTTAGGTG TAGCTGCAAG TGATAATTTA GATTCAATAT TAGTACCATC TTGTACGAAT  
 480  
 GCACGATCTA AATTCTGGTA AGCTAAATTA ATTGCAATCA AGCCATTATT TNCAAGCATN  
 540  
 CCGCCGATAG GTATAACTTC ATTGGCTGTA AAATGAATTG CCCCTGTAGC TACAGTACCT  
 600  
 GCAAGTGGTA ATGCTGTTCC AATGAAGATN GCTGGAAATG GTNTCCAAAA CACANGGGGC  
 660  
 ATCACTGTGA TGCTCGACTA ATGGTAAGAG TC  
 692

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AATATAGCGT TTTNACCCCT TTGTGTNACC CTCCCCAAGA GATATAACAT NCCGCCGTNT  
60  
AAAATCAATT AGAAATATCT TTTTATTCTG ATAATAGACA CAGTATAGAC ACATTTTAAT  
120  
GGGTGATACC ACTTGTAATA TCACGGGGTT GTNATGTNTT GNATATCANT NAAATACTTA  
180  
TATANAAATA TTGCTCGGAA TATAAAAAGN TAAATAGGNT TTTGAGTTTT AAATATGAAA  
240  
TACAAAGCGC CCANTCGAAC AAAGTATTTA TATTAAAATA TGGAAAATCC ATCANTATTA  
300  
AATTAAAATN GTTTTATTAT GATAAAGTGA AAGTAGGTAA GTCTATGGAA GGTCTTAATC  
360  
ATCGAAGAAA TACAGAAAAA GAAGAGACAA CACAAACGCA ATCAGTTGCA CCTAATACAG  
420  
GTGAAGAGGG GATGTCATCA GGCAAGTAAC ACAATCAANT AAGACGTCCG ACATACATAA  
480  
ATGAATCTAT CAATAAACAA ATGGAAGCCA AAGCGCATGA AACAGCGCAA AATGCAGATT  
540  
TAAAAACCGA AGCAAGAAGT TTATTTGATA ATGCAACCAA ATCAATCGGG AGACTAGCCG  
600  
GCAATGATGA AAGCATAAAT CTTAATTTAA AAGATATGTT TTCTGAAGTA TTTAAGCCGC  
660  
ATACTAAAAA CGAAGCAGAT GAAATATTTA TAGCGGGTAC TGCTAAAAC TACGCCAGCAA  
720  
TTTGTGACAT ATCAGAAGAA TGGGGGAAGC CATGGCTCTT TTCTCGAGTA TTCATCGCTT  
780  
TCACAGTAAC ATTTATTGGA TTATGGGTCA TGGCAGCGAT TTTTAATAAC AATGACGCTT  
840  
GTACCGGTGC TCGTGCC  
857

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CTCACTTTGT TTTCCAGTAT GGAACGCTTG CCCTAAGTCC TTAATTGCAT TATAAAATTC  
60  
AGGCGCTAAA ATAATCGCAA TTGCCGCGT TTTAAATCA ATATTATGAA ATACTACTAA  
120  
GCTTAGCGTT GCTTCCAATG CAACCAATCC AATACCTAAC ATACTTATAA ATTCGAGCAT

180  
 TAATCCCGAT AAAAAAGCAC TCGTAAAAAT GCGCATTGTT AAAGTTCTAA ACTGAGTACT  
 240  
 ATCGTCGTAA ATATGCTTCT CTGTTTGCTC TGTACGATTA AATAGCTTTA ACGTCACTAA  
 300  
 ACCTNTAGCA ATATTTAAAA ACCGNCGACT AAATTGATTC ANATAAGTCA TTTGATCTTT  
 360  
 TTGACGCATC GAGCGTTTTT AAACCGAAAA TAATATAAAA CAAAGGAATA AATGGTGCAG  
 420  
 NTATTAACAT AATTAATGCG GNATTGAAAT GGATGAAAAA CAATGCAATG ATTATGATGA  
 480  
 GCNGAACCAT CAATCGATTT GAACAACTTG AGGCAAATAA CTCTTATAAA AAGGTGCTAA  
 540  
 ACCATCAATG TTTTCTGTGA GTATAGTCAT TTGTTACCG ATTGGATGAC CATTATTTTT  
 600  
 ATAAATAACC CGCTGTCTAA GCATATGCTT AACTTTAAAT GCTAATGTAT CACCTAACCA  
 660  
 TTGATTTAGA AATTGCACAG NTGCTCTTAA AAGTAAAACA CCTAATAAAA TAAATAATAC  
 720  
 AATCCATAAA CCTTGAAATT GATGTCTTAT AATTTTAGCT AAAAAATCTG CTATTAAAAT  
 780  
 ATTGTGCGTT ATAACGAGTA TGCCCGAGAC CAGTACTGAC CAAGAACATG AGTACCGGAA  
 840  
 AAATTTTATA TTGAAACAGT ATTGTTGTTA ATTTTTCACA ATTATATCAC CTAACCTATA  
 900  
 TAAAGTT  
 907

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

AATTTTAAAG ACCCCNCGCA TAAATANCCA TCCCACCTAC TTATCCAAAA GTTANGTGGA  
 60  
 TGGTTTTTCA ATTAAAATTA ATATTAGTGT AANCCAATCA AAGATTTAAT CNAATATGCC  
 120  
 CCTGCTCAA ACATTTCTC ATTTAATTTG CTTTACTTTC AATTTAATAT CATTATCCAC  
 180  
 AACACTTGGC GTGTCATCGT TATTATTTTCG CATCTTTGAC ACGTTTATCA TCATTAGGAN  
 240  
 TCGGCACCGA ATAAAATTGC GATAAATGCC ATGATTCCCA TTAATACGTT AACCCAAAGT  
 300  
 GCAATCATCG CACCTGTATG AATGCTCGTT GCAGCAACTG CACCAACATA TACAGCACCA  
 360  
 CTAATTGCGA CACCGAATGC GCCACCAAGT GATGAAGCCA TTTTATAAAT ACCTGAAGCA  
 420  
 ACGCCAACTT TATCTAACGG TGCATTGCGA ATAGCTGTAT CTGTAGAAGG TGTTGCATAA  
 480  
 ATACCTAAGC CTAGTCCGAA ACATAAATAT CCTACGACAC AACTGATAAC ATAAAATATG  
 540  
 CCTGGTAAGA ATACTANTGA AATAAGTGCA ATNCCAATGA CCACAATGNA TGTACCTNAT  
 600  
 AACATTGGTC GCTTAGAACC CANTTNTGGT NATAATAATT TTTCACCAAC TCGAATCATC



660  
AATAACAACA TGATTAAATA AGTAANTGAT NAGTATCCTG CCTGCCATNC TGTATAACCT  
720  
AAACCTTGTT GCACGCATGT ATTCGCTACA ATTNATGTAC CTACAACNCC GTTG  
774

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTCTGATTCA ACAAATGAT TATTCTTTAC GTAAACTACC TTTTTTTATT TGAGATGAAG  
60  
CATATGCTTT TAATAATATT GTCCCAATAA TACCAACTGA AATAATATTT AATACTGCAG  
120  
AGATAACACC TTGTGTATAA ACCTTGTTAG CCGGTTTCGTT ATAAATCAAA ATATCTAATG  
180  
TTGGTGCAAT AAGTGCCCAG CAAATAATAT TCGCAATAAT TTGACCGATA TTAAAATAAA  
240  
TCATCGATTT CCTAGAAAAT AGGCATGAAG AAAGATTTAA TTTTAGGGCC AATCCATCCA  
300  
TATTAAACAG GCGATAATTC CTGAACAAAT AACCCAACTC CACCAAGCAC TACCCGTATG  
360  
TCGGGGAAAT CTTTAATAGC GTGNCCAACT AATCCAGGCA TTAAACCAGC AAAAGGCCCA  
420  
AATATTGCAG ATATTAATGC TAAAAATGCA TAAGATGTTT CTATATTCGT ATTAGGAAAA  
480  
CCTGTTGGTA TTACAACAAA ACGCCCTAAA ATCACAATA CCGCNGCTCC TATACCAATC  
540  
GCAACAACAG TTTTAACTGA AATATCNTGT TTTTTCATCT TCATTACTCC TTACATAAAA  
600  
AATTCATTAA ATTGATGGTG CTTTAGATAA ATGAATCGTC CAATCATTTT CAGTACCAAT  
660  
ATGATATAAA TCTGAAAATG AGTCTCGATT GACTGCTACA CCAATATTTA CTAGCGAGTT  
720  
AACATACACA AGAGGTTTAC CCACATTAAC ATCTGCAAAC GATCGCTCGT GCC  
773

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CATAAGACAT GTAAATTCTA AGATGATTTG TTGGATAGGG TAGCTCCATA TAATTCTTGA  
60  
ATCCNATCAT TATTACATTA ATAAAAAAA CACCCACAAT TGTGGGTGAT TGTAATGAAC  
120

GTATTATCTT GGCACGAGTA CTCAACGATT AATTGTTTCGT TAATTTTCAGC AGGTAATTTCG  
 180  
 CTACGTTCTG GTAAACGTAC GAAAGTACCA GTTAAGCTGT CAGCATCAAA GTTTAAGTAC  
 240  
 TCAGGTACGA AATTGTTGAT TTCAACTGAT TCAACGATGA TGTTTAGTTT TTGAGATTTT  
 300  
 TCACGAACTG AAATTGTTTG ACCAGGTTTA ACAGAATAAG ATGGAATATC AACACGTTTA  
 360  
 CCATCTACTA AGATATGACC GTGGTTAACT AATTGACGTG CTTGACGACG AGTACGAGCT  
 420  
 AAACCTAATG AATAACAAC AGCGTCTAAA CGACTTGCTA ATAAAATCAT GAAGTTTTCA  
 480  
 CCCGCGTACA CCCNAATTTT TTACCAGCGA TGTCAAATGT GTTACGGAAT TGTCTTTCAG  
 540  
 TCAATCCATA TTANGTAACG TAATTTTTGT TTTTCACGTA ATTGTAAACC ATATTCTGAT  
 600  
 AATTTTTTAC GTTGGTTTGG ACCATGTTGT CCTGGTGCGT AAGGACGTTT TTCTAATTCT  
 660  
 TTACCAGTCT CGTGCC  
 676

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGCACGAGCG ATGATGGCTG TCGGAACAGG TGCATTTGGT GCGCATGGTT TACAAGGGAA  
 60  
 AAATAAGTGA TCACTATTTA TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG  
 120  
 GCTTAGCATT ATTAATTATA GGTGTAATTA GTGGTACAAC TTCAATCAAT GTTAACTGGG  
 180  
 CTGGCTGGTT AATATTTGCT GGTATTATTT TCTTTAGTGG ATCATTATAT ATTTTAGTAT  
 240  
 TAACTCAAAT TAAAGTTTTA GGTGCGATTA CGCCAATTGG TGGCGTATTG TTCATCATTG  
 300  
 GCTGGATAAT GTTAATCATT GCGACATTCA AATTTGCTGG TTAAATTTTA AACTTTTAGA  
 360  
 TTACCTATGT AACTAAACAT TAAATTTTTA ANAAAAA  
 397

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TATCTTTAAG AACAATTGAA GCCGCTAACC ATCGGAGAAA GCTGTAAAT CCAAGTGTG

60  
 GCCTGCTAAA TACCCACAAT CATCACGGGT CGTTGCCTTG TACCACAATA GAAGGCAGCA  
 120  
 TTATACCCA AATATTTGCA TAGCTAATTG TGATAAAACT GTCGTTTCCG TTTGTGGCAT  
 180  
 AATTCCATAA ACATATGCTA AACCACCGAT ACCAACTAAT AAAAACGCTA AAATTGAACC  
 240  
 CATAGCAATT AACGTTTTTA CAGCATTATT AGCACTTGGT TCTCTAAAAA TTGGTGACCG  
 300  
 CATTTGAAAT AGCTTCAACA CCTGTTAATG ATGAAGCCCC TGATGAAAAA GCTCTTAATA  
 360  
 GCAAGAATAA TGTTACTCCA GGANCCGCAG TTCCTACTGA TGCATGCATA TGTGGTTGAA  
 420  
 TATCTCCTGT CGCCACACGG AAAGTACCCT ATAAATATTA ATATCACTAA CCCATAATG  
 480  
 ANAAGATATA CTGGATAGGA TAATACGGTG NCAGATTCAG TTAAACCCAC GTAAATTTAA  
 540  
 TATTAAAATA AAAAGTACAA GTAAACATGC AATCAGTACT TTATGCCCAT ATAACTTGG  
 600  
 GAATGCAGCA ACANATGCAT CAGCACCAGA TGATATACTA ACAGCGACAG TCAGTATGTA  
 660  
 ATCGACTAAT AATGAGCCTC CTGCAAGCAA TCCCCATTTT TCTCCTAAAT TGGTCTTGA  
 720  
 CACCATATAC GCTCGTGCC  
 739

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGCACGAGCG AGAACGATTG AAGCTACAAT ACCTGATGTT GCTGCGGGAA GTACGACTTT  
 60  
 AGTTGCTACT TCTAATTTAG TTGCTCCAAG TCCATAGGCA CCTTCTCGAA TTTTATTTGG  
 120  
 TACAGATGCC ATTGCATCCT CACTCAAACT TGTGATGAGA GGGACAATCA TAATACCGAC  
 180  
 AACTAAGCCG GGA CT TATAG CATTAAACTC TCCAAGACCT GATATGAAAG ATCTTAATAC  
 240  
 TGGTGTAACA AAGGTTAATG CAAAGAAACC AAACACAATT GTTGGTATTC CTGCTAAAAT  
 300  
 TTCTAATATC GGT TTAATTA TGCGTCGGGC ACGGGCACTT GCATATTCAC TTAAATAAAT  
 360  
 TGCTGCACCA AGCCCGACTG GAACTGCAAA TATAGTCGCA ATAACTGTGA TTTTAAAGT  
 420  
 CCCTATTATC AATGCCAGAT ACCAACTTA GGGTCTGAAC CGGTAGGATT CCAGTAGTAG  
 480  
 AAATAGAAAT CAGTATTGGA ATTCTGG  
 507

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATAGTCTA CTCATTCATC GTCCTTCACC ATTGATGGAT CCAGAACAAG TTGCTGATGC  
60  
ATTAATAAAA CTTGTAAAC AAGGTAAGTT GAAGTCATTC GGGGTGTCGA ATTTTAATCA  
120  
TTCACAATAC CAATTGTTAA ATCAATATAT TATGAAAGAA AGACTACATA TTAGCATCAA  
180  
TCAATTAGAA TTATCGCCAT ATCACGTTGA TAGTTTACAA GATGGAACAA TGGATTCAAT  
240  
GTATCAAAAC CATGTTCAAA TTATGGCTTG GAGTCCTTTT GCAGGCGGTA AAATTTTCGA  
300  
CAAGGAAGAT ATTAAAGCGC AACGTATTAT GAAAGTTGTC AATCAATAGC TGACAAATAT  
360  
GGTGTGAGTG ACACAGCTGT GATGATAGCA TGGTTAGTAA AAATACCGCA TAGTACCATG  
420  
CCGATACTGG GAACAAGTCA GTTAAAGCGT ATNGATCAAG CAATCGAAGG GCTACAACTT  
480  
AATTTAGATG ATCAAGTCGT GGGTTGACAT TTACAACGCT ATTATCGGAC AAGATATCCC  
540  
GTAAACTTAN NNACNCNNA ATCATAAATG GAGCATACCA TGACAAACGA AGATAAACGT  
600  
TTCGAACAAT TAAGATTTGA ACGCAAATTT ATAGTTATCC CGTATTTAAT TTATGCAGTC  
660  
ATTGTATTAC TATTAAATAT TTTCTATTCT GATTTGAAAA TAACAATGAC ATTATTCGGA  
720  
CTTTTCTTTG CGTATAATGT AGTCATTTTG TTC  
753

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 542 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CCCATTATTA TTTNGAAAAT GAATTGGAAA ATACAGTAGA CGAAGTGTGG GTTGTATACA  
60  
CTTCTGAAAG TATACAAATG GATCGTTTAA TGCAACGTAA TAATCTGNCA TTAGAAGATG  
120  
CGAAAGCACG TGTCTACATA CATCAACGCG TACGTAAAGT AATGACTTAT TTATAGTGTA  
180  
ATATTAATCT TCTTCTCCGN AATTCGGNTT TNCAATATAA CCTTCTTCTT CTAACAANCT  
240  
CTCAAGGTTG TGNGTNAATN CAAGTTTATC CCCTAAATTA TCGATAACAT GATCGGCCAN  
300  
TCGGNTNNNN NNATCAATAG AAATTTGGNT TATAGACACG TGCTTTCGCA TCTTCTAATG  
360  
ACAGATCATN ACGTNGCATT AAACGATCCA TTTGTATACT TTCAGAAGTG TATACAACCC  
420

ACACTTCGTC TACTGTATTT TCCAATTCAT TTTCAAATAA TAATGGAATA TCCACGAACC  
480  
ACATTATATC CTTGGTTTTA AATATTCTTG CTTTCTTCT GCCATAATAT CTCGCACGAA  
540  
TA  
542

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TCAATCCANC CTCCAATTGC TGATGAAGAA CCTCCTTCAG CNCCCACCCA TTANNGGGGC  
60  
CANAGTCATA AGTAACAACT TTTGAACCAA TTGTATCTTC AATTGAATCT GTAATCTTAT  
120  
CTCCCGCTTC TTCCCATCCT AAATGTTCTA ACATTAATAC AGAACTTAAA ATTACTGAAG  
180  
NTGGATTCAC TTTATTTAAA CCTGCATATT TTGGANCTGA GACCATGTGT TGCTTCAAAA  
240  
ATAGCATGAC CTGTTTCATA ATTAATGTTT GCACCTGGCG CAATACCAAT NCCACCAACT  
300  
TGTGCAGCTA AAGCATCTGA AATATAGTCA CCATTCAAGT TCATAGTTGC TACAACATCA  
360  
TGCTCAGCTG GACGAGTTAA AATTTGTTGT AAGAAAATGT CAGCAATAGA ATCTTTAATG  
420  
ATAATCTTGC CTTCTTTCAC AGCTTTTTCT TGAGCAGCAT TAGCAGCATC TCTGCCTTCA  
480  
TTTACAACAA TTTGCACATA TTGTTGCCAA GTGAATACTT GCATCACCAA ATTCAGATAA  
540  
TGCTAAATCG TAACCCCACT GCTTAAATGA GCCTTCTGTA AATTTCATAA TATTACCTTT  
600  
ATGAACTTAA AGTAACTTGA TTTACGGGTT ATTTATCGAT AGCATATTGG TATAGCTGCT  
660  
CTACTAATCG CTCAAGTCCT TCTTTTAGAA CTTGGTTTAA TACCAATACC TGAAGGTTCT  
720  
TGGAATCGAT T  
731

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TTTGACATCT CTCAAAAATT AAAGCATAAA GGTTCATCGG AAAGGCGCAA AATTCACAGT  
60  
TGTTTGTTGG TTTGTTATTT CCCTCNCAAT ATTCAGTATT AGACATTTAT AGTTTGAAA

120  
 ATGCGTGATA ATTAGTTGTA TTCAGTTATT AAGTAATAAA TTTTGGAGG CAGAACATCA  
 180  
 TGAAATTAAC ATTAATGAAA TTTTGTGG GGGGATTTC AGTATTATTA AGTTATATTG  
 240  
 TATCTGATAA CAATAACCTT GGGAAAGAAT TTGGCGGTAT ATTTGCAACG TTTCCGGGCA  
 300  
 GTATTTTATAG TGTCTATGTT TATTACAGGT ATGCAATATG GTGATAAAGT CGCTGTGCAT  
 360  
 GTAAGTCGTG GCGCAGTGTT TGGTATGACA GGGGTATTAG TTGTATTTTA GTAACATGGA  
 420  
 TGATGTTACA TATGACGCAC ATGTGGTTGA TTAGCATTAT TGTTGGTTTC CTAAGCTGGT  
 480  
 TCATCAGTGC AGTATGTATT TTTGAAGCGG TAGAATTTAT AGCACAAAAA AGATTAGAAA  
 540  
 AGCATAGTTG GAAAGCTGGA AAATCGAATA GTAAATAGTG TGAACGTAAT CTCTTAACTA  
 600  
 GGACTAACTT TGCAAGCATT GAATAGCATG GAAAAGTTGC ATCATTAAATA AGTGAAATTC  
 660  
 AAGTTGGCAT TGAGAAAATT ACAAGCGCTC GTGCC  
 695

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GGCACGAGCT CGGCTTGACG GTAGGAAATA TCAGCACGAG CTTGATTCAA CANCCGAATC  
 60  
 AGGGAGGAAA TGCAGGTATA ACTCAATCTA AGTTCGCTAA GAGACATCCA ACGTTTTACN  
 120  
 AGGCAAATCC AAGCNAAAAG GATTGCTTCN AATAATATCC CACCAAACAA TTTAAGACAT  
 180  
 TATGCTGTTA AGAGGTCACC AACNATATAT ATAGTGGTTA CGGATCAGTT ATTAGCGTTC  
 240  
 TTTAACAACA GATATTGGCG CTCACAGTTT AACCCAAGAG GTGGTTGGTC TCCAAGTGGT  
 300  
 CCAAGAAGAT ATGCGAATGG TGGTTTGATT ACAAAGCATC AACTTNCTGA AGTGGGTGAA  
 360  
 GGAGATAAAC AGGAGATGGT TATCCCTTTA ACTAGACGTA AACGAGCAAT TCAATTAACT  
 420  
 GAACAGGTTA TGCGCATCAT CGGTATGGAT GGCAANCCAA ATAACATCAC TGTAATAAAT  
 480  
 GATACTTCTA CAGTTGAAAA ATTGTTTGAA ACAAATTGTT ATGTTAAGTG ATAAAGGAAA  
 540  
 TAAATTAACC GATGCGTTGA TCAAAGTGT CTTCTCAGGA TAATACTTAG TTCTATGATG  
 600  
 CACTTAGAAG TT  
 612

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCACGAGCG ACTTTTTCTA GGCATAATCG AATTGACAAT GGTACTCAAG CTTAAAAATG  
60  
GCCCACTTAA TTCAGGCAAT AACAGACTAG GCATAACATT ATTTTTCATC AATTTAAATG  
120  
TGTA AACAT CGATGACATT GTCTGTTGCT GTTGTGATA AACATTCATA TCGTAGCGGT  
180  
CTGCAAATTC TTTAATGCGA TATGCCGGCG GCACGAGACA TGACAGGTAA TGAATCATGT  
240  
TTGAATTGTT CGTCTACGGC ATCTTTTGA ATAGGTAATC CAAAGAAACC TGCAATACCA  
300  
ATCGTTTCAA AGGGCCCTGC TGCTTCGATA TGTCTACGAA ATGGTTCTGA ACGAACATCT  
360  
ATACAAAATG CAATTTGCGC TTTCGTTGAT GTGCCACCT GATTTAGCTC GCTATTATTT  
420  
TCATCAACTG CTTGTGTGTC AATTAACAAT ACTGAATGTG GCTGATTAGC GTTATCATTT  
480  
TCTGAGACAT TTAATTGGTT TACATCTAAT GCGCCCGCCA CACTTTCATG ACTGCTTTAA  
540  
TTTTTGT TTTT AACTGAGATC GTATGTCAAT TTCCAGGCA ATTAGCCATA AATTNTAAA  
600  
TACAT  
605

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGCACGAGCT GATCAAGGGT GTAAGTTGGT AGTGGTCAAT AAAGAACAAT CATTACCAGC  
60  
TAACGTAACA CAAGTGGTTG TGCCGGACAC ATTAAGGAGT AGCTAGTATT TCTAGCAACA  
120  
ACAACATTAT ATGGATTATC CGGAGTCATC AGTTAGTGAC ATTTGGTGTA ACGGGTACAA  
180  
ATGGTAAAC TTCTATTGCG ACGGATGATT CATTTAATTC AANGAAAGTT ACAAAAAAAT  
240  
AGTGCATATT TAGGAATAA TGGTTTCCAA ATTAATGAAA CAAAGACAAA AGGTGCAAAT  
300  
ACGACACCAG AAAACAGTTT CTTTAATAA GAAAATTAAA GAAGCAGTTG ATGCAGGCGC  
360  
TGAATCTATG ACATTAGAAG TATCAAGCCA TGGCTTAGTA TTAGGACGAC TGCGAGGCGT  
420  
TGAATTTGAC GTTGCAATAT TTTCAAATTT AACACAAGAC CATTTAGATT TTCATGGCAC  
480  
AATGGAAGCA TACGGACACG CTCGTGCC  
508

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```
GGCNCGAGAC TGTCGAATAT TTAGTAGTAA CTTCAGATTA CAAGCGTATG ACTTATCGAC
60
CGAACGGTAC AAATAAAGTA TTTGTTAAAA GAAAAGAAGC GGGNTCATGG TCTGAGTGGT
120
CAGAATTAGC TATTAATGAT TACAATACAC CTTGTGAAAC TGNTCAAAGT GCCCANTCAA
180
AAGCTAATAT GGCCGAAAGT AACGCTAAAT TATACGCAGA TGACAAGTTT AATAAAAAGGC
240
ATTCGAGTTA TTTGTGGATG GAACAGCAAA TGGTGTGGGC TCTACATTGN ACTTAAATGA
300
GAGTTTAGAC CAATTTATTT TATTAATTTT TTATGGGACT TTTCCAGGTG GTGACTTTAC
360
AGAGTTTGGC AGTCCTTTTG GAGGAGGAAA GATTTCATTG AATCCCTCAA ATCTTCCAGA
420
TGGTGATGGA AATGGTGGAG GTGTTTATGA GTTTGGATTA ACTAAATCTA GTCGTACATC
480
TTTAACTATA TCAAACGATG TCTATTTCTGA CTTAGGAAGT CAAAGAGGCT CTGGTGCGAA
540
CGCAAATAGA GGGACAATTA ACAAATTAT AGGAGTGAGA AAATAATGCA AATATTAGTT
600
AACAAGCGTA ATGAGATAAT TTCATACGCT ATCATTGGTG GCTTTGAAGA AGTATGATAT
660
TGAAATTACA GAAATTCTCT CAAGTTT TAG ACTAAGCTTT AAATATCAAT GGGGAATAGTT
720
TTACGAAGAT ATCCGAGAAA AGATGACTGC
750
```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
AAATGCCGGG GGAGCTCAAG TATATGACTG AAATAACATT CAAAGGTGGA CCAATCCACT
60
AAAAAGGTCA ACAAATTAAT GAAGGTGATT TTGCACCTGA TTTTACAGTG TTAGATAATG
120
ACTTAAATCA AGTAACATTA GCAGATTATG CTGGTAAAAA GAAATTAATT AGTGTGGTAC
180
CATCAATTGA TACAGGTGTT TGTGATCAGC AGACTCGCAA ATTCAACTCT GAAGCTTCTA
240
AAGAAGAGGG GATTGTGCTT ACAATTTT CAGACTTACC ATTCGCACAA AAAAGATGGT
```



300  
 GCGCTTCAGC AGGTTTAGAC AATGTCATTA CATTAAGTGA CCACCGTGAC TTATCATTTG  
 360  
 GTGAAACTA TGGCGTTGTT ATGGAACGAA CTTCGTGCCG AATTCGGCAC GAGCTCGTGC  
 420  
 AGTATTTGTA TTAGATGTAG ATAATAAAGT TGTTTATAAA GAAATCGTTA GTGAAGGTAC  
 480  
 TCGATGCCCC AGATTTTGAT GCTGCTTTAG CTGCATACAA AAATATTTAA TCATTAAAGA  
 540  
 GATAAATCTT AAAATGTATA CATCGTGTCC ATCGTTGTCA ACAGCATTAA AATAGAATTG  
 600  
 TTTTCTATGA TTGCTAAGAC CTATGGGCAC TTTTATTGG AGAGGGACGA ATATGGCAGA  
 660  
 ACAACAAACA ATTATGGAAC GCTTGTTTCA TACATTAGAT GAAAAAGCTA AAACATTAAA  
 720  
 TAATGAAAAT GGCCAAAGTT TTATTGAAAA TCTTGGGCTA GCAATGGAAC AAGTATATAC  
 780  
 CAATGAA  
 787

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGCACGAGCG CGTCATATAA TGAAAGTAAT GATAAAAAGA AAGGATAACT TAATGTGAGT  
 60  
 CAAGAACGTT ATTCAAGGCA AATTTTATTT AAACAAATAG GTGAAATAGG TCAAAGCAAA  
 120  
 ATAAATCAAA AATGTGCGTT GATTATTGGT ATGGGCGCAT TAGGTACACA TGTGGCCGAA  
 180  
 GGACTTGTTA GAGCAGGCAT TGCTAAACTA ATCATTGTTG ATAGAGATTA TATTGAATTT  
 240  
 AGTAATTTAC AAAGACAAAC ATTGTTTACT GAAGAAGATG CTTTGAAAAT GATGCCTAAA  
 300  
 GTGGTTGCAG CTAAAAGCA TTTGCTAGCG TTACGTAGTG ATGTTGATAT TGATGGTTGT  
 360  
 ATTGCCCATG TGGATTATTA TTTTTTGGGA AACACATGGA CAGGACGTTG GACGTTATTA  
 420  
 TTGATGCAAC CGATAACTTT GAAACACGAC AACTGATTAA TGATTTTGCA TATAAACATC  
 480  
 GTATTACCTG GATTTATGGC GGGCGTTGGT CAGAGTACAT ATTCAGGAAG CTGCATTTAT  
 540  
 ACCTGGNAAA CACCTGCTTT ACTGTTGG  
 568

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
CTACNNTAAT AAGAAAATAT AACATACNAA TCAAAAACTA AAGGGATGTG ACGTTAATGA
60
AACTCGTATT TGTGGCACGA GCTGGTAATA TGGCACAAGC TATATTTACA GGAATTATTA
120
ACTCAAGCAA CTTAGATGCC AATGATATAT ATTTAACAAA TAAATCTAAT GAACAAGCTT
180
TAAAAGCATT CGCTGAAAAA CTAGGTGTTA ACTATAGTTA TGATGATGCG ACATTATTAA
240
AAGATGCAGA TTATGTTTTT TTAGGTACCA AACCGCATGA CTTTGATGCT CTAGCAACAC
300
GCATCAAACC ACATATCACA AAAGACANTT GCTTCATGTC AATTATGGCA GGTATTCCGA
360
CTGATTATAT TAANCAACAA TTAGAATGCC AAAATCCAGN TGCTAGAATT ATGCCANACA
420
CAANTGCGCA NGTTGGACAC TCAGTTACTG GCATTAGTTT TTCAAACAAC TTTGAACCCT
480
AAATCCTAAA GATTAAATTA ACGATTTAGT TAAAGCATTT GGTCTGTATT GAAGTATCCA
540
GAGATCATTT TACATCCAGT TACAGCTATC ACC
573
```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
CTCTATTATA AACATATTAA AACGCATTTT TCATGCCTAA TTTATCTAAA TATGCATTTT
60
GTAATTTTTG AATATCACCT GCACCCATAA ATAAAAACAAC AGCATTATCA AATTGTTCTA
120
ATACATTAAT AAGAATCTTC ATTAATGAAC GATGCACCTC CAATTTTATC AATTAAATCT
180
TGTATCGTTA ATGCGCCAGA ATTTTCTCTA ATTGAGCCAA AAATTCACA TAAGAATACA
240
CGATCTGCTT TACATAAACT TTCTGCAAAT TCATTTAAAA ATGCTTGTGT TCTAGAGAAA
300
GTGTGTGGTT GAAATACTGC AACAACTTCT TTATGTGGAT ATTTCTTTCTG TGCTGTGTCA
360
ATTGTAGCAC TAATTTCTCT TGGATGGTGT GCATAATCAT CTACAATAAC TTGATTTGCA
420
ATTGTAGTTT CATTGAAACG ACGTTTAACA CCACCAAACG TTTCTAATGC TTCTTTAATA
480
TTTGTAACAT CTAGCTTCTC TAAATAACTA ATCGCAATTA CAGCTAATGC ATTTAAAACT
540
GTATGGTCAC CATATTGTGG AGACAGGAAG TGATCATAAA ACTCACCATC CACATACACA
600
TCAAAAGCAG TCTCGTGCC
619
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
GGCACGAGCG TGTCAATATT TACATGATGA TTTCATTTAA TAGCCTTTTT TAGCATCAAC
60
TTCATTCTCA ATTAGACCAT TCTTATTGAG AAAATTAAC AGATTGTTTT TAAAAATATC
120
TAATAAGTCA TACTTTGCCT CATAATCATT ACCAGTTATA TGCGCTGTTA TAGTTACATT
180
TTCCAATTCA TATAATTCAT GATTAGGTTT CAAAGGTTCA TTTTCAAACA CATCTAAATA
240
TGCATGTCGA ATAACCTTAC TTTTAAATAC TTCTATTAAG AGCGCTTCCT TTAACATATGC
300
TACCTCGTCC TATATTTATA AAAAGTGCTT CCATCCTTTC ATTAATTCCA AAATGTTTTT
360
TTCCTTTAGT TAAATGAATC CGTTTCCTTG CGTTTCCTGG TAAAGCATTT ATAATAATGT
420
CAGCATTTGG TAATGTGCTT TCA
443
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
GGCACGAGCT ATGTGGTTTG AAGTCAATCG CCAAATGTTC CACCTACCAT TCTGATAAAA
60
GTATTTACTT GTTCTTTATT CCATAACACA TATACTTTAT GATCTCTATT TTCAAATTGT
120
CTATGCACAT ATTTTTGTAA AGGATGCAAC TTTCCTTTTT CTTGCTTCAT TTCTACAAAA
180
TATGTTTTTC CTTCTGGCAT AATAATAATT CTATCTGGCA CACCTCTTGT TCCAGGTGCG
240
ACCCATTTTA AACATAAACC GTTTAGCTTT GTTATCTCTT TCACTAAATA TTTTCTAAT
300
GTCGATTCCCT TTCATTTATT CACCTTGAT ACAAATTTA TATTTGTGTT CCGAATGTTT
360
GTTATCAATT CCTTGCCAAA CTTTTTAAAA ATAGCTGTTT AGAGGGTTTA CCCCTATACC
420
CCCTTTACTC CCCTAAACAC TACTTTTTTA AACTTTATAG TGAATTTGAA TGCAACATTG
480
GGAAACAAAC AGGTTTGAAC CCCTACAGCT AGAAAGAAGA GTGTTTGTA TCATTGTTGC
540
ATCATGTTGC ATCACC AAAA TGATACAAC
569
```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GGCACGAGCG CAAAATATTT CAAATAAAAA TGATTGTAAA AAGGCAAAAT ACAAATTTTC  
60  
ACTTAACAAC TAGTACATAA AGTAATACAA TTAAATTAAT TCTATCTGAA AGATGTGTGG  
120  
GGCATCGTTA TTTTAGGTGG ATATGAGCAA TTTATTAAAA GTCATTTACG GAAAATATAT  
180  
ATAGACGGGG TGAGTAATAT GCAAGAACAT GTGGTGGTTA CACTTGATGG AAAAGATTAT  
240  
CTTGTAGAAC CAGGTACGAA TTTACTTGAA TTTATTAAAT CACAAGATAC TTTTGTCCCT  
300  
TCAATTTGTT ATAACGAGTC GATGGGCCCA ATTCAAACAT GTGATACATG TACTGTTGAG  
360  
ATTGACGGTA AAATTGAACG CTCATGTAGT ACGGTGATTG ATCGCCCAAT GACTGTAAAT  
420  
ACTGTGAACA ATGATGTGAA AGATGCTCAA AAAGAGCCTT GATCCGAATT TTAGAAAAGC  
480  
ATATGCTGTA TTGGACAGTA TGTGATTATT A  
511

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATCCTTTATT TNTAAGGCGT TTCATCAAGC TAACACTTCA TTATCTTTAG TCGCTTTAAT  
60  
GCCCTTCTAT TAAACTCGGA ACTAAAAATG GATTGNCTTT TCAACCACCC GANCACTAAA  
120  
ACATTGTCNT TTTTGATGGC CNATTAAGAC ACAATTTCCC GCTGTTTGCT TCAAAGTAGC  
180  
TTGCTTCTTG NATTNATTTT CAATATCTTT CTTGTTAAAA ACAAGANTGT TGCACAGTTT  
240  
GATTGGCATC TTTATTTAGA NCAATGGCAT CTGCTTGCCA CTTATCAATG CCTTCTTTAT  
300  
TCATATTGAT AAGACCATTG GCCAATCCAG ATAATAAAAA TAGCAAGTAA CTAATCATCG  
360  
TTAACACACC AATAATTAGT CCAAACCTCA ATTTGTTGCG CCGTATTTCA TTCCAAGCTA  
420  
AAAACATGCA TTTCTCTCCC TACTACTATG ATTTAAACAT TGTTTATATT CTTAGATGCA  
480  
CGTACGTCGT GTTGCGCTCT GTAATGTTAT ACATACACTT ATCCTTCATT ATACCCGANC  
540

TTTTATATT AAAACCAAAT TTATGGAAAA TGCAANNANT TGTCTATTAT TTTTGTGCGG  
 600  
 TACATTTAAA ATTAAGGATC AATTTAAAAA CGCCTACATA TACCTTTAAG TACATGAAGA  
 660  
 CGTCCAATTC ATATATTATT TAACTTCGCC TGTTTTAGGA TCGGATTGCT TAATAGCATT  
 720  
 TTTACGTAAT TTATCTTTTG CTTTGTCACT TGCTTTATAG TTATTGTTGT AAATCGTAGC  
 780  
 TTCCCAACTA CCATACATTG GGTTAGGGAA AATGATATAT TTCTTACCGA AATCGTCTTT  
 840  
 ATGTTTTTCA ATTAATGCTT CACGAGATTC AGCTGTAGCT TCTTTTGGAT CTGTAAAGTC  
 900  
 TAATAAATTA TCTCCAAATA GCATGACAAG TTTATGATCC TTTTGAACCA TTTGTCTGCG  
 960  
 TGATTCTTTA CTCTTATCAT CTTTACCTTT TAGTAAAATA TGACTCTTCT TAGCTTGAGG  
 1020  
 GATACCTTGT TGTTTTAAGT TCTTTTGTGT TGCCTTTAAA TCTTTTCTT TATCTCTATC  
 1080  
 AGAAATATAG TAGATATCGA CACCTTTTTT GTCAGCATAT TTCAA  
 1125

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

AGAAGCATAT AAACAAAACA TGTTTCGATT ATTAGGTAAA ACTGGTTTTG AAGACTTGAA  
 60  
 AAAAGAATTA GAAGAGCGTT TATAAAATAC ATTACTTCAA TGATTAGTGA AGTTTGAAAA  
 120  
 GATAGAACTA GACGTTAAC TTTTAAAGCA TATTTTCGAG GTTGTCATTA CAAATGTAAA  
 180  
 AATGTAATGA CAACCTCGTT TTTATTTATA TGCAAGAACT AGGTACTAG CTAATGTGAC  
 240  
 AAGATGTTAA GAGAAAATTA AAGAAAAAAT AACATCTGTC ATACAATAAT ATTGTTATAC  
 300  
 TACTAGAGAC TGATTTATTA GCATGATTAC ATGTTAATGT TTCTTTACTT AGTAATTAAC  
 360  
 TTTATAATGT AAGAATAATT ATCTTCAACC AAAGAAAGGG ATTGATGATT TGTCGTTTCA  
 420  
 TCAAGTAGAA GAATGGTTTG AGATATTTTCG ACAGTTTGGT TATTTACCTG GATTTATATT  
 480  
 GTTATATATT AGAGCGATAA TTCCAGTATT TCCTTTAGCA CTCTATATTT TAATTAACAT  
 540  
 TCAAGCTTAT GGACCTATTT TAGGTATATT GATTAGTTGG CTTGGATTAA TTTCTGGAAC  
 600  
 ATTTACAGTC TATTTGATCT TGTAACGAT TGGTGAACAC TGAGAGGATG CAGCGAATTA  
 660  
 AACAACGTAC TGCTGTTCAA ACGCTTGATT AGTTTTATTG ATCGCCAAGG ATTAATCCCA  
 720  
 TTGTTTTATT TACTTGGGNT TTCCTTTTAC GCCAAATACA TTAATAAATT TTGTAGCGAG  
 780  
 TCTATCTCAT ATTAGACCTA AATATTATTT CATTGTTTTG GCATCATCAA AGTTAGTTTC  
 840

AACAAATTATT TTAGGTTATT TAGGTAAGGA AATTACTACA ATTTTAACGC ATCCTTTAAG  
 900  
 AGGGATATTA ATGTTAGTTG TGTGTTGTG ATTTTGGATT GTTGGAAGAAA AGTTAGAACA  
 960  
 GCATTTTATG GGATCGAAAA AGGAGTGACA TCGTGAAAAA AGTTGTAAAA TATTTGATTT  
 1020  
 CATTGATACT TGCTATTATC ATTGTACTGT TCGTACAAAC TTTTGTAATA GTTGGTCATG  
 1080  
 TCATTCCGAA TAATGATATG TCGCCAACCC TTAACAAAGG GGATCGTGTT ATTGTAAATA  
 1140  
 AAATTAAAGT TACATTTAAT CAATTGAATA ATGGTGATAT CATTACATAT AGGCGTGTTA  
 1200  
 ACGAGATATA TACTAGTCGA ATTATTGCCA AACCTGGTCA ATCAATGGCG TTTCGTCAGG  
 1260  
 GACAATTATA CCGTGATGAC CGACCGGTTG ACGCATCTTA TGCCAAGAAC AGAAAAATTA  
 1320  
 AAGATTTTAG TTTGCGCAAT TTTAAAGAAT TAGATGGAGA TATTATACCG CCTAACAATT  
 1380  
 TTGTTGTGCT AAATGATCAT GATAACAATC AGCATGATTC TAGACAATTT GGTTTAATTG  
 1440  
 ATAAAAAGGA TATTATTGGT AATATAAGTT TGAGATATTA TCCTTTTTCA AAATGGACGA  
 1500  
 TTCAGTTCAA ATCTTAAAAA GAGGTGTCAA AATTGAAAAA AGAATTATTG GAATGGATTA  
 1560  
 TTTCAATTGC AGTCGCTTTT GTCATTTTAT TTATAGTAGG TAAATTTATT GTTACACCAT  
 1620  
 ATACAATTAA AGGTGAATCA ATGGATCCAA CTTTGAAAGA TGGCGAGCGA GTAGCTGTAA  
 1680  
 ACATTATTGG ATATAAAACA GGTGGTTTGG AAAAAGGTAA TGTAGTTGTC TTCCATGCAA  
 1740  
 ACAAAAATGA TGACTATGTT AAACGTGTCA TCGGTGTTCC TGGTGATAAA GTAGAATATA  
 1800  
 AAAATGATAC ATTATATGTC AATGGTAAAA AACAAGATGA ACCATATTTA AACTATAATT  
 1860  
 TAAAACATAA ACAAGGTGAT TACATTACTG GGACTTTCCA AGTTAAAGAT TTACCCGAAT  
 1920  
 GCGAATCCCA AATCAAATGT CAATCCAAAA GGGTAAATAT TTAGCTCTTG GAGGATAATC  
 1980  
 GTGAAGTAAG TAAAGATAGC CGTGCGTTTG GCCTCATTGA TGAAGACCAA ATTGTTGGTA  
 2040  
 AAGTTTCATT TAGATTCTGG CCATTTAGTG AATTTAAACA TAATTTCAAT CCTGAAAATA  
 2100  
 CTAAAAATTA ATATGAAACA AATACAACAT CGTTTGTGCG TTTTAATACT GATAAACGAT  
 2160  
 GTTTTATTTG GTTAGTACCA CAATAAAAGC TAAGTTCGAA ATGAACCTAT AATAAATCAA  
 2220  
 TCACAATCAC TTTGTGTTAA AATATGTGTC AAAGGAAGTG AGGGTTTGTC ATGACATTAC  
 2280  
 ATGCTTATTT AGGTAGAGCG GGAACAGGTA AGTCTACGAA AATGTTGACC GAAATAAAAC  
 2340  
 AAAAAATGAA AGCAGATCCG CTTGGAGATC CAATCATTTT AATTGCGCCA ACTCAAAGTA  
 2400  
 CATTTCAATT AGAACAAGCC TTTGTCAATG ATCCGGAATT AAATGGTAGT TTAAGAACAG  
 2460  
 AAGTGTTGCA TTTTGAACGA TTAAGTCATC GTATTTTCCA AGAAGTTGGT AGTTATAGCG  
 2520  
 AACAAAAGTT ATCTAAAGCT GCAACGGAAA TGATGATTTA TAACATTGTT CAAGAACAAC  
 2580  
 AAAAGTATTT AAAACTTTAT CAATCACAAG CAAAATATTA TGGGTTTAGT GAAAAATTAA  
 2640  
 CAGAACAAAT TCAAGATTTT AAAAAATATG CAGTAACGCC TGAACATTTA GAACACTTTA

2700  
 TTGCTGATAA AAATATGCAA ACTCGAACTA AAAATAAGTT AGAGGATATT GCTTTAATAT  
 2760  
 ACCGTGAGTT CGAACAACGC ATNCCANAAC GAGTTTATTA CTGNTGAGGA TTCATNACAA  
 2820  
 TATTTTATTG ATTGTATGCC GAAATCAGAG TGGCTAAAAC GTGCTGATAG ATATATTGAT  
 2880  
 GGTTTTCACA ACTTTTCAAC GATTGAGTAT TTAATAATCA AAGGATTAAT TAAATATGCG  
 2940  
 AAGAGTGTCA CAATTATATT GACGACAGAT GGTAACCACG ATCAATTTAG TTTATTTAGA  
 3000  
 AAACCATCGG AAGTGTTACG ACATATTGAA GAAATAGCAA ATGAACTCAA TATTTCTATT  
 3060  
 GAACGTCAAT ATTTCAACCA ATTATATCGC TTCAATAATC  
 3100

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGTGGCGAGA AAATACCGCA AGGTCATAAA GATATCTTTG ATCCAAACTT ACCAACAGAT  
 60  
 CAAACGGAAA AAGTACCAGG TAAACCAGGA ATCAAGAATC CAGACACAGG AAAAGTGATC  
 120  
 GAAGAGCCAG TGGATGATGT GATTAAACAC GGACCAAAAA CGGGTACACC AGAAACAAAA  
 180  
 ACAGTAGAGA TACCGTNTGA AACAAAACGT GAGTTTAATC CAAAATTACA ACCTGGTGAA  
 240  
 GAGCGAGTGA AACAAGAAGG ACAACCAGGA AGTAAGACAA TCACAACACC AATCACAGTG  
 300  
 AACCCATTAA CAGGTGAAAA AGTTGGCGAG GGTCACCCAA CAGAAGAGAT CACAAAACAN  
 360  
 CCAAGTAGATA AGATTGTAGA GTTCGGGTGG AGAGAAACCA AAAGGTCCCA AANGGACCTG  
 420  
 AAAACCCAGA GAAGCCGAGC AGACCAACTC ATCCANGTGG GCCAGTAAAT CCTAACAAATC  
 480  
 CAGGATTATC GANAGACAGA GCAAAACCAA ATGGCCCAGG TCCATTCAAT TGGATAAAAA  
 540  
 TGATAAAGGT TAAAAAATCT AAAATTGCTA AAGAATCAGT AGCTAATCAA GAGAAAAAAC  
 600  
 GAGCAGAATT ACCAAAAACA GGTTTAGAAA GCACGCAAAA AGGTTTGATC TTTAGTAGTA  
 660  
 TAATTGGAAT TGCTGGATTA ATGTTATTGG CTCGTAGAAG AAAGAATTAA AATAATTCAT  
 720  
 AATTTAAATA ATAGTTGATT TGCATTCACT ATATTTAGTT TGTTAAAAAC AACCTAGAAT  
 780  
 ATGATGAGAA TGATATACAA CCCCAAAAGT TGGCTTG  
 817

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
CCATCGACTA AGCAATGGTA TTTGTTTCATT AAATCCTCAT GTTGATCGTT TAACGTTAAG
60
CTGTGCGCATG GAAATCGATG CTAGTGGTCG CGTTGTTAAA CATGAAATTT NTGATAGTGT
120
TATACATTCT GATTATCGAA TGACGTATGA TGCGGTAAAT CAGATTATTA CTGAAAAGGA
180
TCCTAACATT CGCGAACAAT ATAAAGAAAT TACGCCTATG TTAGATTTAG CACAAGATTT
240
ATCTAATCGN TTGATTCAAA TGAGAAAACG ACGTGGGGTG AAATCGATTT TGGATATTAG
300
NGAAGCAAAA GTATTAGTTA ACGAAGTCGG GTATACCAAC AGATGTTCAA TTAAGACAAC
360
GTGGCGAGGG TGAACGTCTA ATTGAATCAT TTATGTTAAT TGCAAATGAA ACAGTTGCTG
420
AACATTTTAG TAAGTTAAAT GTACCTTTTA TTTACCGAGT GCATGAGCAA CCTAAATCAG
480
ATCGCTTAAG ACAATTCTTT GATTTTATTA CAACTTTGG CATCATGATT AAGGGCACTG
540
GCGAAGATAT TCATCCAACA ACACCTCAAA AGGTTCAAGA AGAAGTAGAA GGTGCGACCTG
600
AACAAATGGT CATTTCAACA ATGATGTTAC GTTCAATGCA ACAAGCGCAT TATGATGATG
660
TGAACCTGGG ACATTGTGGC TTATCAGCTG AATATTATAC GCATTTNACA TCACCAATTA
720
GACGTTATCC TGATTTAACA GNTCATCGTT TAATCCGTAA GTATTTAATT GAGAAATCAA
780
TGGATAACAA AGAAGTGAAG CGTTGGGAAG ACAAATTGCC TGAGTTAGCT GAACATACTT
840
CTAAACGTGA ACGTCGTGCT ATTGAGGCAG AACGTGATAC TGATGAATTG AAAAAAGCAG
900
AATATATGAT TCAACATATT GGTGATGAAT TTGAAGGTAT TGTCAGCTCA GTAGCTAACT
960
TCGGTATNTT CATTGAATTG NCAAAACGA TAGAAGGTAT GGNTCATATT GCGAATATGA
1020
CTGATGATTA TTACCGCGTT GAAGAGCGTC AAATGGCATT AATTGGGTGA GCGTCAAGCT
1080
AAAGTATTTA GAATTGGTGA CACAGTTAAG GTTAAAGTGA CGCATGTTGA TGTAGATGAA
1140
CGATTAATTG ATTTTCAAAT TGTTGGAATG CCTTTACCTA AAAATGACCG CTCACAGCGA
1200
CCAGCAAGAG GTAAAACGAT TCAAGCTAAA ACGCGTGGCA AATCTTTAGA TAAATCGAAA
1260
TCTGATGATA AGGGTCGGTA AGAAAAAAGG TAAGCAACGT AAGGTAAAAA CCAACGTAAT
1320
AATGATAATC AGGTAATAGT AAGCATAG
1348
```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 982 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```
ATGAAAATTA TTTTAATTTT AGCATTAGCG CGTGTCGTTT CTAGACATAA TCAATTCACA
60
TTCAATAAAT CATTCCAAAG TGATTTGTTA TTATTTTTC AATTATTGG TGTCTCGTTA
120
GTACCAAGTA TTTTAATATT ACTGCAAAAT GACCTAGGAA CTACATTAGT ATTAGCTGCT
180
ATTATTGCAG GTGTGATGTT AGTAAGTGGT ATAACATGGC GTATCTTAGC ACCTATCTTT
240
ATTACAGGTA TTGTTGGTGC AATGACAGTC ATTTTAGGTA TTCTATATGC ACCCGCATTA
300
ATTGAAAATT TATTAGGTGT CCAACTGTAT CAAATGGGAC GAATCAATTC AAGGCTTGAC
360
CCCTATACAT ATAGTAGGGG GGGGGATGGC TATCAATTAA CTGAATCACT TAAAGCTATC
420
GGGCTCTGGA CAAGGTACTA GGTAAAGGAT ACAATCACGG GGGAGGTTTA TATCCCTGA
480
AAATCATACT GACTTTTATC TTNCAAGNG AATGGGAGAG GAACTTGGCT TTATCGGTTC
540
TGGCAAATTG AGNCTTAATA TTTTATTTT TAATCTTCCA TCTAATAAGA TTAGCTGCGA
600
AAATTGGAGA TCAATTTACC AAAATCTTTA TCGTTGGTTT CGTCACTTTA CTTGTGTTCC
660
ATATTTTACA AAATATTGGT ATGACAATTC AGTTGTTACC AATCACTGGT ATTCCATTAC
720
CATTTATTAG TTATGGTGGT AGTGCGCTAT GGAGTATGAT GACTGGAATA GGTATAGTCT
780
TATCAATTTA TTATCATGAA CAAAACGAT ATGTCGATTT ATACCATCCA AAAAGTAATT
840
AATTTAACT ATTTTGAGTT TCAAATATCA TAACTTTTCA AGATGACGTT ATATAGTCTA
900
TTTACGTCGT CGATTTAAAA TGTCATATAT AGATATTACT CGATAATAAC AATCCCTCTT
960
TGAAGTACAC ATTGTAAAAT GG
982
```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
GGCACTAACT TCATTTGAGC ATCCTCCTAT CAATTGCTAT ATAAATTAGT ACCCTTTTGC
60
CACTTAATTA TAACAAATTC TCAAATTTTA AAAATTGAAA ATCTAGTTAA TGTATTAGCT
120
CGATTTTGAA ATCTAATAAT AATTGGCATA AAATGGAAGT AATATTATGT GAGGAGTGTT
180
ATGAAATGAC AAAAATATCA AAAATAATAG ACGAACTGAA CAATCAACAA GCTGATGCAG
240
```

CATGGATTAC AACACCGTTG AATGTATATT ATTTTACTGG ATACCGTAGC GAACCCATGA  
 300  
 AAGATTATTT GCATTATTGA TTAAGAAAGA TGGTAAACAA GGTACTATTT TGTCCAAANA  
 360  
 TTGGAAGTCG GAAGAAATCA AAGCATCACC CTTACACAGG TGAAATCGTT GGATATTTAA  
 420  
 GACACTTGAA ATCCTTTTTT ACTTTATCCA CAACNCAATC AATAAATTAC CTAATTGTAA  
 480  
 GCGGAGCACC TTAACAAGTA GCACCGCCAC AAACAATTAA TCTCTGTTTC NATGTCAATT  
 540  
 CATTCGGAGA TGTTGAGTTA ACAATCACAC AATTAAGAGA TATTAAATCC GAAGATGAAA  
 600  
 TTAGCACAAT ACGTAAAGCT GCTGAGTTAG CAGATAAGTG TATCGAAATA GGTGTTTCTT  
 660  
 ATTTAAAAGA AGGTGTGACT GNACGTGAAG TAGTCAACCA TATTGAGCAA ACTATCANAC  
 720  
 AATATGGCGT CAATGAAATG AGTTTTGATA CGATGGTTTT ATTTGGAGAT CATNCCGCAT  
 780  
 CACCTCATGG CACACCAGGA GATCGCAGAT TAAAAAGCAA TGAATATGTA CTATTTGATT  
 840  
 TAGGTGTAAT TTATGAGCAT TATTGTAGCG ATATGACACG TACCATTAAA TTTTGGTGAA  
 900  
 CCTAGCAAAG AAGCACNAGA AATTTATAAT ATTGTATTAG AAGCAGAAAC ATCTGCAATC  
 960  
 CAAGCAATTA AACCTGGAAT ACCTTTAAAA GATATCGATC ATATCGCTAG AAATATTATT  
 1020  
 TCAGANNAAG GTTATGGTGA ATATTTCCCT CATCGCTTAG GTCATGGTTT AGGATTACAA  
 1080  
 GAACATGAAT ATCAAGATGT TTCAAGTACT AATTCTAATT TGTTAGAAGC TGGCATGGTT  
 1140  
 ATTACAATCG AACCAGGTAT TTATGTACCA GGTGTTGCAG GTGTAAGAAT TGAAGATGAC  
 1200  
 ATACTTGTCA CTAATGAAGG ATATGAAGTA TTAACACATT ACGAAAAATA AGGAGTGGGA  
 1260  
 TAAAAATGAA AAGCTTGTTA CAAGCACATT CTCATTTCAGT CAAACACTGC CAATATAACA  
 1320  
 TTGTAGCGCC TAAGACATAA ATTTTATCC AAGTCTAAAT GCAATATGTA ACAAACAAGC  
 1380  
 TAGAAACACA TATGCAGGTA TGTTTCATCAG TAACATGTAA TGAATCAAAT CAATATCATT  
 1440  
 CATGTTTCGAT GATTTCTTCG CATTGTTTCT AGCTTTAATT TATCATTATT TAATTTTAAT  
 1500  
 AACCAAGGAG ATGATAACGT CAGTCTTTAG TACGCTGTAA TCCATTCCCT TTTCATCAAA  
 1560  
 TTCAAATTAT AATTGTAATG CTTCTTCTAC AGATTTATAT TCCATTTCAA ATGCCTCTGC  
 1620  
 AACGCCTTTA TTGGTTACGT GACCTTTGTA AGTATTTAAA CCTAATGATA ATGGTTGATT  
 1680  
 TGATTTAAAT GCTTCTCTAT ACCCTTTAG  
 1709

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

AAAGAGGAAG ATGTGAACCA CCACTAGTAT TGAATCTAAA GATTGAGGAC GTTCCTTTAT  
60  
TAATTGGCTA NNNAAGNNAN ATCNNNAAGA TAGCCAATCC AAAGCCAAAA AGTCAGCATC  
120  
AAGAAATACT TCTANNAAGG TAGCAGCTNN NNAGAAGNGN NAGAAATCTA AGANAAATNN  
180  
NAAATAATTT GTTTCTTTGC TAAATAGAGG AGCACCGATT GACATCACAT CAGTCGGTGC  
240  
TCCTTTTATT TATTCTTTTT AATTAATTTA TACAAANCCN ATTCCCTGTT GAGCGTGTTG  
300  
AATCGCCTTC CNTTGTTTTG TTCTCNCGGT ANCCCATTTA ACCAAATNAT AAACCNANAT  
360  
CTTTNTCCAA ATATTTCTAT TTGATCAAAA TAAGGTTTGA AATTTGCGTT TTTCACATAA  
420  
CCAGCTCGTG CCAATGCTAT CGTGCAATTA GCTTTGAGTC TGTATATAAT AGTGCGTTTT  
480  
GAACATTTAA TTCACGTGCA TGTTCTAGTG CATAAATACA TGCAGCCCAT TCTGCAGTGT  
540  
GGTTATCCAT TTCGCCTAAC TCATGTGTAT ATGTATNATG CTGCTTATCT TCTTTGATTA  
600  
CAATGGCACA NGTACTTATG CCTGGATTTT CTNTTCGTCG CAGCATCAAA ATTTATGTGC  
660  
GCCATAATAA ACCTACTTTC TATTCAATAC TTAGTTAAAG TTACTATTAC TGTAATACAA  
720  
AATATGTTGG GTAATCCATT AAAAAACACG CATCACTTAA ATAAGTAAAC ACGTTGTAA  
780  
AAATACTTCG CTTGATTCAA AAGATGATTT TCTAAATACG TAGTNCTTGT AAAATACTTC  
840  
CTAAANAAAT CATCTTCAGG CTGGGGACAT AAATCAATGT TCTATGCTCC TNCCGAAGTT  
900  
ATATTGGCAG TAGTTGACTG ANCGAAAATG CGCTTGTAAC AAGCTTTTTT CAATTCTAGT  
960  
CAGGGGCCCC AACACAGAAG CTGNCGAAAA GTCAGCTGAC AATAATGTGC AAGTTGGGGA  
1020  
TGGACCCCAN CAAAGAGAAA TTGTATTCCC AAATTCTACA GACNATNCAA GTTGGGGTGG  
1080  
GNCGACGAAA TAAATTTTGC GAAAATATCA TTTCTGTCCC ACTCCCTTAA AACTTATTCT  
1140  
TTTGTGTAGT AAGTGCGTTA ATAGCCTTGA TCTAACTTAT CAATCTTACC TTTACGATAA  
1200  
AATGATTTAG CAATATATCC ANNTGGTACA TTGAAACTG TTGAAGCTAA TTTTAATACG  
1260  
TAAGTTGTAA TAAATATTTT NAATNCAACT GTACCAGGTA AACTTCCGAT AAAAGCGATA  
1320  
GCTACAAATA AAGCTGTATC CAATTATTGA GCTTG  
1355

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

CCAATTTTCC CTTCTACCTG CGTGGGTTAGT ATTCAAGCCC AAAGTTCAGC GGGAAAATAT
60
TGACAATTAA CCGGATCCAG CTAATCGGAG GTCGGATAAA GATGTTGAGT TGTAAGTTAT
120
TTGGAATATT ATTTTAATAG TGTCATCCCC CTTTGTAATA TAATTGTCTT ACTTTTAAAT
180
TAAAAGCCAA ATTAATATAA GAAANCTAAG ACTTAGTACN GTATCAATTT TGTGCGTTTC
240
AATTGAGTTC TAGTTTTTTT TAATATGTTA ATATTAAACT TATAACTTTA TGGGAGTGGG
300
ACAAGAATGA TAAAGAGCCA CTAAATGATT TATTATGTAG TGGTTCTTAA TACATTAGCC
360
ACANCTAATG TGTACTTAAA AATAGGAATA CATGAGTAAA ACTCATGCAT AAGAAATACT
420
AATTTCTATA GAAAAAGTAT TACTTTATCG TTGTACCACA CCAACTTGCA CATTATCGTA
480
AGCTGACTTA TCGTAAGCTT CTGTGTTGGG GCCCACACCC CAACTCGCAT TGCCTGTAGA
540
ATTTCTTTTC GAAATTCTCT TTGTTGGGGC CCACACCCCA ACTTGCATTG TCTGAAGAAA
600
TTGGAAATCC AATTTNCTCT GTGTTGGGGC CCACACCCCA ACTCGCATTG CCTGGAAGCT
660
GAATTTCTTT TCGAAATTCA GCTTCTGTGT TGGGGCCAC ACCCCAATT GCATTGCCTG
720
TAGAAATTCT TTTCGAAATC CAATTTCTCT GTGTTGGGGC CCCTGACTAG GATTGAAAAA
780
AGCTTGTTAC AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT
840
AGAACATTGA TTTATGTCCC AGCCTGATAT CACCATTAAA TACAATTCAT TTAGTNTTCA
900
ATTGGAAACA ATTNATCGAT ATATTGAATC TCATCATCTG ATAAAACGAT ATCTGCAGCT
960
TTAATATTTT CAATGACTTG TTCTGCACGT TTTGCACCAG GAATAATCAC ATCGATAGCT
1020
GGTCTCGTTA AATAAAATGC TAATACAATG TTCGCAATTG AAGTTTGATG TGCTGCAGNT
1080
AGNCTTTCCC AAAGCTTTTA CGCTCGTGAC GCACATTCTC TTCAAAAACA CCAGGTATAA
1140
AATCCCGACG TGTAGTACGA TGGTCACTAA ATTTAGTGTT CTCATCATAT TTTCCAGCTA
1200
AAATACCGGA TGCTAATGGG AAATAAGGAA TAAATGTGAT TAGGTGATCA ACACAATATT
1260
GCAATACTGC CTCATTTTCG CGGTGCAATA AATTATATTC TAACTGTACA ACATCAACGT
1320
AACCATCTTT ATTTGCTTCT TTAAGTTGAT CTAATGTGAA ATTTGATACA CCAATGGCTT
1380
TAATCTTCCC TTGTTCTTA AGCTCGTGCC
1410

```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GTGTTACGGT AGGTTGTTGA TCCTAATTTT CCCTGNCAGT TGGTCCCAGT ACCCACCCTAT  
 60  
 TTCCCAACTT ACTAAAAAAG AAATCCAATT ANNCCGAAAG AAAATATTGA AGTCATTGAA  
 120  
 ATTAACCGAA GCGTTCCAGT GCACAGGTAG TTGCCTCCCC AACCAAGCTT TAAATATTTT  
 180  
 CAAATACGCA ATTAAATATA TGGGGTGGTG CATTAGCATC AGGTCATCCA TACGGTGCAA  
 240  
 GCGGTGCCCA ATTAGTGA CTGATTATTTT ATATGTTTGA CAAAGAGACT ATGATTGCAT  
 300  
 CTATGGGGAT AGGGGGAGGT CTAGGAAATG CAGCATTATT TACTCGATTG TAACCAGCGA  
 360  
 TTAAATGTGT CATTTTCTAA GGATAGTGTG GCTGCATATT ATCAGTGTTT TANCCAACCT  
 420  
 TATAGAAAAG AAGTCTCGTG CCCATTAATG TGTNCGTCAT TATGGCCACA ATTTGATTTA  
 480  
 TTTAAAAAAA TATCCAAATA GCGAGCTGAT TTTACCACAA ATCAGCAATT AATCAAATC  
 540  
 NCAAGATAGA AGTAGACACA ATATATGTAG GGCATTTAGA AGATATTGAA TGCCGACAGA  
 600  
 CTCGCAATAT CACACGTTAT ACAATGGCTT TAACATTAAC TAAAAATGAT CAACATGTCA  
 660  
 TANCGGTTAC ACAAACTTTT ATTAAGGCGA TGAAGTAGAG ATGAAGTTTA ATGAGATATG  
 720  
 GATAAATGAA TATTTGGCGC TCGTAAATGA TGATAATCCA ATACATAATG AGATTGTGCC  
 780  
 AGGACAATTA GTGAGTCAAA TGATGCTGAT GGCTATGTCA TTAGAGACAA ACCAGTGTCA  
 840  
 AATTAACCTAC GTTAAACCTA TTTTAATAAA TGAAAAATATC GAATTCATTG AACAAACGCA  
 900  
 ACACGAAATT ATAGCAATTA ATGACGATGG AGAGATTAAA ATAAAAATTT CTTTGAGCAC  
 960  
 AAAAAAATAA CCGATATTAG CTGCATGAAC GCATATTAAT TAGGAGATGA AAGGACAGCT  
 1020  
 AATATCAGTT ATGTATTGTT ATTATTATTG GGAACAGAGA TGAATATAGG TTACGTTTCT  
 1080  
 TTCTTTGCAC GGGGATGCAT TAATCTAAAA TAATAATAAC AACTATATCA ATGTTTAATA  
 1140  
 AATTCTGGAT TATTGGAACG ATTAGTCAAT TTAACCTAAT TNCATATGAT CTATATCGTC  
 1200  
 TTGTNATAAA GAGAGCAATT TGAATATTTT AGTATCACTA AATGAATCGN CACATTTAAT  
 1260  
 TGAAACATGC TGAAACGTTT GGGTTATAAT TTCATAAACT GGTGCGCCTT CATGGTGATA  
 1320  
 CTGTCGAATA AATAATCATA ACCATATTTA CCTCCTTNGG CTACTCTATG GGTATATTAT  
 1380  
 AAATAACATT TTTATGTGTG ACATCAACCT TAAGTATCAA CTTTTTATCA GACATAGAAC  
 1440  
 GTANGATTTA CTAAGACTAT TTATGTATAA AAGTTCTAAA TAAATATATA TTTATAGAGT  
 1500  
 CGCCTGGCAG NCATTTGGGA AATATAACAT ATATGATTAG AGAGGCATCT ATCGCAAAAG  
 1560  
 AATGATAATG ATAGAGGTAT TGAGCATATA GATGAGTTTA AGTTCATCTT GAAAATAAAG  
 1620  
 GGTTATTTAG TCATAGATGT AGATGTATAG GAAATATTTG TATGTATTGN TCGATATGTA  
 1680  
 TGAAATTTTC AATAAAAGCT AATAACGCTT ATATGTAAC TTTCAAATTTA AATTATATAC  
 1740  
 AGAGCATGAT GATTATAAAA AAATANCCAC ATCACATAAA TTGAGTTCAT ACCCAATTTA  
 1800  
 AGTGGTGTGG CTAATAATGT TGATTTATAG ATGAACCGCC TAATCGTTAA ACCTCTGTTA

1860  
 CTTCAACATC GATATGTTCA ATACGTTGT ATGCACCGTG ATCCACAGGA CCAACAAAAT  
 1920  
 CATTCAATTTT CCAACCGTTT TTAATAGCAG AAGCGACGAA AGCTTTCGCT CGTGCTAATC  
 1980  
 ACAGCTTCTT TCGGTGACTT ACCGTTAGCT AAATATGCAG GTGTTGCCGC AGCAAATGTA  
 2040  
 CAACCAGCAC CATGGTTATA ACTTTGTTGG AACATGTCTG TTGTTAGTTG ATAAAATGTG  
 2100  
 TGACCATCAT AGTATAAGTC ATACGATTTA TCTTGATCTA AAGCTNTGNC ACCTTTAATG  
 2160  
 ATGACATGCT GTGCGCCTTT ATCAAAGATA ATTGNTGCAG CCTTTNACAT ATCTTCAATT  
 2220  
 GAATTTAATT TACCTAATCC TGATAATTGA CCCGCTTCAA ATAAGTNTGG TGTCACTACC  
 2280  
 GGTGGTTTAG GTAGTAAATA TTTAATCATC GCCTCAGTAT TTCCAGGATT AAGCACTTCA  
 2340  
 TCTTCGGCCT TTACAANCCA TGACAGGATC TTACTACAAA ATATTGTGCA ATTAGATGCT  
 2400  
 CATATACTTC TCCAGNACGG GTGGATATCT CCTCAAG  
 2437

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TTTCCCCNA CTCCATAATC TTGGCCAAAA TCATGTTTAA ATTTGATCTT GATTGAGACC  
 60  
 CAAAGATAGC TTGCATATTG TTTCCCAACT TCTAANACAC CTGATGCGCC TAAAGCTTTA  
 120  
 AATACCTGCT ACATCTACTT TTGATTTATC CAACCCACTT CTACGCGCAG ACGTGTAATA  
 180  
 CATGCATCTA AATGTTTAAT GTTTTCTTTT CCACCCCAT TGNATCTAAGA CATCANATGG  
 240  
 TAATTTTGCG AACTAGAGT TACGAATTC AGTTTCTTCA TCTTCACGAC CTGGTGTTTT  
 300  
 CAATTTAAAC TTACGAATTN CACAGTCGAA TGAGANGTAA NACACGATAG CAGACACGAC  
 360  
 AGCGTTCTNN GACTGGTAAT NGGGCATTNN GCCCAACCCA ATTTATGTGA GCTAACTCAG  
 420  
 GTTGAACNTT GACCATCTTT NNATTCTTCA ACCCANAACC TGCAGGCGTA TTCATAANT  
 479

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CCAAAGTGTT CTGGTCTAAG ATATTATCGC TAATCCGTGT TAAGCCACTC AGCTGTTTAA  
60  
TATCAATTAC CTTTTTNAAA TCCCTCCAAC CTAAAATCTT GATTCCCACC TTGCTTTAAT  
120  
AAAATCTTTC GTTTTAGTTG TATTATGTTT AAACCTCTTG CCAGTCTTTT CGGTAAGATA  
180  
ATCAATAATC TCTTTATATG GGATGCGTGT CGGGTTTCCC GACAATATAT CTA CTACTCTATT  
240  
TATATTGTTA TTA CTCTGTAT TATTAATACT TGTATTGTCT CTTTAACATT TGTGATAATA  
300  
GGGGTATTAA CAGAATTGTT AATAGGGGTA TTATCATTTG TGTTAATAGG TCTTATCATT  
360  
TCTGTTAAGG GGTATAGCTT TCTTTGTTTA ATTTCAATTAC CATTTCTAAT GATTTCAACA  
420  
TGTAATATC CACATTCTTT TAAGTTGGCT ATACGGCGTG ATACAGTAAC TTTTGTAAC T  
480  
TCATATAGTT TCGCAAAGTA ACCATTACTT GCTGTGCAGT ATCCGTA CTT GTTACTTAAA  
540  
GACGTTATTT CTGCAAAAAG TAAC TTTTCG CTGTCAGTAA GTCGGTTATC GTATCTGACA  
600  
TTTGCCGTTA TTATTGAGTA GTA ACTTGGT TGTT CAGTCA TTCTCAGCAC CTTCTTT CAG  
660  
TGCTTTGAAC TTGTCTGGTA TCTCCAGTT AGATATGAAT TCTTTCAATT CATCAGTCAT  
720  
AGGTA CTTCG TTTAGTATTG CGTCATCACC AAACAGATAT AAAACTATCT TGTTATATGC  
780  
TAATGCCGCT TTTTCTGTGC TATCAAAATA TTCCGTAGTA TATAGCTTGC CATCAATTTT  
840  
TTTCCTAACA GAAAATCGAT GCGGCATATC AGAGTGGTTT CCAATTCCTC TG TAGCCATA  
900  
TTTACTAGCG TTTCTTGTGT TGTTAATATT TTTATGAGGA AAATAATCTC TAACTTTACG  
960  
CATATCTCTT CCAATTATGT TTTTAAAACC TTCCACCACC CCAAACTCA TCTACAGCTT  
1020  
NGTTATACGC TTCAGCTGCT AATTCTTCTT GTTTNAAAAA TACCTAAACG TTTTNGGATT  
1080  
TCCTTCAACA TTTATATTGG CTGTCCATTT ATTGCAATCT TNACGCCAGT TAACACCTTT  
1140  
ANACTTAGAA GAACCATTAC TTTTAGGTNT CTCCCATCTT GANCNGTTNN NACCTTTTGT  
1200  
AGTTAAATTA GATTTAGTAA AATTATTATT TTTAATTTTT TGAAA ACTTC CTTCTTTTAT  
1260  
AAAGGTTGTT AATAGTACAA CCTTCTCTC GTTGCCAATC CTAGTATGGA TATATCTTGT  
1320  
ATTACCTTTA TAGTATTTGA ACCATTTATA TCTGTTCCAC TCTTTCATAA TCTTCATCAT  
1380  
CAACAAAAAT TTCTTCTCCA TCTTGTA AAAA ATATCGATTT AACCATTATT CTCTTCCTTT  
1440  
CAGCATTTTG TTGAGCCTCT CATCAACTTT TATCCACGAG TCATGCAAGT GATATTTATC  
1500  
ATCAAACGAC TTAACACCAA TCGCATGTTG CTCGTTGTGA TGTTGCGGAC ATAACGCTAA  
1560  
TACATGTTTG TTGTAGTGAT TCATTTTGT TCTGTTCAAT CCTCTGCCGA CTGCTTCATA  
1620  
ATGCGCTAGG TCTGCGTGAG GCTTTCCACA AATTACACAG TTGCGGTTGA TTGTAGCCCA  
1680  
ATACAATAGT GCTTTATCCT CACTTAACAA CTTGCTCTCG TGCCTATGCT CATAGGTATT  
1740  
TGATGATGAA ACATAAACGC TATAATCAGT TCTATTA ACT CCCTTGCAAC TTTCATAGAA

1800  
 CAGTCGCGCA GACTGATTTC TTCATAACCT TTCATAATTT CCAATTCTGT TTGTAATAAT  
 1860  
 TTNCTAATTG ATTCCACCGG TTCTCCCCAG TGAAGTTCTA TATCTCTACA CATNGCGAAT  
 1920  
 ATTTTTTTGC GTTGTCTAT AGATAGTTTT TTATTATCCG GAACCTCTAC TTCTGCTTTT  
 1980  
 AGTGGATATC CGTTTTCTAG TAAGTCAATG TGACTTTGTT CAAGTCAAC ACCANTAGCA  
 2040  
 ACGACGGAAT AAGTNCCGTC ATTGTCNNTC TGGNATCTTG TAATGTATTG CANNTAAACC  
 2100  
 CACACCTTAA ACGCTAAATC TTGGTCGTCA TATCCAAATT GCCCCCTGCT TTCAAATGGA  
 2160  
 TTGCTTTGTT GAGACATTGA TGTGTGTTGT TGTGCCCCGT TATTTTCTTC AGCTTTTTGC  
 2220  
 TTATCTGTCT TCGGAATAGG TTTGTTAACA ACATCATCGC CCTTTTGTGA AGGTTTAATA  
 2280  
 AATGAAAAAT CCGTAAAATA CTTACCTTCA TCTTCATTGA ATTTCCATTT CAATACCAAG  
 2340  
 TGACANAAC TACCAATAAG ATCATTGGTA TCANAATCTA AGCTAGGAAG ATTTAACTTA  
 2400  
 ATACCTAATC GAGTAACTAA TTCAATCAAT TGTTTTTCTT GGAAATCATA TTTATACGGC  
 2460  
 GGTACAAATT GATTATGTTT ATATTGTTTG CCTTCATCAT TTTCAAATAC GATTGTGAAA  
 2520  
 TATCTATTTT CTCTATCATT AGAAGAAAAC CTGATCATCT TTTTtaggtt TCTTAGATTG  
 2580  
 GAATTGTTGA GGG  
 2593

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCCCAGTCT CATATGAAGT AGTTGGATTA GTTCCGAAGT ATGAGGATGG GAATTTCTTG  
 60  
 ACATAGTAAA GTGCCGGATG ATAGTGCAAG AGGTATCGTT GCACAAAATA TGACAACTGC  
 120  
 TGAGATTGAA ACATTTGGTT CAGATCCAGT TATTATGCCA ACGGGGTGCC CCTGGTATTA  
 180  
 TTTTCGGTAA AACAACAAAC TCAATGATTA ATACAGGATC AGCGGCTTCC ATTGTTTACC  
 240  
 AACAAAGGCGC TATTTATGCT AATGCTGAGT TCATTCAAAT TCATCCTACT GCAATCCCTG  
 300  
 GTGATGATAA ACTCCGACTA ATGAGTGATC AGCACCNTTG TTGAAGGTGG ACGAATTTGG  
 360  
 ACATATAAAG ATGGTAAGCC TTGGTACTTC TNAAGAAGAG AAATATCCTG ATTATGGTAA  
 420  
 CTTAGTACCT CGTGATATCG CAACCGCGTG ANATTTTCGA TGTATGTATT AACCAACAAA  
 480  
 TTAGGNATAA ATGNCGAAAA CATGGNATAT CTTGATTGT CACATAAAGA TCCAACATGA  
 540  
 GTTAGATGTA AAACtaggtg GTATCATTGA AATTTATGAN AAATTCAGTG GTGATGACCC



600  
 ACGCAAAGTA CCAATGAAGA TTTTCCCAGC TGTTCACTAT TCAATGGGTG GTCTATATGT  
 660  
 AGATTATGAT CAAATGACAA ATATTAAAGG GTTATTTGCA GCTGGAGAAT GTGACTTCTC  
 720  
 TCAACATGGT GGTAACCGCT TAGGTGCCAA TTCATTGTTA TCAGCGATTT ATGGTGGTAC  
 780  
 AGTAGCAGGT CCAAACGCGA TTGATTAATA TTTCAAATAT TGATCCGATC CATATACTGA  
 840  
 TATGGACNGA AGTATTTTTG AAAAACGTAA AGCTGAAGAG CAAGGAACGT TTTGATAAAT  
 900  
 TATTAGCTAT GCGCGGTACA AGAAAATGCC TATAAATTAC ACCGTGAACT TGGTGAAATT  
 960  
 ATGACACCAA ATGTAACGTG TGTTTCGTGAA AATGAAAAAC TGTTAGAAAC AGATNAAAAG  
 1020  
 ATTGTTGAAT TGATGAAACG TTATGAAGAT ATTGATATGG AAGATACTCA AACTTGGAGT  
 1080  
 AACCAAGCGG TATTCTTTAC CCGTCAACTA TGGAACATGT TAGTACTTGC ACGTGTTATT  
 1140  
 ACGATTGGTG CATATAACCG TAACGAATCA CGCGGTGCCC ATTATAAACC AGAATTCCTG  
 1200  
 ATAAGTATTT TCGTCAGAAG TACATAATAT TTAAATCATT TAATTTTGAG AAGCATGGAA  
 1260  
 AATTTTGGA CAAATGGTTT TACGTAAGAA AATGGAAACA TAAGATTTTA GATGGTCATC  
 1320  
 AGCTTAATCA AAATATATAT GATCAGCGTC ATTTAATGAC AATCAATACT GATGAAATTG  
 1380  
 AAAAAATGAT TATAGAGACA AAGAGGGCAG AGTTGATTCA TTGGATATCG ATACTTCCAG  
 1440  
 TCATCATATT CAATAAAGGC TCTCGTTTAG TAAAGTATAT AAATATTTTC TATGCAATGA  
 1500  
 TAGCTAATGT TCCAATCATT ATTGTGCAAC GCTATAATCG ACGAGATTAA CGCAGGTACT  
 1560  
 ACGCATTTTA AAACGAAGAG GTGAACGTCA TGAATAACA TATCATCCGN TATTGGGTGG  
 1620  
 GNGGCTTAGG TGGGATTTTCN TGCAGCAATT CGAATGGACA AAAGTGGCTA TTCGGNCTCA  
 1680  
 TTATATGAAC AAAATACTCA TATAGGAGGC AAAGTGAATC GNCATGAATC AGATGGCTTT  
 1740  
 GGCTTTGATT TAGGTCCATC TATTTTAACG ATGCCTTATA TTTGTGAAAA ATTATTCGAA  
 1800  
 TATAGCAAGA AGCAAATGTC AGACTACGTT ACAATCAAGC GTTTGNCACA TCAATGGCGT  
 1860  
 AGCTTTTTTC CAGATGGCAC GACTATCGAT TTGTATGAAG GTATTAAAGA AACAGGTCAG  
 1920  
 CATAATGCGA TATTGTCGAA ACAGGATATA GAGGAACTGC AAAATTATTT GAATTATACA  
 1980  
 AGACGAATCG ATCGTATTAC TGAAAAAGGG TATTTTAACT ATGGTTTAGA TACACTATCT  
 2040  
 CAAATTATTA AATTTTCATGG GCCATTAAAT GCTCTTATTA ATTATGATTA TGTACATACT  
 2100  
 ATGCAACAGG CCATAGACAA GCGTATCTCG AATCCATACT TGCGACAAAT GTTAGGCTAT  
 2160  
 TTTATCAAAT ATGTAGGTTT TTCATCATAC GATGCGNCAG CTGTATTATC TATGTTATTC  
 2220  
 CATATGCAAC AAGAGCAAGG CCNTTGNTAT GTAGAAGGTG GAATCCATCA TTTNGCCAAT  
 2280  
 GCCTTGGAAG AGCTAGCGCG TGAAGAAGGT GTCACAATTC ATACAGGTGC ACGTGTGGAC  
 2340  
 AATATTAAAA CATATCAAAG ACGTGTGACG GGTGTCAGAT TAGATACAGG TGAGTTTGTA  
 2400

AAGGCAGATT ATATTATTTT AAATATGGAA GTCATACCTA CTTATAAATA TTTAATTCAC  
 2460  
 CTTGGATACT CAACGATTAA ACAAATTAGA GAGGGAATTT GAGCCGGCAA GCTCAGGATA  
 2520  
 TGTGATGCAT TTAGGTGTTG CTTGCCAATA CCCGCAATTA GCACATCATA ATTTCTTTTT  
 2580  
 TACGGAAAAT GCTTATCTCA ATTATCAACA AGTTTTTCAT GAAAAGGTAT TGCCAGATGA  
 2640  
 TCCGACCATT TATCTAGTAA ATACGAATAA AACTGATCAC ACACAAGCGC CAGTAGGGTT  
 2700  
 ATGAAAATAT CAAAGTCTTA CCACATATTC CATATATTCA AGATCAGCCT TTTACCACTG  
 2760  
 AAGATTATGC GAAGTTTAGG GATAAAATTT TGGATAAATT AGAAAAAATG GGACTTACTG  
 2820  
 ATTTAAGAAA ACACATTATT TATGAAGATG TTTGGACACC GGAGGATATT GAAAAAAATT  
 2880  
 ATCGNTCTAA TCGTGGTGCA ATATATGGTG TTGTCGCAGA TAAAAAGAAA AACAAAGGAT  
 2940  
 TTACCTTTCC TAAAGAAAGT CAGTATTTTG AAAACTTGTA CTTTGTAGGT GGATCAGNAA  
 3000  
 ATCCTGGTGG TGGCATGCCA ATGGTTACAT TAAGTGGGCA ACAANTCGCA GACAAANTNA  
 3060  
 ACGCGCGAAG AAGCGAANGA ATAGGANGGT GANATCTATT GAAATCGGTN NTCACGACTA  
 3120  
 TTTAANAGAC AATAGTGGNN ACCCATCNTC TTNTGGGGNC TTGGGAGCAT TTGGATNTTC  
 3180  
 NNCGGGGGNC A  
 3191

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1189 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCTGGAATAA TTGGTGGTCC GTAATTGATG GGCCAAGTTG AAATTGGAAG CTAAAAAAGT  
 60  
 CTTAATCCGC CCAAATTGTT AACAACACAC CTATTGACTT TGTCAATCCA ACCCATCAAT  
 120  
 CCTTCATTAT TAACATGTCC CAGGTATCTT TAAGNTTGAT GAAACATTAG ATACCAGTTG  
 180  
 TTGGCGAAGG CTTAAAGCTT TGCCANCTTG AAAAATTAAG CCGGAATTAA GATGCATTGC  
 240  
 GTCGCCTATT TGAATCCAAA CCGATAGTGT TAAATATGAT AAATTAAAAG CACGTTATGA  
 300  
 GCGTTTCCAA AATCAATCAT TCAAAAACCTT AGATTATGAT TTCGAAAGCG TCGTACTTTC  
 360  
 AAGACAATCA CCATTGCGCG AACGTATTGA ACAACAACAA AAACGTTTGA ACTTACCGGA  
 420  
 TTTACCAACA ACAACTATTG GATCATTCCC ACAAAGCCGA GAAGTTCGAA AATACCGTGC  
 480  
 AGATTGGAAG AACAAACGCA TTACAGACGA AGCATATGAA ACATTCTTAA AAAATGAAAT  
 540  
 TGCTCGATGG ATTAAAATTC AAGAAGACAT CGGCTTAGAT GTATTAGTTC ACGGTGAATT  
 600

TGAACGTAAT GACATGGTTG AATTCTTCGG AGAAAAATTA CAAGGTTTCT TAGTAACTAA  
 660  
 ATTCGGTTGG GTGCAATCAT ATGGTTCACG CGCCGTAAAA CCACCAATCA TTTATGGTGA  
 720  
 TGTAAGATGG ACAGCGCCTT TAACTGTTGA TGAAACAGTT TATGCACAAA GCTTAACAGA  
 780  
 TAAACCAGTT AAAGGTATGT TAACTGGACC TGTAACAATT CTAAACTGGT CATTTGAACG  
 840  
 TGTGATTATA CCACGTAAAG TCGCTCAAGA TCAAATTGCT TTAGCAATCA ACGAAGAAGT  
 900  
 ATTAGCACTT GAAGCTGCAG GAATCAAAGT TATCCAAGTT GACGAACCTG CATTACGTGA  
 960  
 AGGCTTACCA TTACGCTCTG AATATCACGA ACAATATCTT AAAGATGCTG GTTTTATCAT  
 1020  
 TTAANCTTGC AACGTCTTCA AGTTCGGTGA TGAANCTCAA ATCCATACAC ATATTGTGTT  
 1080  
 ATTCTCAANT CGGGCAAATC AATCAATGCT ATTCAAGATT TAGATTGCTT GATGTTATTC  
 1140  
 AATTGAACAC TCCGNGCCNT GGGGATTTAA TTAAGNTTGG AGGTTTTAT  
 1189

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGAGCATAAT AAAGAGCGTA TCTTAAACAT TAATTTTAAG TGTGATCCCA AAGTAATTTT  
 60  
 CGTGATTCAT TGAAAATTGT TCCGAAAGNA CCGTTGTTCA TCCAAGACAA TATTACCTT  
 120  
 AACAATATTG ATTTGGGGTT ACCTGGAACG ATGTTATTAA GTTTGGTTAG CTGACAAAAA  
 180  
 TAGTCGTTAC CGCCATCGCA GGACCCAATG CCGATTGTAA TGGTTAGCAT TATTAAATCA  
 240  
 ATGATGCATC CAAAAAATGG AATATATAGA TGCAAGTCAT ATTGTGATTG CGTTGTTAAT  
 300  
 CATCCTTGTTG ATAATCACAT TGTTTATCTT ATTATTCATT GAATTAGTAG AAGTGAGAAT  
 360  
 ACCATATATC GATTTAATGA ACGTTTCCGC AACAAATATG AAATCTTATT TATCTTGGAA  
 420  
 AGTTAACCCCT GCAGGCAGTA TTAAGTTAAT GATGAGTATT TCAGCATTTG TTTTCTTGAA  
 480  
 AAGTGGCATT CATTTTATTT TATCTATGTT TAATAAAAGC ATATCAGATG ACATGCCAAT  
 540  
 GCTGACATTT GATAGTCCAG TAGGTATTTT AGTATATTTA GTGATTCAAA TGTTATTGGG  
 600  
 TTATTTTTTA TCGAGATTTT TAATCAATAC TAAACAAAAA TCCAAAGATT TCTTAAAGAG  
 660  
 TGGCAATTAT TTTTCAGGAG TTAAACCTGG TAAGGATACA GAACGTTATT TAAATTATCA  
 720  
 AGCAAGACGC GTATGTTGGT TTGGATCGGC ATTAGTTACA GTCATTATTG GTATACCGCT  
 780  
 TTATTTTACA TTGTTTGTAC CGCATTTATC TACTGAAATT TATTTCTCAG TACAACGTAT  
 840

TGTATTAGTT TACATCAGTA TTAATATTGC AGAAACAATT CGTACATATT TATATTTTGA  
 900  
 TAAATATAAG CCATTTTAA ACCAGTATTG GTAAGGAGGT AATTATGAAA TACTTTATTC  
 960  
 CAGCTTGGTA CGATGACCAA CGATGGTGGC AAGACACGAC TGTGCCGTAT TATCAACTAC  
 1020  
 AAAATAAGAC GGAATTTGAC GATATGATTA GTTTAATGGG AATGCACCTT GAAAATGACT  
 1080  
 TAGATTATCA ACTGATTGTT CTCAATCATG CACCAAATTT AAGAACATTT TTACATCGAT  
 1140  
 ATGACTTATA TGAAACAAAG TATTCGTCTG TGTTTGATGA AATTCAAGGA TTCAGTCACC  
 1200  
 ATGCGCCACA AGCGATTAAT TATCATCACT TAAAATGGNC GGATGATGTT GGAGTNTGGG  
 1260  
 TACACGCCCG NATTTATTAA AAATGTGTGA CGAGTGAACA GACCTATACA NATATTTATT  
 1320  
 TNAGNCAAGA AGGGTATTCA NTTGGGTTTG NAGANTGATT NGAAAGAGAT CAAGTNACAA  
 1380  
 CGGCGTTATA TTTTGTGATGA CAGAGGTTAT TTATCAGCGA TACGTTATTT TGATGATCAG  
 1440  
 GGAGAGGCTT CTTACCAACA ATATTTAACG GATTAATGGA GATTGTGTAA CTTCATGGAA  
 1500  
 GATTGGANAA ATGGCAGGAG TCACTGTATC NANAAGGATA TTCAACATCA CTATCAACAA  
 1560  
 ACAGAAATATA ACAATATGGC TCAACTAATT GGAAGAAAAA TTTCAAGCAA TGATTGCACA  
 1620  
 ACAAATACAT GAAGATGATC ATGTGATTGT GGCTTCAGAT GCTAGGCACA ATCGACAAAT  
 1680  
 AGCCAATCAT ATTCCAGCGA AATTGTAAAG TTATTCATTT TTTAAAAATA GAAATGAANC  
 1740  
 TGTGTCAGAT GAGGAATATC AATCTATCGT AAAGAATGCC CATTTAATTG TTGATAGTGT  
 1800  
 GCAACTAGAA CGTGATTTAA TTAGTCATCA AGAGAAGTAT CAGCGGGAGA ATACAATGAT  
 1860  
 TCGAATCACA CCATTTGAAA CGAGACAATC ACCTAATATA AGTAGTCAAT TGATGGAAAC  
 1920  
 ATTTATAGGT GTATGGATAG ATGGTATGAG TGACGCTGAT TTGCAACAAA TGATGCAACG  
 1980  
 ACTTGTGGAT TATATCGCAC AGGAAGATTA TTACCGTTTA ATTTTATTAT CGCGCCATCA  
 2040  
 AAATGACATA CCGATGTGGC TTCGTGAATG TATTACGTCG GTAAATGAGG AATACCAAGC  
 2100  
 TAAACAGAAT GCGGATGTTA ATGTTTCAGC ATTAATGACA CCTGAAGATC AAGATGACAT  
 2160  
 CATTGCTGTT AAGACGATAC ATGCTGAACA TGATGTTGTA GAAGCATTGC GGACGTTGCG  
 2220  
 ACTTGTGATA GATATGTCAA AAGAACCTGA TTTGTATTTA CAAATTAGTG CAATTAGCGC  
 2280  
 TGGGATTCCA CAAATTAATG GTCAACAAAC AGATTACGTC TCTGATTATG ACAATGGCCG  
 2340  
 TATTATAAAT ACAGCTGGAT GAATTAGATG ATGCGTTAAA TTATTATTTA TTTTATTTGA  
 2400  
 AAAATTGGAA TTATGCGTAC GCCTATTCTT TAAAATTAAT AGATGCATAT GCTTCTAAGA  
 2460  
 ATATTATTAA TCAGCTCGAT GAGTTAATAG AAGGTGAAAA TGATGCCACG TAAATTTAGA  
 2520  
 GTTTTGCAA TTGGAGGAGA CGATTTAGAA CCTATTTTTC AACACAAAAA AGGTGTGAGT  
 2580  
 TGGGATTACT TCGATATTGG ATTGTTTGAA TTTGATAGTG GTTATGTAGA GGCTATTGAA  
 2640  
 GCGATTGTTG AAGCAGAAGG GCGCTTTGAT TTTATCTATA TTCAAGCACC ATACTCGGAG

2700  
 ACATTAACGA ATTTATTACA AATGATAAGC GAACCATACA ATACGTATGT TGATGAATCA  
 2760  
 TTTTGGTCAG TTGAATATGA ACAAGACGAA AATTGTCCAA AAATACGTTG TTCAACCAAT  
 2820  
 TACATTACCG GAATATTGGA AGGAACGTAA TAATNAATTA GAGGCAGGNT AGCTTCTCAA  
 2880  
 GGACAAGGAT TGGAGATAAA GTTTCCCCTA AGTTAGCACT TGTGCATCCG AATTTTAAAG  
 2940  
 GAGATGTCGA ATACCCAAGG TAATTCAAGA GCTCACGTTG AGTGGAGAAT TTGGAAAAGA  
 3000  
 ATTTAAACCT ATCGCATCTT GNCAAAATAA TCTCGTTTAC GATAAAGATA AAGTCATTCA  
 3060  
 NATATGGCCA GAATTTGATA TTGATGGTGC GGTGAGTTG CAATATACAT TTAGATTGAT  
 3120  
 TCAGACTGGC GCTGATGGTG CATTAAATTGA ACAAATCATA TTAAGTATG ATATGTTAGA  
 3180  
 CAGTCCTTTA GAGATACCTG CGAAACCATT TGATGCTTAT ATAAGTGTA CTGTTAAGGC  
 3240  
 GCGTGGGAAC GGGACGGTAC ATTTAGGACC TAAACACACA CGATGGTCCA GANTAGANAN  
 3300  
 GGNTCAATTT TTACNTGGTG GGAATCGTTT CGAAGATANN CNCCGNCNGG AATTTAATTA  
 3360  
 TTAATCCNC CCTGGTGATA TGANACCCCC ACTAAACGTA AATTTTAGTG GTTATCGANC  
 3420  
 ACCGGAAGGT TTCGAAGGAT ATTATATGAT GANACGTATG AATGCNCCGT TTTTACTTAT  
 3480  
 CGCCGATCCT CGTGTTGANG GTGGTAGCTT TTATATCGGT TCATCTGAAT ATGAACAACG  
 3540  
 TGATTATCAA TGTTATTGAC GAGACAATAT TCATGCTGTA AATCCAACAT CAGGTGCAGC  
 3600  
 TGGTAAGTAT CAATTCTTAC AATCAACTTG GGATTGAGTA GCACCTGCTA AATATNAAGG  
 3660  
 TGTATACCA GCAAATGCTC CTGGAAGTGT TCAAGATGCC GCAGCAGTAA AATTATATAA  
 3720  
 CACTGGTGGC GCTGGACATT GGGTTACTGC ATAAGCCATT TATGCATAGC TAATCAATAG  
 3780  
 TTATATAAGT AACTTTTAGA TCGGAATATA TCGGG  
 3815

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GGCNCGAGAC GCTTAATTAT GGAACNCCAA GATGCNATTG GACNCGGTTA TAACATTGGN  
 60  
 ACAGGCACTT TTAATAATTT ATTAGAGGTT TATCGTATTA TTGGTGAATT AAATATGGNA  
 120  
 AATCCAATCG AGCNTTGAAT TTAAAGGAAG CACGAAAAGG AGATATTAAC CATTCTTATT  
 180  
 GNAGATATCT CTAACCTAAA GGCATTAGGA TTTTGTGCTC CTAAAAAATA CAGTAGAAAC  
 240  
 AGGTTTAAAG GATTACTTTA ATTTTGAGGT AGATAATATT GAAGAAGTTA CAGCTAAAGA

300  
 AGTGGAAATG TCGTGAAAAT GACATTGAAG CTGTCCATAA TAATAAGGGT TATGCCTATC  
 360  
 AAAGAAAATT AGATGCACTC GAAGAAGTGA GAAAAGGCTA TTACCCAATT AAACGTGCGA  
 420  
 TTGACTTAGT ATTAAGTATC GTTTTATTAT TTTTAACATT TCCGATTATG TTCATATTCTG  
 480  
 CCATTGCTAT CGTCATAGAT TCGCCAGGAA ACCCTATTTA TAGTCAGGTT AGAGTTGGGA  
 540  
 AGATGGGTAA ATTAATTAAA ATATACAAAT TACGTTTCGAT GTGTAAAAAC GCAGAGAAAA  
 600  
 ATGGTGCGCA ATGGGCTGAT AAAGATGATG ATCGTATAAC AAATGTCGGG AAGTTTATTC  
 660  
 GTAAAACACG CATTGATGAA TTACCACACC TAATTAATGT TGTTAAAGGG GAAATGAGTT  
 720  
 TTATTGGACC ACGCCCGGAA CGTCCGGAAT TTGTAGAATT ATTTAGTTCA GAAGTGATAG  
 780  
 GTTTCGAGCA AAGATGTCTT GTTACACCAG GGTAAACAGG ACTTGCGCAA ATTCAAGGTG  
 840  
 GATATGACTT AACACCGCAA CACAACTGA AATATGACAT GAAATATATA CATAAAGGTA  
 900  
 GTTTAATGAT GGAACATATAT ATATCAATTA GAACATTGAT GGTTGTTATT ACAGGGGAAG  
 960  
 GCTCAAGGTA GTCTTAATTT ACTTAATAAG TTCAAATAAA AGTTATATTT TAAAGATTGT  
 1020  
 GACCAATNGT TACAGTNTAA CGAGGANTCC CTTGNGACNG TATCAAATGG CATTAAAGAA  
 1080  
 ATATGTNCCA TCNTTTGATT TGCNTGGCCA ATAAATACTA TTCATCTTGA TGAGATAAGC  
 1140  
 CATGTTAAGA AATTGAAAGT ATAGCATTA NGGGGTTTGT AACAGTTGAA AATTATATAT  
 1200  
 TGTATTACTA AAGCAGACAA TGGTGGTGCA CAAAACACAT CTCATTCAAC TCGCCAACCA  
 1260  
 TTTTTCGTA CACCATGATG TTTATGTCAT TGTAGGCAAT CATGGACCAA TGATTGAACA  
 1320  
 NCTAGATGCA AGAGTTAATG TAATTATTCT CGAACATTTA GTAGGTCCAA TTGACTTTAA  
 1380  
 ACAAGATATT TTAGCTGTCA AAGTGTTAGC ACAGTTATTC TCGAAAATTA AGCCTGATGT  
 1440  
 TATCCATTTA CATTCTTCCA AAGCTGGAAC GGTCGGACGA ATTGCGAAGT TCATTTTCGAA  
 1500  
 ATCGAAAGAC ACACGTGTAG TTTTACTGTC GCATGGATGG GCTTTTACAG AGGGTGTTAA  
 1560  
 ACCAGCTAAA AAATTTCTAT ATCTAGTTAT CGAAAAATTA ATGTCATGTA TTACAGATAG  
 1620  
 CATTATTTGT GTTTCAGATT TCGATAAACA GTTAGCGTTA AAATATCGAT TTAATCGATT  
 1680  
 GAAATTAACC ACAATACATA ATGGTATTGC AGATGTTCCC GCTGTTAANC AAACGCTAAA  
 1740  
 AAGCCAATCA CATAACAATA TTGGCGAAGT AGTTGGANTG TTGCCTAATA AACAAGATTT  
 1800  
 ACAGATTAAT GCCCGACAA AGCATCAATT TGTTATGATT GCAAGATTTG CTTATCCAAA  
 1860  
 ATTGCCNCAA AATCTAATCG CGGCAATAGA GATATTGAAA TTACATAACA GTAATCATGC  
 1920  
 GCATTTTACA TTTATAGGCG ATGGACCTAC ATTAAATGAT TGTCAGCCAC CAAGTTGTAC  
 1980  
 AAGCTGGGTT AAGAAAATGA TGTCACATTT TTGGGCAATG TCATTAATGC GAGTCATTTA  
 2040  
 TTATCACAAT ACGATACGTT TATTTTAATA AGTAAGCATG AAGGTTTGCC AATTAGCATT  
 2100

ATAGAAGCTA TGCCTACAGG TTTGCCTGTT ATAGCCAGTC ATGTTGGCGG TATTCAGAA  
 2160  
 TTAGTAGCTG ATAATGGTAT ATGTATGATG AACACCCAAC CCGAAACTAT TGCTAAAGTC  
 2220  
 CTGGAAAAAT ATTTAATAGA CAGTGATTAC ATCAAAATGA GTAATCAATC TAGAAAACGT  
 2280  
 TATTTAGAAT GTTTTACTGA GGAGAAAAATG ATTAAAGAAG TGGAAGACGT TTATAATGGA  
 2340  
 AAATCAACAC AATAGTAAAT TACTAACATT GTTACTTATC GGTTTAGCGG TTTTATTCA  
 2400  
 GCAATCTTCG GTTATTGCCG GTGTGAATGT TTCTATAGCT GACTTTATCA CATTACTAAT  
 2460  
 ATTAGTTTAT TTACTGTTTT TCGCTAACCA TTTATTAAAG GCAATCATT TTTTACAGTT  
 2520  
 TTTCATTATT TTGTATACAT ATCGTATGAT TATTACGCTT TGTTTGCTAT TTTTGTATGA  
 2580  
 TTTGATATTT ATTACGGTTA AGGAAGTTCT TGCATCTACA GNTAAATATG CATTTGTAGT  
 2640  
 CATTTATTTT TATTTAGGGA TGATCATCTT TAAGTTAGGT AATAGCAAAA AAGTGATCGT  
 2700  
 TACCTCTTAT ATTATAAGCA GTGTGACTAT AGGTCTATTT TGTATTATAG CTGGTTTGAA  
 2760  
 CAAGTCCCCT TTACTAATGA AATCGTTATA TTTTGATGAA ATACGTTCAA AAGGATTAAG  
 2820  
 GAATGACCCT AACTATTTTCG CTCGTGCC  
 2848

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CCCCAAAGAA ATACANTTGT TGGTAGAAGA ACCCCCAACC CACAAGNTGG GGACCCTTCA  
 60  
 TTTCCAACCN TATGGCGGAG GGTAAAGTA AATTCTTGAA GCTTTGGTTG CCCNCAAATA  
 120  
 ATATGATATT TCCGAAATGG GCCGGAGCCG TATCCAACAA TTAAAAATCT GCCGGAGGTA  
 180  
 TTAAAGCATT ACTTAACCGC TCCGATTAAG ATGNNATTGA AGGAGAGATT AATATGGTAG  
 240  
 AATCAATGCT AACTTTTATG CTTGGGCCAT TAAGACAAAT CNCTGATTTT TATATGGAAC  
 300  
 ATTTACTCGT AAGTAATTCC ATCGTCATTG CAGGTATTTT TGCGACAGGT ATTTTAAAAA  
 360  
 AGAAAAAAGT TGTGAATTAA ATCANATTTG AGGTGATTTA CAAGTGAAAG CATTGAAATT  
 420  
 ATATGGCGTA GAAGATTTAC GGTATGAGGA TAATGAAAAG CCAGTCATTG AAAGTGCGAA  
 480  
 TGACGTTATT GTTAAAGTAC GAGCGACTGG CATATGTGGT TCAGACACGT CACGAAACAN  
 540  
 AAANATGGGG CCATACATTA AAGGTATGCC ATTTGGTCAT GAATTTTCAG GTGTAGTAGA  
 600  
 TGCCATTGGA AGTGATGTTA CGCATGTTAA TGTGGGCGAC AAAGTGACAG GTTGCCAGC  
 660

AATACCTTGT TATCAATGCG AGTAGTGTTT GAAAGGTGAA TATGCACGAT GTGAAAAAGT  
 720  
 TATTCGTCAT TTGNCTCAAT ATGAACCTTG GATCGTTCNG CGGAATATGT CAAATTCCCA  
 780  
 CCCCCAAAATG TTTTNAAGGG TTCCAAGCCA ATGTTGATTA CCATTGAANC AACCAATGGT  
 840  
 TTGAGCCATC AGCCCGTTGT TGCGCATGGG TTTTATAAAT CCGAATANAC AACCTGGTAT  
 900  
 GACTGTTGCA GTAATGGGGT GTGGCAGTAT AGGTTTGTTA GCTATTCAAT GGGCACGAAT  
 960  
 ATTTGGTGCT GCACATATCA TCGCTATAGA TATAGATGCG CATAAACTAG ATATTGCAAC  
 1020  
 ATCATTGGGC GCACATCAAA CAATCAATTC AAAAGAAGAA AATCTTGAGA AATTCATCGA  
 1080  
 AAATCATTAC GCCAATCAAA TCGATTTAGC TATAGAATCA TCAGGTGCTA AAGTTACGAT  
 1140  
 TGGTCAAATA TTGACGCTAC CTAAAAAAGG TGGCGAGGTG GTATTACTCG GAATACCATA  
 1200  
 TGATGATATT GAGATTGATC GCGTTCATTT TGAAAAAATT CTGCGTAACG AGTTGACAGT  
 1260  
 ATGTGGCTCT TGGAAGTGT TGTCCAGTAA TTTTCCGGGC AAAGAGTGGA CGGCAACCTT  
 1320  
 ACATTATATG AAGACGAAAG ATATTAATGT AAAGCCTATT ATTTCTCATT TTTTACCGTT  
 1380  
 AAGAAAAAGG CCCGGAGACA TTTTGATAAA TTAGTTAATA AGAAAGACCG ATTTGATAAA  
 1440  
 GTCATGTTTA CGATTTATTA GTATGCACCT TTGAGGACGA AAACGCTGGT ATAGTTATAG  
 1500  
 CTATGAAAGT GCGAATGCCG TCTGGTCTAC AGATACTATC GAAATAATTC ATCTTCGAAT  
 1560  
 ATACGTTGAT AAATAGCCGG TTTACTTGTG TGAAATATGC TTGTGAATCG GTTGTTTTGC  
 1620  
 ATTTTGTATA CTTAAAATGA GATGGCAATA TTTGATAATT TTTAAAGTGA AAATCAAGTA  
 1680  
 CAGCCACTTA ATAAGATAAA TTTATTATAA TATATGGTAA AATGATGGCA GTAATAATGA  
 1740  
 ATTTGAAAAA GAGTAAACAT TAATACCTTT AACAATTTAA TATCGTCAGA GTTAATGATT  
 1800  
 AACTGCATGG CAAAACAACT TAGAATGGTC AGTTACNNAA ATACATTTTT ATAAAAAATT  
 1860  
 ATCACACTAT TGTGACAACT ATCTTTGGAT TAATAAAAGA GGCAAGTGAG CAATAGGTTA  
 1920  
 GGCTTATGTG CGGGCATAGG TCAGTAATGT AGAAATGGAA ATGATGTAAT ACGTTAATTC  
 1980  
 GTTTGAATCT TTAAAAGTAT TGGATAAATC AGATAATCGC CTGTTATACG CATCAATCAA  
 2040  
 TGTTTTATAC ATAAATATGT CTGATATTTT TAAGTCGTTA TTTTGAATG GAATAAATGG  
 2100  
 AATCTTACCC CACGACCCTG TACTAAAATG CGTTTTTRRD CTNS  
 2144

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CAAATAACGG ACCCTTTNGT TAATATCCCA TTTTTTTGGC GGAGTATGGG ACCTTAGCAG  
60  
AGAAAATAGC CATAAGATAA GATTTTCGCCC CANNCGTTGG AGCCCAACTT ACATTGTTTG  
120  
TAGAATTTCT TTTTCGAAATT CTTTGTGTTG GGCCCCCACC CCAACTTGCA TCGTCTGNAG  
180  
AAATTGGGGG TCCAATTTCA CTGTGTTGGG NCCCCCTGAA CTAAATAGTA TGGAAATATA  
240  
TATATCTAAA TAATTAAAC GGNCAATAG TTTAATATGG CAGTAACAAT TTTTATAATT  
300  
TAGATATTTT GATATAGACT AATGCTTAA TTAAGCAACT TTTCTANNNA GGGAGTATGA  
360  
AAATGATTAG TACTTTGAAT GAAATTATGA AATGTATCGG AAGACCNCGA TACAATTATT  
420  
AATACACAAG ACATGTTAGA CCAGATCCAG ATGCATATGG TTCACAACTT GGTTTAAAT  
480  
ACTATATTCA GCAGAAATTT CCGCAAAAGC AAGTATTTGC AGTGGGTGAA GCGGAATCAT  
540  
CATTAAGTTT TATTGGAGAG TTGGATAACA TTGATGATAA AACATATCAA GATGCGCTTG  
600  
TAATTGTATG TGATACTGCC AATGCTCCAC GAATTGACGA TGAACGATAT AGTACAGGTA  
660  
GTAAACTTAT TAAAATAGAT CATCATCCTG CAGTTGATCA GTATGGTGAT ATTAATTTAG  
720  
TTAATACGAA CGCGTCATCT ACAAGTGAAA TCATTTATGA TTTAATCTCA CATTTTAATG  
780  
ATGAAGCAAT TGTTAATAAA GGCACGAGCG AGTGTTTTAT ACCTTGGTAT CGTCGGTGAT  
840  
ACTGGGCGAT TCCTTTTTTA CAATACCTCA GAACATACTA TGGAAATTGC TGGAAAGTTA  
900  
ATTGGGCATG ATATTGATCA TAATGCGCTA TTAAATAAAA TGATGGAGAA GGACCCAAAA  
960  
ATGTTGCCGT TTCAAGGTTA TGTTTTACAA CATTTCGAAC TTATGGATGA TGGATTCTGC  
1020  
CAAGTTAAAA TAACTGAAGA TGTATTGGAG CAATTCCGTA TTCAGCCAAA TGAAGCATCT  
1080  
CAGTTTGTTA ATACAATTGC TGACATCAAA GGTTTGAAAA TATGGGTGTT TCCAAGTTGT  
1140  
TGAGGGTAGT GAAATAAGAT GTCGCTTACG CTCTAAAGGG CAATTGATTA TTAATGATAT  
1200  
TGCGCAAGAT TTTGGTGGCG GTGCCCATCC GGAATGCGTC AGGAGTTTCA GTGAACAGCT  
1260  
GGGATGAATT TGAGCAACTT GCTACAGCTT TACGCACAAA ACTTAACTAA TAGAAAGGAG  
1320  
CCATTCAATC ATGGTGGCAT ATTTAAATAT TCATACGGCT TATGATTTGT TAAATTCAAG  
1380  
CTTAAAAATA GAAGATGCCG TAAGACTTGC TGTGTCTGAA AATGTTGATG CACTTGCCAT  
1440  
AACTGACACC AATGTATTGT ATGGTTTTCC TAAATTTTAT GATGCATGTA TAGCAAATAA  
1500  
CATTAAACCG ATTTTTGGTA TGACAATATA TGTGACAAAT GGATTAAATA CAGTCGAAAC  
1560  
AGTTGTTCTA GCTAAAAATA ATGATGGATT AAAAGATTTG TATCAACTAT CATCGGAAAT  
1620  
AAAAATGAAA ACAATGGAAA ATGTTTCATT TGAAGTATTG CAACAATTTT CATCGAATTT  
1680  
GATTATCATT TTTAAAAATG TTGCAGACGA ACATCGTGAC ATTGTTCAAG TTTGTGATTC  
1740  
GCATGAAGAT ACGTATTTAG ATCATCAAAG TGTTTTAGTT CAGGGTATAA AGCACGTATG

1800  
 GATTCAAAAT GTTTGTACC AACACGTCA AGATGCCGAT ACGATTTCTG CATTAGCAGC  
 1860  
 TATTAGAGAC AATGCAAAAT TAGACTTAAT TCATGATCAA GAAGATTTTG GTGCACATTT  
 1920  
 TTTAACTGAA AAGGAAATTA AACAAATTAGA TATTAACCAA GAATATTTAA CGCAGGTTGA  
 1980  
 TGTTATAGCT CAAAAGTGTA ATGCAGAATT AAAATATCAT CAATCTCTAC TTCCTCAATA  
 2040  
 TCAGACAAC AAGCATGAAT CAGCTAAAAA ATATTTGGTG GCGTGTCTTA GTTACACAAA  
 2100  
 TTGAAAAAAT TAGAACTTAA TTATGACGTC TATTTAGAGC GATGGAATAT GAGTATTAAG  
 2160  
 TTATTACTAA TATGGGTT  
 2178

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCATTTTTTTT GATTGAGCCA AAAGGAGTCC CCCCTGTGAG CGGAATATTT AATTTATTGA  
 60  
 GCTATTTAAT ATTAAACGTA CGCTTAACCC CCCTANAGTG ATATCGTTTC TAGCGTTGTC  
 120  
 ATTATCATTA AGCGAAACAT TTTAAAGACA AATACACACT GTACGATCAC CAAACTGCAT  
 180  
 GTCGAACAAT GTAACATTTG GATTGATAT TTAAAATTGC TTGTGATGAT AAACTTTCTC  
 240  
 ATTTAGAAAA CGCTTCCACG TACATTCAAA AAAATAACTT TGTTAACCAT ATTGTAACAT  
 300  
 TATTTTCATAT ATTTTGGGGC ATGAGAATGA TTCTCACGCC CAGTAATTTA TTTATGCAAT  
 360  
 TGTTTCATGTA GGTTCCTTGC GACGTTTTCA GGAATACCTA TATTTTTAAA ATCTTCAAGT  
 420  
 GTAGCTCGTG CCTTCATTTT CTTGATTGAA CCGAATGAAC GCAATAATAA TGTTTTAACG  
 480  
 TTTGTTACCG ATACCATCTA TATCATCAAG TATTGATTTT AAGCCTGTCT TTTGACGTGT  
 540  
 TTGTCTATGA AATGTGATTG CGAATCTGTG AACCTCATCT TGGATACGGA TGCAACAAAT  
 600  
 AAAATGCCTG CCTATTTTTC TTCAGTGGAC AATTCCTGC ACTAGCGCCA TAATAATAAT  
 660  
 TCAGATGTTT GGTGTTTATC ATTTTCTGTC AAACCTGCAA CAGGGATATC AAGACCTAAT  
 720  
 TCGTTTTGTA GCACATCAAT AACCCCGTTC ATATGTCCTT TACCACCATC GACTATTATT  
 780  
 AAATCAGGTA ATGGTAATCC TTCGTTTAAA ACGCGAGAAT ATCGTCGTCT TACTACTTCT  
 840  
 CTCATTGATT TGTAATCATC TGGACCTTTA ACCGTTTTGA TTTTATACTT TCTATAATTT  
 900  
 TTCTTATCTG GTTTACCGTC GACAAATGTA ACCATTGCTG AACTGGATC CACACCTTGA  
 960  
 ATATTAGAAT TATCGAATGC TTCAATTCTA ATTGGTGTTT GAATTCCCAT TTGTGTTCCA

1020  
 AGTTCTTCAA TAGCTTTAAT CGTTCTTGAC TCATCACGTG ATATTAATTC AAATTTATTA  
 1080  
 TTTAAGGATA CTTTAGCGTT ATGTGCAGCT AGGTCAACCA TATCTTTTTT GGGACCTCGC  
 1140  
 GCGGGTTGAA CGATTTTAGT GTCCACAACA GATTGAATCA TTTCTTTATC CAAATTACGT  
 1200  
 GGTACATGAA CTTCCTTAGG TAAAATATGT TGGTTTAAGC TATAAAATTG TCCAATAAAT  
 1260  
 GTATAAAATT CTTCTTCTTC TGTTTGGTGT AATGGAATCA TCGNGTATC TCGCTTTATC  
 1320  
 ATATTACCTT GTCGGATTAA AGAAACTTG GATACACATC CATCCTTTAT CAACACAATA  
 1380  
 ACCAAAGACA TCACGAATCG GNTTATCTGA TGACATAATT TNGGGTGGGT GGGCAAGATT  
 1440  
 TGGATATTGT TGGATTAAAT CTCTATATTC TTNAGCCGCN CAAAATCAAG TGATTCACTT  
 1500  
 GGAGGNCACA TNCGCTCTTC TAANCTTT  
 1528

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AGGTTGATAC ATATGTCTTG TAAATACATG TGTCATTGCT TGACCAATTG CAGCAATCTG  
 60  
 GACCCAGGAT NGGTGCCTAC CCAGTTATCT CCAAATTTCA CATTTCTGCG TAATCTGGTG  
 120  
 CTACTTGAAA TGACTTTTGT ACCTTAATAG CGGACTTCTG TCATAAAATG TGCATCCGGA  
 180  
 GTACGTGTTA AAGGTACATT AGAGCCCCAC ATAATAATGT ATGATGCGTT ATACCAGTCA  
 240  
 CTTGATTCAG GCACATCTGT TTGCTCTCCC CAAATTTGTG GAGAGGCAGG TGGTAAATCT  
 300  
 GCATACCAGT CATAAAACT AAGCATTTCA CCACCAAGCA AATTGATGAA TCGAGCACCT  
 360  
 GCTGCATAAC TAATCATTGA CATCGCTGGA ATAGGTGTAA ATCCTGCGAT TCGATCTGGA  
 420  
 CCATATTTTT TTATTGTATA CAGTAATTGT GCTGCGATTA TCTCTGTAAC GTCTTTCCAA  
 480  
 TTTGAACGCA CGTGCCCTCC CATACTCGG GCTTGCTTAT ATTGTTTGGC TTTGTCTTCA  
 540  
 TTTTCAACAA TAGACGCCCA TGCAGCAACG CGATTACCAT AGTTTTCTTC TAATGCTTCA  
 600  
 GTCCATAAAT CCCAGAGTTT TCCACGAATA TATGGATATT TGATTGGAAG CGGACTGTAT  
 660  
 TCATACCAAG AGAATGACGC ACCTCGTGGA CATCCTCTCG GTTCATATTC AGGCATATCC  
 720  
 GGACCACAAC TTGGATAGTC AGTTTGTTGA TTTTCCCAGG TAATCACACC ATTTTTCACA  
 780  
 AATACTTTCC AAGAACATGA GCCTGTACAG TTAACACCAT GTGTTGTTCT TACTTCTTTA  
 840  
 TCGTGGCTCC AACGTTCTCT GTACATTTTT TCCCATTCTC TACTTTTACT TTCTAGGATC

900  
 GACCAATTCC CATTAAATTT TCTGTTGGCT TAAAGAATTC AATCCAAATT TTCCCATATT  
 960  
 TATATCCTCC TACGTATAAA AAATACGATG TGTAGATGTC GTGTTNTTAA ATACTTTAAA  
 1020  
 ATGCCCAAGA CTATTGCTTT AATTAGATTG TACATTTTTT CACAAATATA AAATATTAGG  
 1080  
 GAATCACCTA ATTACTTAAG GAATTTCCCT ATCAATAACG GGATTTTCATT GAAATAATAC  
 1140  
 ACAATCATGT ATGGTCGTGC TTATTGCCAA TCTAAATCGT TCAAATTTGC CACAACGACA  
 1200  
 AATAAGGCTT CAACACGAAT ATATTCTCTC GGTTGAAACC TTACTTATTC ATTTATTTTT  
 1260  
 TATAAATTAG TGACATAACA CTGTATTAGC ATCTGCACGA TCGGTTGAAA TATATGTTAC  
 1320  
 ATTTTCTTGC TGCTTAATAA ATGCATCATA GTAATCATAT TGCCGACCGG AATGATATGT  
 1380  
 CCCATTGAT GTATCATTTG GGTTTAGCAA ACAGCCATAA CCTTCGTCAT ATAAATGTTC  
 1440  
 ACAGAGCATA AGGGCGTCAT GTCTAGAACC ACTTACTACA TAAATTGCT GAGTCGGATT  
 1500  
 AGAAGTTGTT GAGACATTTT CAGTATAACC CACTACTTCG CCTATAATAC ATATACCTGG  
 1560  
 TTTGCGCTCA ATTGCGTAAT GCTCCAGTTT CCCAACAATA TTACTTAAAC GCCCCTTAAC  
 1620  
 AACAACTCG TTAAACACG ATGCTTGAAA GACAATCGCT ATCGGATAAT CAATATCTGT  
 1680  
 GTACTGTTGT ATCTGGGCGA TAATTTTCCC TAAACGTTTA ACTCCCATAT ATATCGCCAA  
 1740  
 CGTACCACCA TTTACTAAAG NGTTGACATC TACGTCATTT TCTTCTGAAT CTNTNAAGTG  
 1800  
 ACCTGTAGAA AATGTCNCAC TCTTAGCAAC AGCACGCNTC GNTAATCCTG TTTGCATCGT  
 1860  
 AGCAGCTGCA GCACTCGCAA GATGTCACAC CAGGTACAAT GTCANACGCA ATAGTAAAAG  
 1920  
 TTGTTTAGTG TGTCAACTTC TTCTTGAAC CGNCCAAATA TTGCTGGGTC GCCACCTTTA  
 1980  
 ACCCTCACCA ACCTTGTTAT ATCGACGTGC TGCTTCCACG ATACATTCAT TTATTTTTTC  
 2040  
 TTGCTGAATG TGTTTTGCAT ACGGCTTTTT ACCAACATCG ATAATTTAG TAGTCAAATT  
 2100  
 CGCATATTGT AAAATTAACG GATTCATAA TCGATCATAT AGTATAACAT CCGCTTCACG  
 2160  
 TATTAAACGC TCAGCCTTTT TAGTCAAATA ATTTCGATTA CCTGGTCCCG CACCTATCAA  
 2220  
 GTAAACCTTG CCATATTTAT CTACAGACAT ATATATACGT TCCCGTCTGT AACTTCTACC  
 2280  
 TCATAACAT CTACACAACC TTCATCAGGT TCTTGTAACA TCCCAGTATT TAAATCAATC  
 2340  
 TTTTGATCAT GAAGTGGACA GAATACATAT TCACCACTCA CTGTTCCCTC TGACAATGGT  
 2400  
 CCTTGTTTAT GCGGACAAAT ATTGTGGAAT CGCGTGANTT GTACCACTTT CAGATAAAAA  
 2460  
 CCAATCCTAC CTCTTTGCCT TTGNCAATAA CCTTTTTTCC AATTAGGGGT GTTAATTCAT  
 2520  
 CTATAGTTGT CACTTTAATT TTTTCTTTTG TTTCCATGTA TTACACCTTC TCCACTTCAA  
 2580  
 AAATTTTACG TGCTTGCGCA TTGCTAGNTA TTGCTTCCCA AGGTTTCAGT TCGACTGCTT  
 2640  
 TTTTAGCATC CATAATGCGT TCAAATAGTT CATTTTGTCT TTCTGGGTCA AGTAAGACTT  
 2700

CTTTTACATT TTCAAATCCA AGTCTTCTTA ACCATGGCGC TGTTCCTTCA GCATATATAC  
 2760  
 CTGTTTCGCG ATATAGTGCA TCAAAGCACC ACATAATGTG NTTACTTCAT CTTCTGTTTC  
 2820  
 TACAGTTGTT AAAAATTCAG CTTTTTCGAC TTCTGTACCA CCATTACCAC CGATATAGAT  
 2880  
 TTGGAATCCA TTTTCAACTG AGATAATACC AAAATCTTTA ACACCTGATT CAG  
 2933

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TAAAGTTCNT TCCCCTGCTN AATGTCCAAN TTTCCCCCAT AGCAACTTTC AAATATTTTT  
 60  
 CATGACTTGC TTTAGCCCCAA TCAAGTTCTT TACCTGAAGG TATATTAAAT TGATTTGTTG  
 120  
 AAAAGTTCCA AAAATTCTGC GCTTGGGTAA GTCCTTGTGG GACAATTTTT TGAAATCCTC  
 180  
 CAACTTCTTA AATATTTCTG GTGATTTTTG ATTAAAACTC ACGTAATTTA CGTAGTTTCT  
 240  
 CTTCTAATTC ATGTTTTTTG TTGACCTAAT GTTTGTATTA TTTGTTGGTT CGATGAAATG  
 300  
 GCTTGCTGAT TATCGGAAGC ATGCTTTTTT AAATTGTTAG TTAAATTTTC ATATCGCGTA  
 360  
 ATTTGTTGAC TTAATGATCT GATATCTTCT TCAAGCTCTG ATTCTTTTAA AGATATGCTA  
 420  
 TCAACCTCAC TCGTATAACG TGACACAAAA TTATCGCAAG CTTGCTTCGT TAAATCACTC  
 480  
 AATGTTTTCA TACTTGTTGA TAATGGAATT AACACCGTAC TAAAAAATTG CTTAGCTGAC  
 540  
 GTATACGCTT TCCCTTTAAG CGCATCATCA TTGATAAATT GAGTAATTGC TTTTCCAAC  
 600  
 GCATCATAAT TTGAATTCAT TGTTTGACTC AAATTCCCCA CACTTGAAGC TTGGTTTCGA  
 660  
 GATCTGTCTA AATACATGTC AATACTCATC GGCATGCTCC TTTTCAAAA ATATATGATT  
 720  
 TTCAAACAT TTAATAATCAA ATGCTTTTTT CATCTACAAA GTTGTAATAA TTTAAACTC  
 780  
 GGCGATGATT ATTTCTTATG TAAAGGAGTC TAGATGCAGG TAAATTGAGA TAACATGTCG  
 840  
 CCTTTTTTCT TATTTTAGCA TATGGATATA ATGGTGTCTT TGTATATTCG CAATTAATCA  
 900  
 ATAAAAATTA TCTTTCAATA TTTTAATTTT ATTGCGACAA CATCCTTAAC ATTAAATATA  
 960  
 TTAATATCTC AAAATATATT CACTATTAAA ATATGTCATC AGTTGTAAA AGTATTTCTT  
 1020  
 CATCATGCGA AATATCAAAA CGTATCTAAA ATACGAATAG TTTATCAATC ACACAACATC  
 1080  
 ATCATCCAAA ATTTNATTGC TCTCATNTNC AATATTCATT TCATATCTAT CAGTTCATAC  
 1140  
 ATAATTAATA TTTCAATTGT GCAATCTCAC CGTTAATGCA TCAACTTTCA AACAATAAAT  
 1200

CATCACATA ACCACACCTA ATTCACACT TTTCAAACAT AAGTATTGAC ACATTGAGCA  
 1260  
 AAATGATTTT TAATTGTAAC TAATACAGTT ACAATTATGA GGTGAGAAAC ATTGAATTTA  
 1320  
 GAATTTAACA TTGCCGTGCA TGTATTAGCT TTTTAACTA AGCATCATTC AGAAAAATTC  
 1380  
 AATAGTAGTT CATTAGCAGA ATTAACCTGT TTANATCCTG TTCAATTACG ACGCGTGACG  
 1440  
 ACTCAACTTG TCGATTTAAN AATGATTGAC ACAATACGAG GTAAAGATGG CGGTTATTTA  
 1500  
 GCAATGATC AAAGTGCTGA TGTCTCTCTA GCAACATTAT ATAAACATTT TGTCTTAGAG  
 1560  
 AAAGAACAAC ACACACGTCT ATTTACTTGG CGACGAAGGC AGTCACTGTC AAATTGCTCG  
 1620  
 TAATATTGCA ACTACCATGT CACATTATCA GCAAGACGAA CAGAATATCA TTATTAATTT  
 1680  
 TTATAATGAA AAAACAATCA AAGATGTCAT TGAAGACATT CAAAAGGAGG ATTTATGTCA  
 1740  
 TGAAAACATA TGATTTAATT GTAATAGGAT TTGGGNAAGC TGGTAAAACT TTAGCGAAAT  
 1800  
 ATGCTGCATC AACAGGTCAA CACGTTTCGA GGTATCGAAC AATCTTCCAA AATGTATGGN  
 1860  
 GGCAC  
 1866

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ACAATGCCTC CAAGAGGTAC ANCCGATAAC TGTCTCACAA AACTAAATAA ATTTAACTCT  
 60  
 GTGTCCTCTT CCCATCCGTT CACTTTAATA TCTTCTCCAT AAGCATCAAC GGAAAGATAA  
 120  
 AANCCGGACC TGGAAATGTA TGTGCCATCT CTTTAACCCA ATCAGTATCT TGAATGCCTT  
 180  
 TCGNTCCCAA CCTATGCAAT AATTAATCCC TGCGGCAAAG TAGTCCATGA TTTGGTGACT  
 240  
 TCGTACGAAT GCCACCACCT ACTTCAATAT CTTTGTTTGT TAATCTCCTC AATGACTTAA  
 300  
 TATAATCAAA CTCTCGGGCA TACTGTGCCT TAGCACCTAT CAAGTCGACG ATATGAATAC  
 360  
 GATTACACA TTCAAATTGA CTATAGTAAG CAATACTTCC TTCAGCCGAA CGCGACATTT  
 420  
 TTTCTTCACT ATCATATTTA CCCTCTGTTA ACCTCACACT TGTGACCCA ATCAAATCAA  
 480  
 TCGCTGGCCA TAATTCAATC ATTTATAAAT CCCCTTGTA TTGCCTGACG CAAAATTTGT  
 540  
 AACCCATATG TACCGCTTTT TTCAGGATGG AATTGAATAC CAATATAATT GTTAAATTGA  
 600  
 ACAATTGCCG GAATATCAGC CCCATACTGC GCATATGCAA TGACATTTTC TGACATCGGC  
 660  
 GCTTGTAAG AATGTACGAA GTAAACATCT TGATTTAACA TAGGATGCTT ACTCACTAAA  
 720

TTATTCCAAC CTAAGTGC GG CACTGGGTAT TCTGTTGGGA TACGCGAAAT ATTCCTGGG  
 780  
 ATAAACCCTA ATCCAGATGC ATCGCCTTCA TCACTATGCT CATAATTAA TTGCATGCCT  
 840  
 AAACAAATAC CAATCATCTT CTTATCAGTA TTCTTAGCCA ATATTGCATT GAGATTTAAT  
 900  
 CGTTTTATCT CTGACATCGC ATCTTTAAAA TGGCCGACAC CGGGCAATAT GATTGTTTCT  
 960  
 GCTTGATCGA TTATTTTTGA GGTATTTGAG ACAACCACCT CATACCCTAA ATGTTCAATA  
 1020  
 GCGCGTTTTA CATTACTAAT ATCCCTAAT CCATAATCAA CGATGACAAT CATTCAATCA  
 1080  
 CACCTTTTGA TGACGGCACA CGCTGATCAT CAGTTGCAGT TAGCGCTATG CCTAATGCAC  
 1140  
 GGGAAAACGC TTTGAATATA GCTTCAATTT CATGGTGTGT ATTACCTCCA CGAATTAAAT  
 1200  
 CAATATGCGT TGTTAATCTT GCATTGATTA CGACCGCTCT AAAAAATTCT TCTACTAACT  
 1260  
 CCGTATCAA CGTACCAACT TTTTCTTTAC TTAATGATGC ATTGAATGAT AGGTATGGGC  
 1320  
 GCCCACTTAT ATCCACAACG ACACGTGCTA ATGTTTCATC CATTGGAATG TACATCGTTC  
 1380  
 CATAACGAAC GAAATGCTTT TTATCTTTAA TCATTTCAAG TAACAATTGG CCAATGACAA  
 1440  
 TGCCGATATC TTCAGTTACA TGGTGATCAT CTACGTCAAT ATCACCTTGT GCCTCAATGT  
 1500  
 TTAATGACAG ACCGCTATGA AATGTAAACA ATGTTAACAT ATGATTTAAA AAGCCCACAC  
 1560  
 CTGTATTAAT ATGCGATGGT GACTGGTCAT CTGATATTGA AATATTTAGT TGGGGTTTCA  
 1620  
 GCTGTGTTTC GGTGGTTGTG AATAAATCAT ATTGTGCGCT CCANTCTTTA ACAATNTCTT  
 1680  
 CCTAATTGCT TTAAGTCCA TGCTGTTGCA ATTGAGTATC TTACATAGCC CTTTCATCAAC  
 1740  
 CGGCTCAACA TAAAAGCGAG GTTTAAATCC TTGTTCAAAT ACGTATTGTC CTAATTGGTG  
 1800  
 CGCTGCTGAA CCTTTAGTAA GTACAAAATT GGCATTTGAT GGAATACTG ACATTTTATC  
 1860  
 TGCAACATGT GTATCAAATA TTTGTTTTAA CTGCTCAGCT AACTGTCGTT GCATCGTTAA  
 1920  
 AAATACTCTT GTCTCTTCTC TATGTCTAAA AATATAAGTC GCAATATTTA GCGTAAATAC  
 1980  
 ATTTAATGGA TATGGATGTT CTATTTTTTG AATATGCTTT ATCGTTCCAG CAGTACTAAT  
 2040  
 TAAGACACCT AATCTTAAGC CGGCAATTCC AAACGCCTTT GATAATGTAC GCATTCTTAA  
 2100  
 GATGTGTGGT GCCAGTTCCA CGTCATATGC CGTACCATAA TCTAAATATG CTTTCATCAAT  
 2160  
 GACAAAGTAT CCGTTTAATG CTTTCATCTT ATCTGCAATA GCTGTTAAAA ATGCCGNATC  
 2220  
 AAATTGCTTG CCTGAAGGGT TATGTGGATT ACTCATAATA AAAAATGATG GNTGTNCTTC  
 2280  
 ATCGATTTTC GTTAAAATGG TTTCCAAATC AAACGTNAAA TCTGATCCNG CATCTTACAA  
 2340  
 ATGCAATTTT ACGATTTACT TGTGCCGCAT ATGCTTGATA CATAAAAAAA TCAGGATTTA  
 2400  
 GCGTTAATGC CGGACCTTCT GGCATGATCA GCATTAACCT TTGANTCANT TCATCAGATC  
 2460  
 CATTTCCTGC AATAANTTGT TCAGGCGATA ACCCGTAAAA CTTAGCATNA GCTTCCGTGA  
 2520  
 ATTGTTTATA TGCTGCATCA GGATATAAAT TATATGGCGT TGCATAATA ATAGACGTCA

2580  
 TTGTTTTTTC ATCCAACGGC GTAACGGAC TTTCATTTTT ATCAATATAA ATCATTTCAA  
 2640  
 TTACACTCCC CTAAGACTGA CGTATTAAAA TAGACTGCTG GTGATTGTAT AATGCTTCAA  
 2700  
 CATGAGCAAT ATGTTGTGCT GAATCAGCAA TTTGTTCAAA CGTATCTTTT GATAAATGGA  
 2760  
 TGACCGTGTT CCGTGTTAAG AAATCATTGA CCGATAACCC ATTGGTAAAT CTAGCTGTTC  
 2820  
 TATTTGTAGG TAATACATGA CTTGGACCTG CAACGTAATC TCCTATGACC TCTGGCGAAT  
 2880  
 AATGTCCAAT AAACAATGCA CCCACATATT TCACTTNCNC AATATATGGN TGAGGATTTA  
 2940  
 CTGTGTGAAT CGACGCATGT TCAGGCGCGA TCGTGCCTTT CATGACATGG  
 2990

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GCATCGGTTA AATGGCGTCA TTCCAATTAC GGGCATCTTN AGGCATTTTG CTTTTCAAGT  
 60  
 GGCTAATTTA GCTTCACCGT TTAAGGCTAT TTTTAGCATC AGTCACTTGA GTTAATGCAC  
 120  
 GGAGTAATGT CATCTGGGTT AAGCGTTGGA TTTGTCGTTT GATTGATAAT ACCTTCCGCT  
 180  
 TGAGACACTG CATTTGTATA TGCTGTTTGC TTATCGACAT CAGCATCGTG GTAGTTCTCA  
 240  
 CTTGCTTTCA CAGTATCTTT ATTTGCAATA CTTGTTTCA AGTTACCCAT TGCTGTATTC  
 300  
 ACATTTTGTG CATTTTGTGTT TAGTTTGTCC AACCTGTAGC TAAAGCTTGT GCTTGATTGA  
 360  
 NTTGGTTTCG TAATGCATCA CGTTGTGGTG ATTTAAGTCA CGTNACGTAT CAAGATTTGC  
 420  
 TAAAGCATCT TGTTTCGCTT GCGCTAATTT TTCATCACCG TTTAATGCAT CTTTCGCTTG  
 480  
 ATTCATAGTT GTAACGTCTT TTGTTACTGT ATCAGGCGCC AATACAGGTG TTGGTGTGCC  
 540  
 ATTTGCGATT TGTTGCGCTT GGTTAGCTGC ATTGTTATAA GCTTGTTGTT TGTCTTGATC  
 600  
 CGCTTGTGTA AAGTCAACTG ATTGTGGTAC TTGACTATTC GCTTGAATTT GTTGTGTCAA  
 660  
 CGTACCCATT GCATTATTTA ACGCATCAGC ATTTTGCTTA ATAGCATTA CACCTGTAAC  
 720  
 AAGTTCTGCA TGCGACACTT GGGTCTTTTA ATGCTGTTTT TTGTGGTTGA TTTAAGTTTG  
 780  
 GTAACGATC AATGGCTGTA TTTGNATTGT CTTTAGCAAC TTGTAAGTTA TGGTTACCGT  
 840  
 TTAAATCACC CTTAGCTCGA GCCACTTGTT GTAACGCTTG AGCCACTTGT TGTGGACCCA  
 900  
 CGCTTGCAAT TGGGTGNACC ACTAATGATT TGGTCCAGCA TGCGCTACCG CATTTGAAAA  
 960  
 ATGCATTTTT GCTTATCAGT ATCAGCATTT GCCAAAGTTA CCATTTGCTT NAGGTGGTCT



1020  
TAATCTGCAA TACCTTGTNT CAATTGTGTC ATTGCTTTGA NNTAAATCTT TGTGCTGTTT  
1080  
GCTTAATCGT GTTNACATTT GCAACAGTTT GCGCAGCATC GACTTGTTGT TTAAAGGCAT  
1140  
CTTTGTGCGC TGGATTTAAA TCATTTGCAT TTGTAATAAC TTGTTTCGCT GCATCTTTTG  
1200  
CACGTTGTAA CATTGTCATT ACCATTCAAT GCTTGTTTCG GCTTCGTTCA CACGTTGCAT  
1260  
CGCTTGTTTC CAACTTCAGT TTGAACTTGC ATTGCTGCCA TTTGCTTTAG ATAAAATACC  
1320  
TTCTGCATGT GAAACCGCAT TAGTATAATC ATCTTTCTTA GCTNGATCTG CATCAGTAAA  
1380  
GTAAATGCTA TCTAATGTCT CAGTTTTATC TTGTAATGCA TTGTTTAAGT TAGTCATAGC  
1440  
ATTATTCAGA TTTTGAGCAT TTTGCTTAAC ATTATTAAC TTTGCAATAT CTGGTGCTTG  
1500  
TTCAACTTGA GTTGTTAGCG CTTGTTTTTG AGCATCATTT AAATGATCTA GTGTACCAAG  
1560  
TGTTGTCTTA GCATCTTGTT TGGCATCAGC TAATTTGTGA TTACCGTTAA GTGCTTGATT  
1620  
TGTGTCATTC ACTTTAGTTA ATGCTTGTTG AATTGTATTT GGATCCATTG TTGGATTTGT  
1680  
TGTTTGTTTT AACAATTCTT CTGCTTGNGT TACTGCATTA TCATATGCTG TTTGCTTGTC  
1740  
AGTATCAGCA TCGTGATAGN TCTCGCTACC TTTAATTTGT GCTTTATTCT CAATACCTTG  
1800  
TTTCAATTGT GTCATCGCGT CATTAAGCGT TGTTGCCGCT TGTTGAATAG CATTGACGTT  
1860  
TGGTACAAGT GTTGCTTGCG TGATTTGTTT GCTGTATTCA TCACGTTGCG CTTGGTTTTAA  
1920  
GTTTGGCAAT TGATCAATAG CATGTTGAAC ATTTTGTTTC GCCGTTGCTA AGTTTGTATT  
1980  
ACCATTTAAA TCATTTTTAG CTTGCGTAAC TNNATCTAAC GCTGCAGGAA TTTGCTAGG  
2040  
TGTAACGACA ACATCAGGCG TACCACTAAT TAATGCTTCA GCTTTGCTA CTGCTTGATT  
2100  
ATATGCATTT TTCTTGTCAG AATCTGCATT GACAAAGTTA CCATCAGCTT TTGTTTGTTT  
2160  
TTTATCTGCA ATGCCTTGTT TTAATTGTGT CATCGCATTG TNTAACTCTT GCGCCGTTTG  
2220  
TTTAACATTG TTTACACCAG CTACAGTAGT TGCATTTCTG ACTTGTTGTT TTAATGCATC  
2280  
TTTCTGTGCT TGGTTAAGAT CATTAGAGTT ATTAATTAAT GCTGTTGCTT CGTCTTNTGC  
2340  
ATGTTGAACG TTGGCATTAC CATTTAATGC TTGTTNTGCT GCATTTACTT GTTGGATTGC  
2400  
TTGNNCAACT TCAGTTTGTG TTGCATTACC ACCATTAGCT TGTGGAAATG ATATTTNCAG  
2460  
CATTTGTAAC TGCAGTGTTA TATGCTTGTT GTTNGGCTTG ATCTNNATCA GNGAAGTTAC  
2520  
CTGNTGCTNG CGTAGCATCT ATATCACCTA TCGCTTGTC CAAGTTACCC ATCGCAGTAT  
2580  
TTAAGTTTTG CGCATTTTGC TTAATTTGAT TTGCTTCATC ACCAGTATGC GCGCCATTAA  
2640  
TTTGATTAGT AACAGCTTGT TTTTGCGCAT TATTTAAGNT GTCTAATGAA CCTAAAGATT  
2700  
GCGTTGCTAG TTGCTTCGCT GCCTCTAAGT TTTTATTACC ATTTAAAGCA TTTTATAGCG  
2760  
TGCTTACTTG TCCAGCAGCT TGATTGATAA CAGTCGGATC TAATGAAGGG TTTGTAGTTT  
2820

GATCAATAAT ACCTTGTGCA GTTGTGACAG CATTATTGTA CGCATCCTTT TTATTCGGAC  
 2880  
 TTGCATCAGT ATAATTTTGG TTTTGTTTTG TTGTCGCATT ATCTGCAATA CTTTGACGTA  
 2940  
 ATTTGTCCAT TGCTGCATCA ACATTGTTTG CTTTTTGTTT ATTACCTTGT GCTTCTGCAA  
 3000  
 CAGTAGTCGA TTGTTGTACC AATTGTTTTA ATGCCTCTTT TTGTGCATTT GTTAAATGGC  
 3060  
 TTAAACCGTC AATTGCTGTA TTTGCGTGTT GTTTCGCTTT TTCAAGGTTT TGAGTACCAT  
 3120  
 TAAGCGCTGC TTTTGTAGTA TTCACTTGAT TCATAGCTGC TTCAACTTGA TCTTTAGGCA  
 3180  
 CGTTCGTACC TGTAGATTTA TTTAAAATAT TTTCAGCATT ACGAACCGCT TCATTGTATG  
 3240  
 CATTTTNCCT CTCTGGATCT TGCATCTTGC AAAGTNNNGG ACTGGCAAGT GTAGTGTCTT  
 3300  
 TATCATTCAA GCTATTTTTC AAGTTANCCA TCGCTGTTTC AAAATCCTGA GNGGGNTTGA  
 3360  
 TTGGTTGGNG TTNACTTCAN CTACAG  
 3386

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATACAAG CGTCTAAATA TTAACAATCT NCCTGTGACG CTATATGGCA TATCTTGCTT  
 60  
 TTTAAGCATC TGTTGTATCT CTGCCATCGA GCGCATTGGC CAGCTTCACA ATAATTATAA  
 120  
 TGAATTGTTT TTATCGATGG AGACACTAAT TGTGTCATTG GGTCACCACC ANAACCATAT  
 180  
 ATTTGATGTG GTTTCATAAC ATCATTTTTTA TCAGAATAAT ATTTATAGGC AGCTAATGCA  
 240  
 ATCGTATCAG TTGCTCCAAC ANCCGCATCT ACTTGCTCCA CATTTTCCAA AACATTTGCA  
 300  
 ACATCTTTTT GTGCTTCCAC ATAAGTAAAA TTTGTTTCAT GTATATTAGG TTTAATTTGG  
 360  
 TATTTAGCTA ACTGGTCCAA GTAAACCCAC GTTTTCTATG AATACCACCT GCAATATCTT  
 420  
 TTTCACTTAC ACTAAACACT TCAACTTGTT GATATCCCTG TTGACCAATC CATTCGCCTA  
 480  
 TAATTTGACC TGCTTTATAA TCATCATGCA CAATACTATG AAGTTGTTCA TGTTGTTGAC  
 540  
 CAACAATAAC GATTGGTACA TTCATTTTAT TAATGACTTC AATATGTCTC TCTGTTATGT  
 600  
 CTGTAGCCAT TAAACAATA CCATCTACTT TACTGCGTGC TAATGTTTCA AGCGCTTGTA  
 660  
 TTTCTGCTTC GATATTTAAA CCTGTGTAAT TTAAATTTAA TTGTGATTCA TATTTTTGGC  
 720  
 ATTGTTTTGC CAATCCTTTG ATTGTTTCAT CTAATGCATA T  
 761

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
CCACCCANCT GATTATAATG TTTTAGCANG AGCTAGACTT GGTTGGTTAC CATCATATCC
60
ACAATTTAAT AAAAATAGTT TGTTGTTTGC AGAAGAAGCT AAAGATGAAG GCATTGAGTC
120
GAATGAGGCA ATTTTAAAAC GAGCGATAAA TGGAAGTTAA GTCAAAACAA ACGCAATTTG
180
CGATAGAAGA TCCGGATTTG AAAAAGAATC ATCCGGAAAT CACTGTTTAT ATGGCGCTCA
240
AATCTAATCT CAAGTTCTGC AAAAGGTCAA GAATACTTTA TGAAGCATTT ACTTGGCACA
300
AAATCAGGGT TATTAGCTAC ACCAAATGAA GATGAAAAGC CAGAAGAAAT TACGTGGCGT
360
GAGGAAACAA CAGGGAAATT AGATTTAGTC GTTCTTTAG ATTTCAGAAT GACAGCAACA
420
CCTTTATATT CTGACATTGT TTTGCCAGCA GCGACTTGGT ATGAGAAGCA TGATTTGTCA
480
TCTACAGATA TGCATCCATA TGTACATCCT TTTAATCCAG CTATTGATCC ATTATGGGAA
540
TCGCGTTCAG ACTGGGATAT TTATAAAACG TTGGCAAAAG CATTTTCAGA AATGGCAAAA
600
GACTATTTAC CTGGAACGTT TAAAGATGTT GTGACAACTC CACTTAGTCA TGATACAAAG
660
CAAGAAATTT CAACACCATA CGGCGTAGTG AAAGATTGGT CGAAGGGTGA AATTGAAGCG
720
GTACCTGGAC GTACAATGCC TAACTTTGCA ATTGTAGAAC GCGACTACAC TAAAATTTAC
780
GACAAATATG TCACGCTTGG TCCTGTACTT GAAAAAGGGA AAGTTGGAGC ACATGGTGTA
840
AGTTTCGGTG TCAGTGAACA ATATGAAGAA TTAAAAAGTA TGTTAGGTAC GTGGAGTGAT
900
ACAAATGATG ATTCTGTGAG AGCGAATCGT CCGCGTATTG ATACAGCACG TAATGTAGCA
960
GATGCAATAC TAAGTATTTT ATCTGCTACG AATGGTAAAT TATCACAAAA ATCATATGAA
1020
GATCTTGAAG AACAACTGG AATGCCGTTA AAAGATATTT CTAGCGAACG TGCTGCTGAG
1080
AAAATTCGTT TTAAATATA ACTTCACAAC CACGAGAAGT AATACCGACA GCAGTATTCC
1140
CAGGTTCAAA TAAACAAGGT CGACGATATT CACCATTTAC AACGAATATA GAACGTCTAG
1200
TACCTTTTAG AACATTAAAC GGACGTCAAA GTTATTATGT GGATCACGAA GTTTTCCAAC
1260
AATTTGGGGA GAGCTTACCA GTATATAAAC CGACATTGCC GCCAATGGTA TTTGGGAATA
1320
GAGATAAGAA AATTAANGGT GGTACAGATG CTTTGGTACT GCGTTATTTA ACGCCTCATG
1380
GANAATGGAA TATACACTCA ATGTATCAAG ATAATAAGCA TATGTTGACA CTATTTAGAG
1440
GTGTCCACCG GTTTGGATAT CANATGAAGA TGCTGNAAAA CACGATATCC AAGATAATGA
1500
```

TTGGCTAGAA GTGTATANCC GTAATGGTGT TGTAACGGCA AGAGCAGTTA TTTCGCATCG  
 1560  
 TATGCCTAAA GGTACAATGT TTATGTATCA TGCACAAGAT AAACATATTC AAACGCCTGG  
 1620  
 GTCAGAAATT ACAGATACAC GTGGTGGTTC ACACAACGCG CCGACTAGAA TCCATTTGAA  
 1680  
 ACCAACACAA CTAGTCGGAG GATACGCACA AATTAGTTAT CACTTTAATT ATTATGGACC  
 1740  
 AATTGGGAAC CAAAGGGATT TATATGTAGC AGTTAGAAAG ATGAAGGAGG TTAATTGGCT  
 1800  
 TGAAGATTAA AGCGCAAGTT GCGATGGTAT TAAATTTAGA TAAATGCATA GGATGCCATA  
 1860  
 CGTGTAGTGT GACATGTAAA AACACTTGGA CAAATCGTCC AGGTGCTGAG TAACATGTGG  
 1920  
 TTCAATAACG TAGAAACGAA GCCAGGTGTA GGGTATCCGA AACGTTGGGA AGACCAAGAA  
 1980  
 CACTACAAAG GTGGTTGGGT ACTAAANTCG TAAAGGGAAA CTTGAATTAA AATCTGGAAG  
 2040  
 TAGAATTTCA CAAATTGCTT TAGGTAAAAT TTTTATAAC CCAGATATNC CATTAATAAA  
 2100  
 AGATTATTAT GANCCATGGA NCTATAATTA TGAACATTTA ACAACTGCGA AATCAGGGAA  
 2160  
 GCATTCGCCA GTTGCTAGAG CGTATTCAGA AATTACAGGG GATAACATTG AAATTGAATG  
 2220  
 GGGACCTAAC TGGGAAGATG ACTTAGCAGG TGGTCATGTT ACAGGCCCAA AAGATCCTAA  
 2280  
 CATAACAAA ATAGAAGAAG AGATTAAATT CCAATTTGAC GAAACTTTTA TGAG  
 2334

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGCACGAGAC TAATACCTGA AATTAATCCA CCACCACCAA TAGCGGCAAA TAAATAATCA  
 60  
 AAGTTAACGG AATTGTCAGT CTTTGATTGT TCTAGCATTT CTTTAGCAAG CGTACCTTGT  
 120  
 CCAGAAATTG TATGAACATT ATTGAATGGA TCTATAAAGT TCATTTGATG TTCACTTGTA  
 180  
 TAAGTTAAAG CTTTCTAGTAA ACAGNGATCA AATGTATCAC CAGTGAGTAC AACTTCAACG  
 240  
 TTACTATTTT CAAAGAACTT TACTTGATTT ACCTTTTGTN AAGGTGTAGT GACTGGCATA  
 300  
 AAGATAACAG CGTTTANATT AAGTTTTTTTA GCTGTATAGG CAACACCTTG AGCATGATTA  
 360  
 CCTGCACTCG CACATGTAAT ACCTTTACTT TTAGCTTCAT CTGATAAAAC AGAAATAGCG  
 420  
 TTGTAAGCAC CTCTTAATTT AAAAGAACGT ACCCATTTGTA AATCTTCTCG TTTTAAATAA  
 480  
 ACTTTACAAT CATACTTTTG AGATAAGTAA TGGTCTAATT GTAAAGGTGT TTCTTTGACA  
 540  
 ATATCTTTAA GTCTTAAAAA TGCTTCATCG ATATCTTNCG TAGAACTGN TGTTTTGACT  
 600

GGCATAATAT TCAACTCCCT TAAAGTGATT TNNCATATTN NTCTATTAAT GATTCATATT  
660  
GTAGGGTGAT TGCAATTGTC ATCTAAGCCA TTTACCAAGT TTATTTTTCC AAAGTTTCAT  
720  
CAATTTCAAA ATGGAAACGC TTGTCTGGTG ATGACACAGT TTGATTGGT AAATCTATTT  
780  
CAATTTCCCTC ATATTGTGCA AGATGTTTAC GAGCACTTTT TTCTAAANCG ATAGGCAACA  
840  
TCGCATTTTT AGTGCAATTC ATATAAAATA TGTCCTGAA ACTTCCTGCA ATAATAATAT  
900  
GNAAACCATA GTCCTTAAGA GCCCAAGCAG CATGTTTACG ACTTGAACCA CATCCAAAAT  
960  
TATCTCCAGT AATTAATAA GAAGCCCCTT TATATTGTGG TTTGTTAGGA TTGAAATCAG  
1020  
GATTATCTGA ACCATCAGGT AAGTACCGCC ATTCATCAAA AGCAAATGGA CCAAAGCCAC  
1080  
TTTTTGAAAT ACGCTTTAAG TGTACCTTAG GAATGATTTG GTCTGTATCG ATATTGTCTG  
1140  
TGAAGAGAGG GACTATTTTA CCTTTATATG TTGTAATAGG TTTGATTGCT GCCATTTAAA  
1200  
CAACCACCTT TCTTACGTCC ACAAATTTAC CATGAATAGC TGCTGCTGCT GCCATAGCAG  
1260  
GGGATACTAA ATGTGTTCTT GCACCTTTGC CTTGTCTGCC TTCAAAGTTT CGATTACTTG  
1320  
TAGATGCACA ATGTACGCCC TCAGGTACTT GGTCAGGATT CATGCCTAAA CACATTGAAC  
1380  
ATCCTGGTTC ACGCCATTCA AATCCTGCAT TTTTAAAGAT AGTATCTAGA CCTAATTTTT  
1440  
CTGCTTCTTT TTTTACTGTA CGAGAACCTG GTACGACAAT AGCTGTAATA TTTGGATGAA  
1500  
CTTTATTTCC TTTAACAATA TGA TAGCTT CAATCAAATC TGATAGTCTA GCATTTGTAC  
1560  
ATGAACCGAG AAAAACATAC CCTAAGTCGA TGTCTTCAGC TTTTGGACCT GGTTCCTAACC  
1620  
CCATATAATC ATACGCACGT TGATCGTTGA TATCATTGAT TTCAGGGAAT GGTTCCTGTA  
1680  
AATTAACACC CATTTTCAAG TTAGTTCCCC ATGTCACCTG TGGTTCTAAT GTTGAAACAT  
1740  
CAAGTTCAAT TACACGATCA AATATCGCGT CGTGCCATCA GAATATAGCT CACGCCACTT  
1800  
ATCAACTGAT TTAGCGAAGT TATCGGCAAA TGGTCTCCCT TTAACATATT CAAATGTTAT  
1860  
ATCATCAGGT TGGATTATGC CGTATTTGGC ACCACCTTCG ATAGCCATGT TACAAATAGT  
1920  
CATTCGACCG TCCATTGAAA GGTTTTTAAT TGTTTCGCCA GTAAATTCCA AAGCATAGCC  
1980  
TGTACCAAAA TCAACACCAT ACGTTTTAAT TAAATGCAGA ATAATGTCCT TAGCATAGAC  
2040  
GCCTGTTGGT AAGGTACCAT TAATATCGAT TTTTAAGTTT TTGGGTTTTG TTTGCCATAG  
2100  
CGTTTGAGTT GCGAAAACAT GTTCAACTTC ACTTGTTCCA ATTCCAAATG CAATAGCACC  
2160  
AAATGCTCCA TGTGTTGCTG TGTGAGAGTC ACCACAAACG ATTGTTTTGC CGGGCTGTGT  
2220  
AAGTCCTGTC TCAGGTCCTA CCATGTGAAC AATACCTTGT TCATCAGAGC CCATATCAAA  
2280  
AATATGCACC CCAAATCTA TGGCGTTTTT TTGTAATGTT GTGATTTGTT TGTGTTGCAAT  
2340  
TTCATCTTTA ATATTGAAAA TATCAATAGT AGGAACATTG TGATCGAGTG TTGCAAATGT  
2400  
TAAATCTGGG CGTCTTAATT TTCTGTTTTG AAGCCTAAGT CCTTCAAATG CTTGAGGAGA

2460  
 AGTAACTTCA TGTATAAGGT GTAAATCAAT GTATAATAGT TGCGGGTCGC CCNATTTCCC  
 2520  
 GNATAACACA TGTCTGTTCC ACACCTTGTC AAATAATGTT TGACCCAGTT ACATCTCCCC  
 2580  
 CTNAGTGATT CAATTTTGA GATAGCATTT CGAAAATATC AGTAGTATTC AATTTGCCGC  
 2640  
 CTAAATCTGC TGTCGTTTGC CCATGTTCAA TCATGTTATA AATATGTTGT TCTAATTC  
 2698

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTAAGANGAT ANTTTAAGCT TGTAACCCAA CAGTTCGCAG GTTAAATCCA ATCCAGTTTG  
 60  
 ACCAAAGAAA TACCGACCCA AACCGCCTTT GNACCGTAGT TGGATAATTA ATGGGGACCG  
 120  
 CCCAAAGATA ATAAGCAGTT AGCCGNNNAG GTTCCGGGAA TAGGNCCGTT TAAATTNAAA  
 180  
 ACCCAGCTGC CTTTTGCTTC TTGAAATACA TTGGGGAATC TGGATTAGAT GGTCCGAAAC  
 240  
 TACCGTCGAC ACCATCACGT CAAGCAGTTG CAATNCCAGC ATCAGATGTG ATTATAAACA  
 300  
 AAGTGATGAC GAGTGATACA CCTGTAACAA TTGTAGCGAC AGGTCCTCTT ACGAATGTAG  
 360  
 CAACGGCATT GATTCGTGAT CCAAGAATCG CTGAGCATAT TGAATCTATT ACTTTGATGG  
 420  
 GTGGTGGTAC ATTTGGAAAT TGGACCGCCT ACAGCAGAAT TCTATCAATA CCTACTTCTT  
 480  
 TCTTGACTAA ATCANACTGT GGCTTCGTTA ACATGCCACT TGGTGTGATA TAAAAACTAT  
 540  
 TTTTAAAGTA ATAGCTTACA GAGTGTTTCA AATGTTTCAGC GAATAAAGCT TCATCCATAC  
 600  
 GTTCTAAGAA GAATGGGATA AACTCACCCC AATGTCCAAT AATCATATTT AACTTTGGAT  
 660  
 AACGATCAAN AATGCCAGAT AATACTAGAT GTATTGCATR RDCTNS  
 706

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTTGTTGGAT CAGATCCAAC ACTACCTGAT GGATCNCTAT CNAGATTGAG CACGCCACCA  
 60

TATCAGATGG AATATCAACC TTGTCATGGG ACAGACTGAC ACCTGAATGA NGGGGTGTCT  
 120  
 GGNCANNCAC ATCATCACCA TTAATGGGAC AGCGAGTGGC ACATNTCCAT GTAGTAAATG  
 180  
 GCACTTATTA CTTACACGGN CATATCGTGN CAGGTTGGCA AGGTGTGAAA AAGACATGTG  
 240  
 ATACAGCGGA AGAGCTTGAC ACATATATAA AGCANAGTGA TGTGGTATAT GAGGAACAGA  
 300  
 AGCATCTANC TTTATTTTAA GNNGGCGGAA ACAATGAAAC TCAANGTTAA AAGAGANATG  
 360  
 AGATTAGATG AATTAATTAA NTGGGCGAGA GAAAATCCGG ATCTATCACA NGGAAAAATA  
 420  
 TTTTTCNCAA CAAGGATTTA GTGATGGATT CCGTCCGNTT TCATCCANAT ACAAATAAGT  
 480  
 GTCTCGACGN CAAGTTTTAT TCCAATTGAT ATCCCCTTCA TAGTTGATAT TGAAAAAGAA  
 540  
 GTAACGGAAG AGACTAAGGT TGATAGGTTG ATTGAATTAT TCGAGATTCA AGAAGGAGAC  
 600  
 TATAACTCTA CACTATATGA GAACACGRRD CTNS  
 634

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGCACGAGCG CCCATTTAAT TAATTCATCT AATCTCATTT CTTTTTTAAC TTTGATTTTC  
 60  
 ATTGTTATAT CTCCTCTTGA ACAGTAAATT TATCGTTAAT TGATACGTAT CCAGTCACAT  
 120  
 TACATAAGAT GCTATCAACA TCAAAAGTCA CACAACAGTT GCGTTCAACA TCATTTGAAT  
 180  
 AGAATCTTTT ATTACCTGAT AACTTGGCGG TTATCACCAA GCCCATTGAA TAAATTCAGC  
 240  
 TAAATCTCAT TTCTTTTTCA ACTTTGATTT TCATTGTTTC CGCCCTTTTA AAATAAAGTT  
 300  
 AGTTGCTTCT GTTCCTCATA TTCCAGAATC ACTTTGCTTT ATATATGTTT CAAGCTCTTC  
 360  
 CGCTGTATCA AATGTCTTTT TCACACCTTG CCAACCTGGC ACGATATGAC CGTGAAAGTA  
 420  
 ATAAGTGCCA TTTACTACAT GGATATGTGC CACTCGTTCTG TTATCCTGAT ACAGATATCT  
 480  
 CTTAGAGCCG AAAAAATGTT TTAAGTATTC TTTACGTCCG CTATCTGTCA TGGTCATCAC  
 540  
 TCCCGCAAGT CAAATACTCT ATCGACGTAA AACTTCGCCT TTGCTAAATC CTCATGACCA  
 600  
 TTCTTTAACG GTGCTCTAGA CAAGTATTTA ATTGCATTAC CTATTGCGAA TGCTAATTGT  
 660  
 GGTGGGTACT GTGCCGTAAC TTGTTCAATA AAATCTATAA TTTCAATGTT CGCCGTATGT  
 720  
 TGTTAATGCG CAGGTTGCTT AACGTTGTCT TGC GTTTTGT TCATATCTAC TTTTCTGTTA  
 780  
 CTGATTATGC TCATTATGTT TCACTCCATT TCTTGAACAT TTGGTTATAG TTGACATCGA  
 840

ACCAGTACGA TCACGTTGAA TGTTTTTGAG TACATCAAAT AATGTTGCTC CTTCTCTAGC  
 900  
 TCAGCTTCTT TACGTCGTAG CCTAGCCATT TCACGCTCTC GCTCCAAAGC TTTTGTTATT  
 960  
 TGTATTTCTC TATAGTCGTT TAGCTTCATG CCGAAAGGTG CATCAATTGC TTCCGACATC  
 1020  
 TCCCAACCCT TCGCAACTCT GTTTCTAACT ATTTCTGGGCG TGAGTCCTTT CTTTTTCATC  
 1080  
 TGCTCATTTT CATATTCAGT GTATTTAGAA GGGGGTTTTT CTTGTGGTGG CGCAATAAGC  
 1140  
 GCATCGCCCG TTAGCCC  
 1157

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGCACGAGCT CGTGCCGATT CGGCACGAGC TTCGGCTGTA TTGGTACCTA TCAATACAGA  
 60  
 CATTGCCGCT TTTTCTAAAT CTTCAATACT ACCTTGAGTC ACCCGCCGTG TCCAACCGTT  
 120  
 CTAAATAAGC CTTTTGTTGC AGGTGCTTGN CAATATCTTT GNACAAGCTA TCAACGTTAT  
 180  
 TTGTGCCAAT AACTTGCTT GCTAATTTTT GCANTAAANA CGATTCTTCA TTCGTCGCTT  
 240  
 TAGAAGAAGA AATGAATGAT AGTGCATCTG GGCCATACTT TTCTTTAATA GATGTAAAAT  
 300  
 TATCTGCAAT GACATTTAAA GCTTCATCCC ATTCTACTTC ATGGAAGTCA CCATTTTCC  
 360  
 TTACTAGTGG TTTAGTTAAG CGTTGATCTG AATTAATATG TCCCCATGAA AACTTACCTT  
 420  
 TAACACAAGT CGCAATTTTA TTTGCTGGAG AATCATGTGA TGGTTGTACT TTAAAATTT  
 480  
 CTCTATCTTT AGTCCAACT TCAAATGAAC AACCCACACC ACAATAAGTA CACACTGTTT  
 540  
 TAGTTTTCTT AATACGCTCT TAACGCAGTT CTGCTTCTGA ATCTGAGATT GCAAATAGTG  
 600  
 GACCATAACC AGGTTCTGCT TTTTGTAGTTA AATCAATCAT TGCTGCTAAT GAACCAGGTT  
 660  
 CCGTATCAGT CATATAACCC GCATTACCTT CCAGATTCAC TTCCATCATG GCATTACATG  
 720  
 GACAG  
 725

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

AAAATCCAAG GCACAAAGTT CTAAATACGG AGTCAAAAGA ATATTGAACA AGCACATTTT  
60  
CAACAATACT TTGAAAATTT ATTATTTTCAT AAGTTCATCA TTGATCCAAA GTAATATTGC  
120  
CCTTGCCGAT GTTCATCTTA TTGACTATTT ATTTACAGCC ATTAGTTAGA TATATTTTTG  
180  
AGCGAATTGT CATGGCTGTG ATTGTCATCA TTGGTGTTAT TGTCAGTGTG TTTACCATTC  
240  
TGTATTTTTTC ACCGCTTGAT GCGGCTTATA GCATACTGGG ACACAATGCA ACANAGGCAC  
300  
AGATACATCA ATTCAATGTA TTACATCATC TTAACGAACC TTATTTTATT CAATTGTGGG  
360  
ATACCATCAA GGGTGTTTTT ACCTTTGACT TAGGTACGAC TTACAAAGGG AATGAGGTTG  
420  
TGAATAAGC AGTTGGCGAA AGAATTCCAA TTACAATAAT TGTCGCAGTA TTAGCGCTAA  
480  
TTGTGGCATT AATTATTGCA ATACCAATTG GTATTATCAG TGCGATGAAG CGAAATAGTT  
540  
GGCTTGATAT CACGTTAATG ATAATTGCAT TAATTGGTTT ATCTATTCCA AGTTTCTGGC  
600  
AAGGGCTATT ATTCATTTTA GCGNTCTCAT TGAAATTGGA TATTTTGCCA CCATCTTATA  
660  
TGCCAGAACA TCCAATATCG GTGGATTTTA CCTGTACTTG TCATTGGAAC AAGTATTGCT  
720  
GCTTCTATCA CGCGTATTGA CAAGGTCTTC TTGTACTTGA AGGTAATGCG CAGCGATTAT  
780  
GTTTTNACTG CTTATGCAAA AGGATTATCG ACGACACAAG TTGGTTATTA AACATATTGT  
840  
GGAAAAATGC CATTATTCCA ATTGTACGGT AAGTGGGTCT TCCTNGGTGG CAGAGTTACT  
900  
AGGCGGTTCA GCAGTGACGG AACAAGTATT TAACATTAAT GGTATCGGTC GTTATATCGT  
960  
CCAAAAACAA CTAATACCTG ATATCCCAGC AGTCATGGGT GGGGTCGTAT ATATATATCA  
1020  
ATTGTAATAT CTTTAGCAAA CTTAATTATT GATATATTTT ATGCTTTAAT CGATCCAAAA  
1080  
TTACGTAGTG AAATTAACGA AAGGAAGTGA GGCATATGGT AAAACTTACA ACAAAGATAG  
1140  
CTTCCTTAAA ACTATTCGCA AGTTATGCTA TAGCAACTTA TATTTTAGTT ATGTTAACGA  
1200  
GTGCATTAAA TCTTTTTTAAA GGTTATGTGG CCGATACGTT CTATATTGCT GAAACATTGC  
1260  
TAATCATTTT AACCATCATT TTAATTATCA TTTTAACAAC GGAACAAACA TGGAAGCATC  
1320  
ATGACCTATG GCGACGTATC GTCGAAGTGT TGTTATTGTT GATGGCATT A ACAGGCAACG  
1380  
TATTTACATT ATTAATGTGT GTAAGTATTA GACGTTACCA ACGTACATCG CAAATACATA  
1440  
GTFATAACGG GGTGGGAATC CGNTTATACG AAAAATACT' AGACATCCGT ATTTGCGATT  
1500  
ATCGGGGTTA CTTATTTTAG TCTACATGCT GACATTATCA ATNGTGTCAC AATTTAAATT  
1560  
TGATACGACA ATGGCTTACT AAAAATCCAG TCCAATGAAC TNGTACAATG GACCGAGTCT  
1620  
AGCCTATCCG TTTGGTACTG ATGATTTCCG TAGAGACTTA TTTACACGCT CGTGCC  
1676

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
CTAATCGTAT GAACGAGTAC CCAGAGGTTT GAAATTTAAT ATTGATTCTA TNAATGATTC
60
CTTAGTGTCTG CATAACGGTG CAAGAGCACG ATACTTAGGA TCAATAAAAC CTTCGTCAAT
120
CATATGGTCA ATCATTGNTT GTAGTGGNTT GAAAANGCCA TTAATATTAT AAATGGCAAT
180
AGGCTTGTCA TGGATACCTA TTTGAGCCCA ACTAATACAT TTCGAAAAAT TCTTCTAGTG
240
AACCCTGCGC CACCAGGAGC CATGACAAAT GCATCTGCAA GTTCTGCCAT TTTATTTTTA
300
CGTTCATGCA TAGAATCCAA CTAAAATTAA TTCAGTTAAA CGTTGGCTTG TGATTTTCATG
360
TTCATCTAAC ATTTTAGGCA TGACGCCAAT AGCTTTGCCG CCATGATTTA ATACACCATC
420
TTGAATGGCA CCCATAATGC CAATTGACCC TGCACCAAAT ACTAATTCAT AACCTTGTTT
480
AGCAAAATAT TTACCTAAAT CGTATGCTTT TTGTACATAT GAAGGGTCAT GACCTTTGCT
540
TGCACCACAA TAACTGCGA TTCGTTTCAT GTTAATCCAG CTCCTTAATT CGATGAATGA
600
CTTTTAATAG TGATTGTTCA AACACTTTTT GATCTTGCTT TGTAAGAGGT GGGGGACCTT
660
TGTGGCGACC ACCTTGTTTT CTAATTTGTG CATTATATA TCGTTTATCT AATAGTTGTT
720
GAATATTTTT GGAATTGTAT ATCTTCCCAT TATGATGCAT GACAATTAAG ACTTTGTCGA
780
CTAATAAACT TGCGAGTCCA TAATCTTGAG TGACTACGAT ATCATCCTTC GTTGATAATT
840
GAACAATTTT GTAATCAACT GCATCTGGTC CATCATCAAC ATATAATGTT GATACATGTG
900
GAGGATATAA TTGGTTCGAA AAATGGCTGA AGCTCCGAAT AATTGTCACA AAAATGCCTG
960
TCTCAGTTGT TAAATCTATA ATAGAATCNA CAACAGGACA AGCATCTCCA TCAATAATAA
1020
TATGTGTCAC AATTATGCCT CTGTATTGTT TTCTTTATTT TGTTGAGAGG CGCTTTTGGC
1080
AACATAATCT TTATATTTTT TAAATGACTT GATGCGTGCT TTATCAGCTT CTTGTTGGCG
1140
TTTGTTCTTC TTTGTGTCGT TTTTCAATAT TTTTTGTAA CTTTTTATTC ATTTTAGCGA
1200
TTTCTTTGCG ATTTTTTTCA GCTAGTTTAT CGCCTTTTCT CTCAGTTTTT TCATCTAATT
1260
TATTAGGTGT TAAGCCTGCT TTTTCTTCGT ATTTTGTGA TTTTTCATA TCTTTAATAC
1320
GTTGTATTTT ATTCTTTTCG CGGGCTTTTT GCTCTTCTTT ATGACGCTTT TCGATATTTT
1380
TTTGAAGTAT TTTATTCATT TTATCAGCGT CTTTACGATT TTGTTTAGCT AATTTTTCGC
1440
CTTTTTTCTC AATATAGGCA GGATCATGTT CTCTAGCAAA CTTTTTAAGT TCACGTTTAT
1500
```

TTTCAAATC TTGTTTTTTA TCGCCGACAT ATTCTTTAAC ATCACTCGCT GTGTTACTGA  
 1560  
 TTGCTGCAGA TGTTTTTGAA GCAACTTTAC TTGGTAGCAT CTGTAACTTT TGGGACGTCC  
 1620  
 GGATGTTGTT TGATACGTTT ACGTTCAACA ATTAACGGTA CCAATACAAT TGGTAATACA  
 1680  
 TTAATCATAA ATTTGATGAC TTTTTTCTTA TCCATAGATC TTGCCTCCAT AATTACTTTA  
 1740  
 TTAATTTTAC ATACCCTATG ATACATCAAT ATAAACGATG ATAGTAGTGA NTCACTATTA  
 1800  
 AGTATTTTCAAG ATGTTTTTTA NAAGAAGACA ATAAAACTG CCAATCACGT GGTTCCTTAA  
 1860  
 TTGACAGTCT ATATTTTANA CAGGAAATTA AATACCTTTA CCAATGCCAA TCCGAAGTAA  
 1920  
 AGTATAGCAA TANAGATTAC TAATACANTT CTGCTAAATG GCANATGGAA TTAGTCTG  
 1978

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GGCACGAGCG ATGTGCCCAG CTTTTTTC AA TTGCAATACC ATCGGTCCTT GATATTGTTC  
 60  
 TTCTGGTACG TCTTTAAGTC CTAATGTAA TTCCACTTCT TTTGCATCAT CTGACCATAA  
 120  
 TTTTCTGAAA TCTGTTTCTA CTAAATCTTC TTGATATACA TTTTCTGGTA ATGGTGGTAA  
 180  
 CCATGGACGC TTAACTTCTT CAATTTCTAA TCGTGTTGTA ATAGATTCGA TATGATCGAT  
 240  
 AACCGCTTCT AACTCGGTTT GGTTTTCTTT CGTTTCTTCA TCTTCAAGTC CACTCAAGTC  
 300  
 TTTGTTGATT GCTTGAAGTT GACCATAGTC ATTAATCATG TAAATCGTCT TATCTTCAAC  
 360  
 TTCTAATTTA TCGCCTTCGA TGTCATATGT TGCACCACTC CATGCAGATT GGAATAATTC  
 420  
 ATAAATTTCA TTATTACCAA CTTTGTAAT ACGCACGACC TGGTAATGTA ATGTCTGCTG  
 480  
 CATCTGGTGT TTTTAAAATT TCATTACTGT CTTGTCTATC TGGNACGAGT TNTAATGCCA  
 540  
 ATTTAAATTN AGAGTTAGAC CAAATTTGGT CATCAACAAC ACCCGATGGT TTNTGTGTCG  
 600  
 CAAGTATTAA ATGAATACCT AACGAACGTC CAATACGTGN CGGNGATACA AGTTCTNTNC  
 660  
 ACATAAAATC AGGTTGNTCT GATTTTAAAT CGGCAAACCTC ATCGGAAATA ATGAATAAAT  
 720  
 GTGGCATTGG CTCTGNTGCA ACACCTTCTT TAAATAACTT ATGGTATTGA TTAATATGGT  
 780  
 TAACATCATG CTCTCCGAAT AAACGTTGAC GTTTCTCAAT TCGGCTTTGA TTGATGTTAA  
 840  
 GGCACGCATC GCTTCATCGC CATCTAAGTT TGTAATCCGT ACCAACTAAA TGGACTAAAT  
 900  
 CTTTAAATAA GTTCGCCATA CCCCCACCTT TATAGTCAAT CAATAGGAAC GCAACTTCAT  
 960

GTGGATGAAA ATTAATAGCT AAAGATAAAA TGTATGATTG GATAATCTCA AGATTTCCCT  
 1020  
 GAACCAAGTGG TACCAGCAAC TAAACCATGT GGCCCGTGTG CTTTTTCATG TAAGTTCAAT  
 1080  
 GATAAAATAT CATCTTTACC TCTTACACCT AAAGGTACTG CCATCGTTTT GTATGTTTCG  
 1140  
 TTTTGTCTCC ATCGATTAAC CACATCAAGC TGATCTACTT CTTTCACGTT ATACATCTCT  
 1200  
 AAAAATGTAA TACTATCAGG AATTGCATTT TTCAAATGTT CGACGTGTAT CAAATTCGCC  
 1260  
 AAACGTCTCG CGATGATATT CTTTATCAAC GTTATCAATA TTTTCAGGTG TAAATTTCAA  
 1320  
 TTGAACTAAT TCTTTTTCTT TCGTAATCAG TTCGCCTTCA GTACGAGACT TGATATCAAT  
 1380  
 AATGGTATCT ACATGCTCTG GCAAACCTTC AATCACATCT TCAACAAAGA TTAATGAAAT  
 1440  
 ACCATATTCT GATNAATCTT GGNTNACATA GTCTAAAATG ACATGATCAA TAATTAATGA  
 1500  
 CATATCTGTA ATGACAAACA CTAATTGCGG TGTGAAAATA ATTTGCTCAT TACTTCTGCT  
 1560  
 GCGTTCACGC ACAGCTTGGA TACGTTCTTT AATCATGCTA TAAATTGACG TTAAATTTTG  
 1620  
 GTCACGTGTT CGGTGATTGT AAACAAACCC TCTAATGTTT TGACCTCTCA ATGTCATATG  
 1680  
 TGGCAACCAA CGTGCCCAT TCAATGTTTC AACTTCATCT TCACGTGTCA CAAATAGAAA  
 1740  
 CTCTAAATCA TGATAACTAT GGAACGTTGA CAATTGGATT AGCATTTTCT CCAATTCTTC  
 1800  
 TAAATGAGA TGTGCGGCAC CAATATATGC AATTGGTCCA TGATTTAAAT CATTGATTAA  
 1860  
 TGGGTGCTTT GTCCNACANC TNTGANAAAT TCATACAATT CTTTAGCATC GTCGAATAGT  
 1920  
 TCATCACGAC GTTGGTTAAA TTCTCCNTCT TGGTAATCTA ATTTGAATGA CTTTTCTACA  
 1980  
 TTCGCAATAC CTAACTTATA ATGTAAGAAA TCGTGATGAT GCGATGTTTT TTCATATATT  
 2040  
 CTTGGTGCTT TCGTTTCAAC GATATCTTTA ATTTCANCAA CCGTTGGATA ATGGTAATTC  
 2100  
 AAATAAAAC GTTGTGCTTT AATCGCTTTA TTAATTTCTT TAGATTTATT ATCCAAATAA  
 2160  
 GCTTTGTAAT CTTTCTCTCG TTTTCAACA TCTTTGTTAT ACTTTTTCTT TTCAGAGAAA  
 2220  
 TACGTTGTAA TACCAAATAC TATCGTTACT GTACTCATAC CAATCATCAT TAAAATATAA  
 2280  
 ATACCAATTG GTCTCACTAA AAAGATGACA ACAGTTAAAG CAATCATTAC TAATGGCGGT  
 2340  
 ATAATGGAAC GCCATATCAC TGTATTCCGG AATTCCGGAA TTCCGTATTG GCTGTGGCGG  
 2400  
 TCTTTCAATC TTAATATCAT CGGTCGGGTC NCGGTGNATA ATCCTTGGCG AGCGATGGTA  
 2460  
 CGTATTGTAA TCATCTGCCT GTGCATGTGG CATCTCTTGT GTTAAGCGAA TTAATGACGA  
 2520  
 TGCCACTGTA TTCTGACTCA ATACANTTAA ACCATCAG  
 2558

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 668 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
CCGGCTGATT ATTAGCGAAG CGAGATTTTG AAGAGATGCA ACCATTATAT GAATGGTTAG
60
GTTTAACTGC TTCATTAGGT TTTGTTGATA TTGTGGATTA TGAGTATCAA AAAGGGAAAA
120
ACGTAATATA TATGAACATG ATATTATAAA TACAATAAT GGACGTCTCG GTTTTGATTA
180
TTTAATTGAT AATTTGGCTG ATAGTGC GGA AGGGAAATTT TTACCACAAT TAAATTACGG
240
TATTATTGAT GAAGTGGATT CAATCATTTT AGATGCTGCT CAAACACCAT TAGTTATTTT
300
GGGTGCACCA AGATTACAAT CAAATCTATT TCATATTGTG AAAGAGTTTG TAGATACATT
360
GATTGAAGAC GTGCATTTTA AAATGAAGAA GACCAAAAAA GAAATATGGC TGTAAATCA
420
AGGTATTGAA GCGGCACAAT CATACTTTAA TGTTGNAGAT TTATATAGCG AACAAGCGAT
480
GGTCCTAGTG CGTAATATTA ATTTAGCACT GCGCTCGTGC CGAATGTTCC TTGGTTCATA
540
TAAGTCATAT CGATGTAAAA ATGTTCTTAA ATTTGGGTGC ATGATTGGAG AACAACCAGG
600
TGGATAATCT TAGTCATTTT CAAGGGTGCA TTCCCATTA ACTTATCATA TCGGCAAATT
660
CCCGCTTT
668
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```
CCCAAATCCT TTGAAATAAA ACTTAATTAA GTTCAAGAAN TCGNGGTGAT TTTCCCCGGA
60
AGTTTGTTTG AATATTATTA TGGATTGATT TGATAGAGCT TATGGACCCC ACATTAATAT
120
TGAAGTCCTG GGGCCAAGTT CACNCCCCCG TGGGTGGAAT TTCCTATTTG ATCCCTAAAC
180
CCAAACTATG GACGTCCCAA ATTCTAAATA TGAAAAAATG GCTGAGCATC GTTTGATGAA
240
TCATGATTTA TATCCCGAAA AAATAGATAA TCGTTAAATG TATCATTTTAA TAAACACACC
300
AATAAGTTGA TTTTCCTAAC TTATTGGTGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT
360
ACATTAAAT AACATTTTAT ACCCAAAGTA CACCAAAGA ATATTAGTAC ACGAATTANA
420
CAACATTTTT ATAGAAACCT ATTGCACTTT AACGTCAATA AGTATATTTT TATATTATCT
480
CTAATTAATT GTGCGCGCTT AATAACAGAA TATTCTCAAT ATTTTATTTT TTTTGTGATT
540
```

TGTGTGAATA TTTAGTTGAT AAGGCACAAT CAAATTTACT TAAACTATTG TATTAGGGGA  
 600  
 AGAAAAGGATG GGATGTATAC ATGACACAAC AAAACTCCCA TGGAAATCAA ATTCAAGACA  
 660  
 TACCTCAAAC AGGATTTTTC GGGCATCCTC GAGGACTAGG CGTACTCTTC TTTGTAGAGT  
 720  
 TCTGGGAAAG GTTTAGTTAT TATGGCATGC GTGCCCTACT CATTTTCTAC ATGTACTTTG  
 780  
 CCGTAACAGA TAATGGCCTT GGAATTGATA AAACAACAGC TATGTCAATT ATGTCAGTTT  
 840  
 ATGGTTCATT AATCTATATG ACATCCAATA CCAGGCGGAA TGGATTGCTG ACAGAATTAC  
 900  
 AGGCACTAGA AGCGCTACTT TATTAGGTGC AGTCTTTATT ATTATCCGAC ATATTTGTTT  
 960  
 AAGCTTACCA TTTGCATTAA TCCGCTTATT CACATCAATG TTCTNCATCA TTATTGGCTC  
 1020  
 AGGTTTAATG AAGCCAAACA TTCCAAATAT CGGTGGCCGT TTATATCCTG AAAATGATAG  
 1080  
 ACGTATGGAT GCAGGTTGTG TTATTTTCTA TATGTCAGTT AATATGGGTG CATTATTATC  
 1140  
 ACCTATTATT GTGCAACACT GTGTTAATGT TAAAACTTC CACGGCGGAT TCTTGATTGC  
 1200  
 AGCAGTTGGT ATGGCATTAG GTTTAGTATG GTATGTACTT NACANCCGCA AAAACTTAGG  
 1260  
 TAGCGGTGGT ATTGAAACCN ACTAACCCAT TGACNACCAG CTTGNAAAGA AAAAGTATGG  
 1320  
 TCTTTATTAT CGGAAGTGGT GTCTTTAGCA ANTGTATTAA TTATCGGTAT TGGGGCATT  
 1380  
 ACTAACTCAA TATCAANTAA CTTAGGTAGG AATACTGTTT TAGTATTAGG TATTGCATTA  
 1440  
 CCANTCATTT ACTTCACTTT AATTATTAGA AGTANAGATG TCANNGATAC TGNACGTTCT  
 1500  
 CGTGTTAAAG CATTTATTCC ATTATTTATT CTTGGAATGG TGTCTGGGC TATTCAAGAA  
 1560  
 CAAGGGTCTA ATGTATTAAA CATATATGGA ANTGNACATT CAGATATGAA ATTAAACTTA  
 1620  
 TTTGGTTGGA AAACANACTT TGGTGAAGCG ATCTTCCAAT CAATTAACCC ATTATTTATT  
 1680  
 TTATTATTAG CTCCAATTAT TTCACTTTTA TGGCAAAAGC NTGGAATAA ACAACCTAGC  
 1740  
 CTGCCAGTAA AATTTGCAAT TGGTACGTTT TTAGCAGGTG CGTCATACAT ACTAATTGGT  
 1800  
 ATTGTAGGTT ATGCATCAGG TTCATCAAAC TTCTCAGTTA ACTGGGTTAT TTTATCGTAC  
 1860  
 ATTATTTGTG TTATCGGTGA GCTATGCTTA TCACCAACGG GTAATAGTGC TGCTGTTAAG  
 1920  
 TTAGCACCTA AAGCATTTAA TGCCCAAATG ATGAGTATTT GGTACTTAAC TAACGCTTCT  
 1980  
 GCACAAGCAA TCAATGGTAC TTTAGTTAAG TTAATAGAAC CACTAGGTCA AACAAATTAC  
 2040  
 TTTATTTTCC TAGGTGTTGT TGCAATTATT GTTACAACAA TTTGTATTAG CATTCTCACC  
 2100  
 TTTAATCATC AAAGCGATGA AAGGTATACG TTAATATTGT TGGCCTAATT CAAAAACAG  
 2160  
 TAAGTCATTT AAATGGCTTA CTGTGTTTTT ATAGGTTTCT ATTAATTAAA TTCAAGATAT  
 2220  
 CAGTATAAAT AAAAGCTTAA TATGCTCGTT ATAGACAGCT ATA ACTATAT TTTCTCGTCC  
 2280  
 CACTCTATAG ACATCAATGT CAGTTATTAC CATTTTCTCT ATTTAAAAAC ATATTTTGG  
 2340  
 TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTT TAGAA AGTAGGCTAA

2400  
ACTATGGAAA ATAAATATAC ACATGGTGTC CTCTTTTACC ATGAACACAG TGGATTAAAA  
2460  
AATATTAATC AAGGTATTGG GGAAGTTACA ACAGCATTAA GTTCAATTTG TAAGCATCTT  
2520  
TCTATTCAAT TGAGTGAAAA CGAAGGTGAC ATTATTAAAT ATTGCCAAGA AATCAAAACT  
2580  
AAAAACTATC CAAAAGATGT AGATAG  
2606

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTACGATGGC ATCTAAATCT GCGGTGTCGT CAATAATCAG TGCTATTGNC TGGTGGNCCT  
60  
GCNATGTGAG CAATACGCTA CCTGTCCAAA TAAANATTTT GNNGNAGATG CAACAAATTG  
120  
GGTACCTGGA CCNACAATCT TATCAACTTT AGGTATCGTN TCTGCNCCAT AAGTCAATGN  
180  
AGCAATACTN TGAGCACCAC CNNCTNGANA CACTTGAGTA NCTTGCGTAA GATAACATGC  
240  
AGCTAATACC TCTTGGGATA CTCCGTTAGG GTGAGGTGGT GTCACANCAN CAATATTTTC  
300  
TACACCCGCT ACTTGTGCTA AAGTACNCTG TCATTAGANC CGTTGATGGA TAACTTGCTT  
360  
TGCCACG  
367

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GGCACGAGCG ATATTTGTCA GGAAGTTAAA GTTCATGGAG ATAAGGCTTT GAAAATGTAT  
60  
AATCTAACAT TCGATCATAC GAAAACAGAT CATTTAGAAA TTAGTCATGA ACAAATTAAA  
120  
GCAGCATTTG ACACATTAGA TGAAAAAACA AAACAAGCAT TACAACAAAG TTATGAAAGA  
180  
ATTAAAGCAT ATCAAGAAAG TATTAAGCAG ACGAATCAAC AGTTAGAAGA ATCAGTGGAG  
240  
TGTTATGAAA TATACCATCC ACTAGAAAGT GTGGGTATTT ATGTGCCTGG TGGCAAAGCA  
300  
AGTTATCCAT CAACGGTTCT AATGACAGCG ACTTTAGCAC AAGTAGCGGG TGTAGAAAAT  
360

ATTGTTGTTG TGACACCACC TCAACCTAAC GGAGTATCCC AAGAGGGTAT TAGCTGCATG  
 420  
 TTATATTACG CAAGTTAATC AAGTGTTCCTA AGTTGGTGGT GCTCAAAGTA TTGCTGCATT  
 480  
 GACTTATGGA ACAGAAACGA TACCTAAAGT TGATAAGATT GTAGGTCCAG GTAACCAATT  
 540  
 TGGTNGCATA TGCCCCAAAA ATATTTATTT GGACAGGTAG GTATTGTTCC ANATTGCAGG  
 600  
 ACCANCAGAA ATAGCACTTG ATTATTGACG ACACCGCCAG ATGTAGATGC CANCGNCTNT  
 660  
 NATGTTTTTG GGCAAGCNAG AACATNATGA ATTAGNACGT CCATNTNTCA TTGGTGAAGA  
 720  
 TGCGCAAGTC CTNAAAGATT TNGAATCACN TATTGCTAAN GCATTGCCTA ATGTGGACAG  
 780  
 ANACGACATT GTTTCTANAA GTATCGCNAA TCAACACNAC CTNATCCANN ATNGTAATTN  
 840  
 NGATNTGGGN GAAGCATCNC CANCTCATGA ATACAATCGC GCCTGAACAT GCGTCGATTC  
 900  
 AACAGTAAA TCCTCAACCA GGAATTCTTG TTGAACGAAT AATTTCTATC TCGTTATCAT  
 960  
 CGTAAGCGTC ATTATCAACT TGTGTTTCTT GCATTTCTTG TAATTCGGCA ACAAACACTT  
 1020  
 CTTGATCTCC TCGATCACGG CTCTTACGAT TAATACGTGT TTTATATTTT CGAACTTGTC  
 1080  
 TTTCAAGTTT ATTATTAATT AAATCAATAC CTGCGTATAA ATCATCGTTT CGCTCTTCAG  
 1140  
 CTCTTAACGT AACATTTTTC AATGGAATTG TTAATTCAAT TTTAGTAGCT GAATNTGAAT  
 1200  
 AAGTTTTAAC TTAAACATGC GCCACTGCAT NTGGTACGTC ATTAAAATAA CGTTCCAAC  
 1260  
 TACCAATTTN CTCCTCAAAT ATAGNTGCGA ATAGCATCTT GTGATAGGGG AGGGNTATCT  
 1320  
 CCAATGAATT TNCAAATCTA TATCATANGG GAATCTCTCC CTAAACCTC TTTATTGGTA  
 1380  
 ACTCTTTATT ATATTNNNAC ATNNNNACGC TATCGNGCAA ACGCAAACAC TTTGGATTCT  
 1440  
 CTGATATTNT NNAGCATATT AATTTACAAC CCTGCACGAT GATTG  
 1485

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ATGATGTAAA CCCAGTTCCN ANCTTCATCA TTCAGTTGAT GCAATAATGT CACNNAACT  
 60  
 CTACCACCAA GATGCACCAA TAGGTTGTCC CTAAATGCAA TAAGCGCCAC CCTTTAACAA  
 120  
 TTCACCTTT TCAGGGAGGT NATTTTAAAT TCACCGATCC AACAGCTAAT GATTGTCCTN  
 180  
 CAAATGCTTC AATTTAATTC CAAATACATC AATATCGCTT AATTCTTTTT TACTACGTTT  
 240  
 CCAAAGCCTT TTCTACAGCG CCAACTGGTG CAATACCCAT AATAGAAGGA TCTACGCCAT  
 300



GACTTCCCAA AGCCATCCAA GCACTGCCAA TGGTTCGATA TTTAATTCTT TAGCTTTGTC  
 360  
 TTCTGACATG ACTAACATCA TCGCAGCACC ATCATTGATT CCTGATGCAT TACCTNCTGT  
 420  
 AACTGTCCCG TCTTTTTTGA AAGCTGGTCT TAAGCGACTT AATTTTTCGA CTGATACATT  
 480  
 TTCACGGACA CCTTCATCCT TAGTGACTAA GATTGGTTCA CCTTTACGTT GAGGAATCGA  
 540  
 TACTGGAAC TTTCACTAT CAAATTCACC ATTTTGCTGT GCACGTACTG CTTTATTGTT  
 600  
 GTGAGATTAC CAGCAACATG TATCTTTGTT CTTCTCTTGA AATACCATAT TGCTCCTACT  
 660  
 AAATTTTCAG CAGTAATACC CATATGATAT TGAGTAAATA CATCTGTAA ACCATCATAT  
 720  
 ACCATGCTAT CAACCATTGA GTGATGTCCC ATTTTAAAAC CGAAGCGACT GTTGTTGNCA  
 780  
 AGCATTGGTG NCTGAGACAT ATTCTCCATA CCGCCAGCGA GCACGATGCT CATGCCCACC  
 840  
 AGTCAGCNAT AGATTGATAT GCTAATTGAN TCGACTTTAA CCCAGAGCCC ACATACTTTA  
 900  
 TTCACTGTAA ATGCAGGTGC TGTTTCTGGC AAGCCACCTT TCATAGCAGC AATTCGTGCT  
 960  
 GGATTTTGTC CTTGTCCTGC TTGTAGTACG TTACCGATGA TAACTTCATC AATCTCACTT  
 1020  
 GGATTCAAAC CCGTCTCTTT AATAATATGT TCTATTAAAG TCGCACCTAA ATCATAGGCT  
 1080  
 GGCACGTCTT TAAACGCACC TCCAAAAACG CCAATAGGTG TCCTGTATGC TGCTGCTAAT  
 1140  
 ACGACTCTCG TCATGTCATA TTCATCTCCT TATGATATAT ACAATTTTAT TACTAATACG  
 1200  
 TCTAATGAAC CAATACGCCA CTAACATCCA ATTTATGAAA CCAATTGCTA CGTATGTTAC  
 1260  
 ATTTTCATTC TTGTTATGCA TTTAACAAAT CATATTATAC AATGATGTAA TTTGTTTGGG  
 1320  
 CAATCGGAAA CGTAAACGGT TTCACTTTAA CATTTACAC TCTTAAATAT GCTCTATCAT  
 1380  
 CCTCATCTAT AGTACAAAAT TATGCTTTGA TTTACCACAA ATTATCATTA ATCATTTTCG  
 1440  
 TCGTGCCTCT AATTAAATTC TTTCTATCAT TGGATCGNTA TCACAGGTGG NTTCACCACA  
 1500  
 ATTCTCATCA ATTT  
 1514

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGCACGAGCT CAAGTAAAGT GCTACCATTT TTCTTACAGA CATTTGCCGA NATCTTAAAC  
 60  
 TAAGACATAN CCCCTAAAAT ACTCNCTANA GNACCGNACA ACCNCAACAC AATTCCTGTC  
 120  
 ATGATCTTAG GCTTTGTGCC ACCTNCCCCA GTTGNCAAAT GCTTTGTCCA TCCTTCTTGT  
 180

AATGACTGAA ATCCTTCTTG ATACATNCGA AATGCAACAA ATGGAAATCC TTCATAAACT  
 240  
 GTTACGGGCA ATGATTGTGA AGTAGATGCA CTTCTTAAAG CAAATCCTTC AATAAAAATG  
 300  
 ACGGGTCGCA CTTTTATGAC CTCCAGTTGC ATAATAATCT TCTTTATTTG TTAATGTCAC  
 360  
 CGGTCCAAAT GCATGCTGGT TAGTCCGCAC CGTCGTCTAA GGTANAAAAAT ACATTCATAC  
 420  
 CACCGACTTG TCATTAAATT AAATATCGCT GAAAACCCCTT CGTAGAAACG CTTTGTTATA  
 480  
 TGATAAGGCT GTACGCTTAA CAATCCTTTT TCACCTTGTA ATTGATACTG ATTAATCAAC  
 540  
 GTTTCAACAG CATCTTTCCT TAAGAAAGTT ACATCAGCAT CTACAAAGGC AATACGATTC  
 600  
 GTACATGCAT GCGTCACACC TTGATAACAA GCATGTGATT TCCCCATACC ATTTGCCGTC  
 660  
 AGTATCATCA ACAACATCTA CTACAGTCGC ACCATATGAA CGTGCTACAC GTGCTGTTTC  
 720  
 ATCTGTGAT CCGTCATTCA TAACAATGAC ATCTACTGGA ACTTGCTGTT GTATTATCGA  
 780  
 ATGTAGTAAA TGACCTATTC TTTTTTCTTC ATTTCTAGCC GGAATAATAA TTGTTAATGC  
 840  
 TTTATGATTG AAGTTCAGCG TTTTCGTCTT TAGCTGATGT CTACGATTAA ATATCAATGC  
 900  
 ACCACACGCC ATAGACATGG TCACTATTAC TGTTAATATT CGTGATAACC ATTTCATAGA  
 960  
 TATCACTTCC TATTCTTCGC TTCTCGCGCG AGCCCGNGCC  
 1000

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1047 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GGCACGAGCT ATATCCAATT GGGGTAAAGC GGGTAAAGAC CAAGAGAAGA ATTTAAGAAG  
 60  
 ACATTAGCAG AAATTGAAAG GACACCGGCA CGAGCTAGCG CAACAAGTTT AGCGATTGAA  
 120  
 GCATTTGGTG CAAAAGCAGG TCCTGATTTA GCAGATGCTA TTAAAGGCGG TCGCTTTAGT  
 180  
 TACCAAGAGT TCTTAAAAAC TATCGAAGAT TCGCAAGGAA CGGTCAATCA GACATTTAAA  
 240  
 GATTCTGAAA GTGGCTCCGA AAGATTTAAA GTAGCAATGA ATAAACTTAA ATTAGTAGGT  
 300  
 GCTGATGTAT GGGCTTCTAT TGAAAGTGCG TTTGCTCCAG TCATGGAAGA ATTAATCAAA  
 360  
 AAGCTATCTG TAGCAGTTGA TTGGTTTTCA AGTTTAAGTG ATGGATTTAA AAGGTCGATT  
 420  
 GTTATATTCG GTGGTATTGC TGCTGCAATT GGCCCTGTAG TTTTGGGAT TAGGTGCATT  
 480  
 CATAAGCACA ATTGGCAACG CAGTAACTGT TTTAGCTCCA TTATTAGCTA GTATTGTAAA  
 540  
 GGCTGGCGGA TTGATTAGTT TTTTATCAAC TAAAGTGCCT ATTTTAGGAA CAGTCTTCAC  
 600

AGCATTAAC TGGTCCAATTG GTATCGTGTT AGGTGTACTG GCTGGTTTAG CAGTCGCATT  
 660  
 TACAATAGCT TATAAGAAAT CTGAAACATT CAGAAATTGT GTTAATGGTG CAATTAACAG  
 720  
 TGTTAAACAA ACGTTT TAGTA ATTTTCATTCA ATTTATCCAA CCTTACATTG ATTCCGTTAA  
 780  
 AAACGTCTTT AAACAAGCGG TTTCAGCAAT CGGTGATTTT GCTAAAGATA TTTGGAGTCA  
 840  
 AATTAATGGA TTCTTTAATG AAAACGGAAT CTCTATTGCA CAAGCGCTTC AAAATATATG  
 900  
 CAATTTTATC AAAGCTATAT TTGAATTTAT CTTAAAATTT TGTAATTAAA CCAATCATGT  
 960  
 GTGCGATTTG GCAAGTGATG CAATTTATTT GGCCGGCGGC TAAAGCCTTG ATCGTCAAGT  
 1020  
 ACTTGGGAGA ATATAAAGA GTAATAC  
 1047

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGCACGAGCG GTACGAGTTC ACTGTTAATC TGCATTCAA TGTGATTATG ATCTGAGTTA  
 60  
 TCCTGCATTT CGTAACCGAT AGCGATGTTT GTTACTTTTT CAAAATTAAT ATCACTATTG  
 120  
 TTCGCTAAGC TTGAACGTAC AGACTCTAAT TTCGGCAACG TTTTATTATC CTCACTATTT  
 180  
 AACACAACGT CGGTGCGCAA TAACGAACGA CGATAATCAA AGACGCCTTT TTCACCCCAA  
 240  
 GTGACTTGAA TTTGATTAGA GCCTTCTTTA TTAAACGTTG GATAACCGTT AAGGAAACGT  
 300  
 TGATATGTTA ACTCGCCTGA CTGATGGCAT TCGTACTAAA CAATCTGAAG TCTTCGTTTA  
 360  
 AGAAACCACC ATGACCATTA ATAAAATCAA AGGTTCTTGG AATCGTTTCT TCCATTGTGC  
 420  
 TGGAACCTGC TTCATCTTCG GACAGGTTTT TATAATGATA TTTCNCATTT TTATCGTTAT  
 480  
 AGTGTGNGAC ACCTGTATTA TTGNTGTAGG TTGTAACACC ACTCTNTGAN CTACGAACGA  
 540  
 TGGNTGANTC GACAAATAGT ATAGCATNCA TTTTCTCAAC ACTAATCGTG TTAAATACCA  
 600  
 TGCGATATGT TTTTANCTTN NCAGGTTTAC CTTGGGTGCA AAAACATGCG TCGNACGATC  
 660  
 AATTGTATCT NTGTGTGTGA TGATATCTTG TGTATGGGTT GCATATCTTT TCACACTGCT  
 720  
 GCTTAATGCA TCTTAAAAA TGNATCATTT CGCGGTGGTA GNTGNTTAAT TTTACGGTAA  
 780  
 TCGGGGCGGT CTTTACTTAT AGCATAAAGC ACGATATTAT CATCAGCATC ATGATCTATG  
 840  
 ACTAAACGAT TGAAATTGAA ATGATTTGGT ACTTTCGCAT TCAATGTTCA NGAACCTGGC  
 900  
 CAAGATATGT TGATAACGGT AAATCAAACG TAAAATCGAA TAATGTAAAA TCACTGCTTA  
 960

AATCCGGAAT CATCAAGTTA TGATCACGAC GAACATGTTC CACGGACNTC ACTTCTTTAT  
 1020  
 TTTTCAAAGG TTTCGTCAGT TTATTCACAT TAGATACCGT CGCAATCGTA CCTTCTGGAT  
 1080  
 GATCATTTTT CGAATGAATA ATCTGAAATG GCGTAATAGT TGTATCCATT TTGGCTGTCA  
 1140  
 TAGGTGTCGT TAAAGGTTTC GTTTCACTCT TCTTACTATC TGTATTGTCG ACATTTGCAA  
 1200  
 TATCAGGAGA AAAGTTCCAT ACCATATATG TCAATACGAC ACTCATCAAG ACGAGTAGCG  
 1260  
 CTAAAATGAC AGATTTAATA TGTTCTTAT TATTCATCCC AATCACCGTC TTCAATGACT  
 1320  
 TCACATGGAA GTGTGATAAA GATAGATGTA CCTTGACCTT CTACACTGTT TGCCCAAATA  
 1380  
 CGACCATTGT GCGCTTCCAC AATCTCTTTC GAAATGGCTA GTCCTAATCC AGTACCACCC  
 1440  
 ATTTTACGCT CGTGCCGTNC CTTATCTACA CGATAGAATC GGGNCGGAAT ATCTTTATCG  
 1500  
 ACTTTATTGG ATAGGAATTC CCGATG  
 1526

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GGCACGAGCG AGCAATATCA AATAATAAAT CATCATCAAT AGTTCTTCCT TGGAAACGTT  
 60  
 CAGGGATGAT GTTGAATAAT AATGACGTAT CTAATATATG GTCATATAAA GAGAAATCAC  
 120  
 CAACTGGGAT GCTATCTAAG TGATAGTACT TTTGTAATAA TAAATTTTCT TTATGTAGAT  
 180  
 CAGGNAATGN ATGCATCTAN CNACTCNTCN TTAGANNTCN TCNTTGCCCA ANAACTTTCTG  
 240  
 ATGGCTTTTC TCCATTCCCT TTCTCNACCT AATCTTGGGA ANCCTAAGTT TGATGTTTTA  
 300  
 ATTGTTGACA TAATATTGCC TCCTTGAGAG CAGGTAATAG ATTTNGAGTA TGCTGCAAGT  
 360  
 TCTAATGAAT CTTGACATT TNGANACGGT GTGATAATGT ATAAACCATN AAAATATTCA  
 420  
 TGAACAGTAT CGATTAAATC CTTTGAAAGC TTAAGACTTA GTTCTCGCGT TTTGGCTTTA  
 480  
 TCATCTCTAA CTGCTTCAAA TTGGTGGAAT ATTTCANCTG ACATCTTGGA TTCCNNGGCAC  
 540  
 TNCATTATGC AAAAAGAGTG CGTCNTTGTA ACTTGCGATA GGCATAATGC CTATGAAAAA  
 600  
 TGGNTTGNTC AAGTGCTTAG TGGCATGGTA AATTTCAATG ATTTTCTCTT TGCTGTACAC  
 660  
 GGGTTGTGTT ATNAAATAAG ACATTCCGCT TNCTATCTTT NTNCTCTAAT CTTNNGACGG  
 720  
 CACCATCTAA TTTACGAACA TCAGGGTTAA AGGCGCCAGC GATGTTGAAG TGTGTACGTT  
 780  
 TCTTCAGCGC ATCACCCCCA GNGTTAATAC CCTGATTAAA TCTTAGAGCG AGTTCANCNA  
 840

ATCCTTTAGG AATTAACATC ATAGACATTG GTTGACCTG GTAAGTGACC AACTTTGGAA  
 900  
 GGATCACCAG TTATGGCTAA TATTTCTGTTA ACGCCAATGA GCGATAATCC AAGTAAATGG  
 960  
 GACTGCAAGC CGATTAAGTT TCGGTCTCGA CATGTAATAT GTACGAGTGG NTCAATATTG  
 1020  
 TAATATTGCT TAATTAAGCT AGCAGCAGCA ATATTGCTAA TTCTGACAGT TGCCAATGAA  
 1080  
 TTATCTGCGA GTGTTACCGC ATCTACATTA GCTTTATCAA GTTTAGCGAT ATTTTCAAAA  
 1140  
 AATCTATCCG TGTCTAAATG TTTCGGTGTA TCCAATTCGA TAATAACGGT TGGACGTTCT  
 1200  
 TGAACCTTAG ATGTTAATGA TTGTCTAACT TTATTTTGAG ATGGATTGAA AAGTGCTTTC  
 1260  
 GTTGGTATCG GAATCACTTT TNTGNCANTA ACAGGTTTAA GTGTCNGAAT AGATTCTTTA  
 1320  
 ATAAATTTGA TGTGCTCTGG CGTTGTACCA CAGCAACCAC CAATTAAACG AACACCTTCG  
 1380  
 CGAATTAGTG CCATTNTGGN GNAACTTGAC CGAAATATTG T  
 1421

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TTATTTAAAA GTATCCAATA GCCAACAATC TCTTTCATCT TTGAGTAGTA TCCCACGTAT  
 60  
 TTCGGGATTG CATCCGAGTT GATTTTTATN ATTTTCTTCA ATGCTATCAA GCGCAGCTCG  
 120  
 TTTACGTCTT ACTTTAGGTT TTATTTGCTC AATTGCCTTG ATTGTTTGAT TTCTAACATC  
 180  
 AGTAACAGCA GCATCTTGAT TTGTATTTTC TATTTCTTGT TGCGCTTGTT TGAGTGTGTC  
 240  
 GCTAATTAAT TGATTGCTT CATCTAATTC ATCAACTGTT GCATGTGGTG TATCTTTTAT  
 300  
 TGATTCTACT TGATTTTCTG CAGTTGCTTT TATTGCTTGT TGTGCTTCAG GCTTAATTAC  
 360  
 AATATGAGGT TGCACGAGCA CCTTTTAGTG TAGCAATGCC ATTNNGTTTCA ACACGTTTCA  
 420  
 CATCATTANT CGTGACTGCT TGATTGAGGT TTTGTAATGC AAGTTTTTCA TTATTCGCTA  
 480  
 ATTGATTTAA AGCAACTTGT TTTTCTTCAT CAGTCNCATG TTCAGCTTGC TCTATTTCTT  
 540  
 GCTTTTTAGC CTCATATTGT TGCTTTACTG CATCTCNAGC AGCTGCTCTA AAAATATGTT  
 600  
 CAGGCGCTAC TAAAGCAATG CTATCAAGCG CTTGACTTGT TGTATCATCA ACTTGTTGAT  
 660  
 TTGTTCTATT ATTCGTAATA TCTGTCATGG CTTGATTTAC AAATTCNTAT GNTNTTATCT  
 720  
 AGTGCTACGT TGTCNNTCNG CCTGCTGTTG CNTCTTTATC CCTGANTAAT CGTAGCACAG  
 780  
 TAAATCATTC GCNTGTTGGA TTGAGTTTTT CCACGTTGCC AGCTGGNGGT AACTTTTTGT  
 840

TTCAGGGTGA ATAATNTTAA TCGCTGATAC ACCATTTGTT CCTGCTTGAT TCACCTGACN  
 900  
 ATTCGTTTGA GCNTGGTCAA TANCTCCAAG TGCTTTTTCT TTTTCTTTAG CTAATGCTTG  
 960  
 TGAAGCAACT TCTTTCTCAT NATCTGTTGA ATCAAGACTA TTATCAATTT GCTGTTGCTT  
 1020  
 TTCTTTAACA GCTTTTTCAA NATCTGCAAT TGCCTTTGGT TTAATTACTA CTTCAGCTNC  
 1080  
 AACATTATCT ATAGCATTTA CCGCTTGATT TGTAGTTGTG TCTACCTGAT CATTTGTTTG  
 1140  
 GTTTTGATTA ATTTGATTAA TTGCTTGATC TTTAAGTTGA GTGATTTGAT TAACAGCAGC  
 1200  
 CTGCTTTTCT TCGTCAGTTG CATTAGGTGT TTGTTTAACC GCTTCAATAC GCTTCGCCAC  
 1260  
 TTCAGCAGTG ATTTTATCTC GCGCTGCTTG TTTTTTACT ACATCAACTT GAACAGCATC  
 1320  
 GATATTATTC TCTGCTACTG TCGCAGCTTG GTCTACTTCT GCATTTGTGT TAGCTTGTTT  
 1380  
 AATACTCNA ATAGCTNGTT GTCTGTCTTG ATTTAAAGTA TAGATCGCAG CATTTNTCTC  
 1440  
 AGCATTCGTT GCATCTGGTG TAGCATTGAT TTCAGCTAAT TTAGCATTAT AATGCTGATT  
 1500  
 GATTTGTGCT AATGCTGCAG GTTTATTAAAC AATATTTGGC TGAATCGCAT TAATTGCTTT  
 1560  
 TGTACCTAAT TGTTGCGCTT GATCTACTTC CGCATTTGTA TCAGCTTGAT TTATATTATT  
 1620  
 AATTGCCGTT GCTAACTCTT GATCCACTTG ATTTAAAGCC ACTTGCTTTT CTTCAGTTGT  
 1680  
 TGCATTTGTG TTTTGATTAA TTTCTTGCTT TTTAGCAGTT GCTAAATCAT TTAATACACC  
 1740  
 TGTAGCAGGT TGTTTCTTCG TTACATGCGG TTGACTGCGC CGATTTGATG ACTGCATCGN  
 1800  
 CTCTAATACT ATTGACCACC GAGTAGTAGA CGTCACACAA TATCAGTAAT GCTCTATTTT  
 1860  
 AGTGATTGAA ACGAATATCG GTCTTG  
 1886

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCACGAGAC AATATATCTA CCGTGAATAA CTGTGCAAAT AGTGAAGTTG TAGCCGCCAT  
 60  
 ACGCATTTCA TTTTCATCAG TTCTGCCATA AATCAATGCA TAGTCGGCAA TTTGAGCCAC  
 120  
 GTGCCGATTA TTCGGCACGA GCTGTACTAG ATATAGTTAT GATGGGAATA CTGTAATGTG  
 180  
 TGGCCACCTG TGCAATTGAC TGCAATTCAC TATGACTACC TTGATTCGTC AAAAAATCA  
 240  
 TGCAATCTCT ATCATCATGC GTCGCAAATG TTGACACAAG TAAATGCGTT TCATGTAATA  
 300  
 ACCTGACATT TAAGCCAATA CGAGATAACT TTTGAAAAAG ATCACCAATA GTCAAACCTG  
 360

ATGCGCCAAA TCCAAATAAA AATATTGTCC TGGCATT TTTT CAACACATCA CAAATTGCAT  
 420  
 CAATTTGCGC ATCCATAATA TTAGTAGCTA CAAATCGCAT CCGTATTCCG TTGCTCTAGC  
 480  
 AATCATTTTA TTTTCAAAG TTTCTACAGA TTCATTTTCA ATCAATTCTA AATGTGGATT  
 540  
 GGTTGCAATA TCTTCGGGTA AGTATCGAGA TATCGCAATC TTTAGCTCTT GAAAACCTTG  
 600  
 ATGTGTCATT TTCCGACTAA ATCTAACAAT TGATGCTGTA CTAACATTCTG TAACATCTGC  
 660  
 CAAATCATTC ACCGTCATAT CAATGATTTT ATGTGGATT CTTAAAATGT AATCAGCGAT  
 720  
 TATCTTTTCT GTCTTCGTAA AATCACTCAA CTGTTTATCA ATGCGATATT AAAATATTTG  
 780  
 TCATCATTAA TCACCCAACA AATCTGTCTT GTCGCATCGC CTTTGTCGGT CCAAATAAAT  
 840  
 ATGTACAAAC GAATCCACCA GCATATGCAG CAAGTAATCC TGCAATATAA CCTAAATACA  
 900  
 TATTATCTGA GATTAATGGT AAGAGTGACA CACCACTTGG GCCTATTGCT TTGGCACCAA  
 960  
 TATGTCCAAT TCCACCTATT ACAGCGCCAC CAATACCACC ACCAATACAA GCAGTTAAGA  
 1020  
 AAGGTGGAAC TAATGGGCAA AGTCACACCA TAGATTAATG GTTCTCCGAT ACCTAGGAAA  
 1080  
 CCAACTGGCA ATGCACCTTT TAAAGTATTA CGTAATGTTG TGTGCGTTT ACATCTTACC  
 1140  
 CAAAGTGCTA ATGCGGCACC TACTTGTCCA GCACCCAGCC ATCGCTGCAA TTGGCAATAA  
 1200  
 GTAAGTAGCA CCAGATTGGT TAATCAATTT CTATATGAAT TGGCGTNAAA AATATGATGA  
 1260  
 AGGCCCTAAC AATAACTTAA CGGTAGGAAG CTTGGTCCAA ATGATAAATC CACTTAAATT  
 1320  
 ACGNCACCCA ATACTTAATA ATCCCCGTTA CTACTGAAAC TTAANTTGTC TTTGAAACAA  
 1380  
 A  
 1381

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGCACGAGCG TTTTAGTTGA TGTGTATCAC TAATATCTTT GAAAATTTTA ATCAGGTACT  
 60  
 ACGACAATAT GATGTCTGTT TTGTGTCTGA AAGTTTTACA GTTTTAAAA TAAAATGGT  
 120  
 ATAAAGTGTG ATTTGTATAA AAAAGAGTCT CGACGGATAA GAATTGATTA ATAACAGTTA  
 180  
 GCATTTTATT AATTACCTTA ACAATGATTC AAGTTTAGTT AAATGAGGTT TAATTTGAAA  
 240  
 GGGGATAGCG CCTCAATATA ATGTAGGTAG ATTGTTTATA TTACGTAATT GAAAAATCAA  
 300  
 ATTTAAATAN ATAGGGTGGG GCTNNAAATT ATGAAATTTA AAGCGATAGC AAAANCAAGT  
 360

TTAGCATTGG GAATGTTAGC AACAGGTGTA ATTACATCGA ATGTACAATC AGTACAAGCG  
 420  
 ANAACAGAAG TTANACAACA AAGTGAATCA GAGTTGANAC ACTATTATAA TAAACCGGTT  
 480  
 TTAGAGCGTA AAAATGTTAC TGGATATANA TATACTGAAA AAGGTAAAGA TTATATAGAT  
 540  
 GTCATAGTAG ACAATCAATA TTCTCAAATT TCTTTAGTTC GGATCTGAAT AAAGACANAT  
 600  
 TTNAAGATGG AGACAACCTCG NATATAGATG TGTTTATCCT TAGAGAAGGT GACAGTAGAC  
 660  
 AAGCAACNAA TTACTCAATT GGTGGCGTAA CACAAACAAA CAGTCAACCT TTTATTGACT  
 720  
 ATAG  
 724

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

CCTTCACCAA TACGTGTANT ATCNTTATTT GGGCGNTTGT CCACTTACCC ATGTAATCGT  
 60  
 GGCATCTGGA ATGGCACTAC CATTAGATAA CTAAAGTAA TCTGCTGCAC TAGAACCATT  
 120  
 ACCTGCTGGG AAGTCTTGGC CTTGTACAGT GTAATGCGAA TGTGCAACGA TTTCTGGAAT  
 180  
 GACATGCTTT ACAGGTACAG TCACTGTTGA TGTTGTTCCA TCTTGATGAG TAACAGTTAC  
 240  
 TGTGACATTG GCATTATTTT CAGTACGACT GACATTACTA ACTGTTTTAC TAGTGATTTT  
 300  
 ATTTGCGCTT GCTGTTGCAT AGTTTCTATT TGGTGCATTA CTTGTAAACG TTAACGAATT  
 360  
 AATAATTGTC GCTTGATCAG CTTGTGATAC TGTCGCATTA TTCGAAATAT TGGCAATTCT  
 420  
 AACAGGATTA GCAGNCCGTT GATGAAGTAC CAACTCGATA TTTATCACGC AAAGGTTTCA  
 480  
 CTGTTACATT GAATGAAGTT GTAGCTGTAT TACCACTNGT ATCAGTTGCT AATAAATTGA  
 540  
 TTGTCTTACT AGTTGCTGAT GTCACATTTG GTGCCGTTGC AGAAACATGT TGATGGTTAT  
 600  
 TATCAACAGT CTCGTGCC  
 618

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:



TTGTGAGACA CACGCTTAGT GCACATGACA ATGTGAATGT TGTTGCACAA ATTATTAAAA  
 60  
 GAAGACTTAC CACTGTTAAG TTGTATCGAG CCGAATGATA CATTTGATTT TCCACNAAAC  
 120  
 TAGGGAGTGT AAGAAGTGAT GGAAAATAGT AGGCCCGAGC GTAATGAAGC GACGATGCAT  
 180  
 CTTGATGAAA TGA CTGTGGA AGAGGCTTTA ATTACGATGA ATAAAGAAGA TCAGCAAGTC  
 240  
 CCGTTAGCAG TTCGAAAGGC AATACCACAA TTGACAAAAG TAATAAAAAA AACCAATTGCA  
 300  
 CAGTATAAAA AGGGTGGACG ATTGATCTAT ATCGGTGCAG GTACAAGTGG AAGATTGGGT  
 360  
 GTCTTAGATG CAGCGGAGTG TGTACCTACA TTCAATACTG ACCCTCATGA AATTATAGGT  
 420  
 ATTATTGCTG GTGGACAACA TGCTATGACG ATGGCTGTAG AAGGTGCGGA AGATCACAAA  
 480  
 AAATTAGCGG AAGAAGATTT GAAAAATATA GATTTAACAT CAAAAGATGT CGTTATAGGA  
 540  
 ATTGCCGCGA GTGGCAAAAC GCCATATGTT ATAGGCGGTT TAACATTTGC TAACACAATC  
 600  
 GGTGCTACAA CAGTATCTAT TTCATGCAAT GAACATGCAG TTATAAGTGA AATTGCGCAG  
 660  
 TATCCAGTAG AAGTTAAAGT TGGTCCAGAA GTATTAAGTGT GTTCANACG TTTAAAGTCT  
 720  
 GGTACAGCAC AAAAGTTAAT TTTAAATATG ATTTCAACCA TCACAATGGT TGGTGTGCGA  
 780  
 AAAGTTTACG ATAACCTCAT GATTGATGTT AAAGCAACCA ATCAAAAACT GATCGACCGT  
 840  
 TCAGTGCGTA TTATTCAAGA AATATGTGCT ATCACAATATG ATGAAGCAAT GCGGTTATAT  
 900  
 CAGGTATCTG AGCATGATGT TGAAAGTTGC GACAGTTATG GGTATGTGTG GCATTTCTAA  
 960  
 GGAAGAAGC AACAAGACGG TTATTAAAC AATGGTGACC TTGTT  
 1005

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GGCACGAGCG ATGACAGGAA TATGATATTG TTTTGCAGCT AACGCAACGC CTACGGGTGT  
 60  
 TTTACCAAAG ATGGTCTGAT AATCCATGCG TCCTTCTCCA GTAATAACGA GGTCTGCATC  
 120  
 TTTAATTCTT TGATGAAAAT CTGTAATGTC AAAGACGACA TCAATACCTT TTGTTAAAGT  
 180  
 TGTCTCACAA AACGCTAATA ATGCTGCGCC CATAACGCCA GCTGCACAG AACCTGGTAT  
 240  
 TTGATTATAC GGACTTTCCT GTGCACATTT TTATCTTATC ATGACAATGN GACATTGCGA  
 300  
 AATCCAAATT AGGTATGCAT CTTTGCATCA GCGCATTTTT GAGGACCATA AATATAGGTA  
 360  
 GCACCATTTT CACCCAATAA AGGATTTGAA ACATCACAGG CCACTTTAAA GGTACCTCT

420  
 TTTANTCGCG AATCGGCCAG ATTGGTTATA TCGATTTGTG CAATGTGAGC AAGATTAGCA  
 480  
 CCATTCATTT GTAATAAGTC CCCGTTTACA TCAGTAAACT TTACGCCTAG TGCACCTAGC  
 540  
 ATACCTGTAC CACCATCATT TGTTGCACTG CCACCAATCC CTAAAATAAT GGTCTTAGCA  
 600  
 CCATGATTTA ATGCATCTTT AATTAGTTCA CCGGTACCAT ATGATGATGT GTATAAAGGA  
 660  
 TTACGTTCCCT CTTTTTCTAA TAAATCCAAA CCTGACGCTG CCGCCATTTT AATAATTGCA  
 720  
 ATTTGTTGTT CGTCTGCGCG TGCATAACAT GCTTCAATAG GTCGCATTAA AGGGTCATTA  
 780  
 ACGATGACTG TATACTTAGT GGCANCTGNT GCATGAATTA ANGCACTCTGN GGTACCTTCA  
 840  
 CCACCATCAG GCATCGGAAT GATATCATAA TGAAGGGTAT TCCCATAAAC ATTAGTAAAT  
 900  
 GCCTGTTTTTA TAATATTGNC AACTTGGTGT GNGGNCATAC TTTCTTAAA TGAGTCAGGA  
 960  
 GCGATGACAA TTTGTTGGGA ATGGATGGNA GNCACCNCTC AATATGNNGG CGNTCTTTTG  
 1020  
 GTTTTANATT NTAGTGA CTN  
 1040

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TGTATAGGCC TATTTGTATA NAAAGTAATA TGATGTTTAG TGGCTATGTA AGTGAAGCAA  
 60  
 TGTATAAATA ATGATGAGTG GTTTGTTACT AATGATAATG GCTATGTAAA AGAGCAGTAT  
 120  
 TTATATTTNG CGGGACGTCA ACAGGATATG TTAATTATTG GTGGGCGAAA TATATATCCA  
 180  
 GCACATGTTG TNCGCCTTTT AACGCAATCT TCGAGCATTG ATGAAGCAAT TATCATCGGT  
 240  
 ATTCCACATG AGCGTTTTGG TCANATAGGC GTATTGCTTT ATTCTGGTGA TGTGACACTT  
 300  
 ACACATAAAA ATGNAAACA ATTTTTNAAA AAGAAAGTGA AACGCCATGA AATTCCATTC  
 360  
 GATGATTCAT CATGTAGAAA AGATGTATTA CNCTGCAAGT GGTAAAATTG CTAGAGAAAA  
 420  
 AATGATGTCG ATGTATTTGA GAGGTGAATT ATAATATGAA TCAAGCAGTC ATAGTTGCAG  
 480  
 CTAAACCGAA CTGCATTTGG GNAATATGGT GGCACCTTAA AACATTTAGA GCCAGAACAA  
 540  
 TTGCTTAAAC CTTTATTCCA ACATTTTAAA GAGAAGTATC CAGAGGTAAT ATCTAAAATA  
 600  
 GATGATGTAG TTTTAGGTAA TGTTGTTGGG ANTGGTGGCA ATATTGCAAG AAAAGCATTG  
 660  
 CTTGAAGCGG GGCTTAAAGA TTCAATACCT GGCGTCACAA TCGATCGGCA ATGTGGGTCT  
 720  
 GGACTTNGAA AGTGTTC AAT ATGCATGTCG CATGATCCAA GCCGGAGCTG GCAAGGTATA

780  
 TNTTGCAGGT GGTGTTTGAN AGTACAAGTC GAGCACCTTG GAAAATCAAA CGACCGCANT  
 840  
 CTGTGTACGA AACAGCATTA CCNGAGTTTT TATGAGCGTG CATCATTTGC ACCTGAAATG  
 900  
 AGCGACCCAT CACATGATTC AAGGTGCTGA AAATGTGGCC AAGATGTATG ATGTTTCAAG  
 960  
 AGAATTACAA GATGAATTTG CTTATCGAAG TCATCAACTG ACAGCGGAAA ATGTAAAGAA  
 1020  
 TGGAAATATT TCTCAGGAAA TATTACCTAT AACCGTTAAA GGAGAAATAT TCAATACTGA  
 1080  
 TGAAAGTCTA AAATCACATA TTCCGAAAGA TAACTTTGGC CGATTTAAGC CCGTAATCAA  
 1140  
 AGGTGGGACC GTTACCGCTG CGAATAGTTG TATGAAAAAT GATGGTGCAG TTTTATTGCT  
 1200  
 TATTATGGAA AAAGATATGG CATACTAATT AGGTTTCGAG CATGGTTTAT TATTTAAAGA  
 1260  
 ATGGTGTAC GGTAGGTGTT GATTCTAATT T  
 1291

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CATTCATCTA ACCTNTTCAT CAGTTGAGTG ATTTTAATCT ATCCTTCAAA AGTTNGNGGA  
 60  
 TCAGGTCCAA TTCTCTTATC TAGATTTAAA CCAGGCACGA GCGTCATTTG TTCATCTGAT  
 120  
 AATTGCAAAAT CAAATATTTG GAAGTTTTCA GAGATTCTGT TTGGTGTAC CGATTTAGGG  
 180  
 ATTATAACCA CACCATGCTG CACATTCCAT CTAAAAACAA CTTGGGCAGG TGACTTTCCT  
 240  
 AATTCTTGAG CAATGTCTTT AATTGTCTCA TCATTTAAAA TTTGTGCATT CATCAATGGT  
 300  
 GACCAAGATT CCATCACGAT ATGTTGTGCT GCCAAATATA ATTTCAATTT ATGTTGCGTT  
 360  
 AAATATGGAT GATATTCAAC TTGATTAAAT ACAGGTTTAA TTGACACTTG TGCCAACAAA  
 420  
 GCTTCCAAAT GTTCAGGTTT AAAAAATTGCT GACACCTATA TTTTGTAGCTT TATTATTTTT  
 480  
 ATATAAATCT TCCATACCTT TCCATGTTAT CAACCATTAC GGCTTCGTTT GTGCCTGGCC  
 540  
 AATGTTACTA RRDCTNS  
 557

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GGCACAATTC GGCACGAGCG TTGGTATGTA GAATATGATG GTGAATGGTA TGTGTATAAC  
60  
GATGGGAGGC TTGAATAAAT GAACTGGAAA CTGACAAAGA CACTTTTCAT TTTCGTGTTT  
120  
ATTCTTGTCA ACATCGGGTT AGTATCGATT TATGTTAATA AAGTCAATCG CTCACACATT  
180  
AATGAAGTTG AGAGTAACAA TGAAGTTAAT TTTCAGCAAG AAGAAATTAA NGNACCGGCT  
240  
AGTATATTGA ATAAATCAGG TAAAGGTATA AAATGAGAGC AAATTACAGG GCGATCAAAA  
300  
GACTTTAGTT CTAAAGCTAA GGGCGATTCTG GATTTGACCA CATCAGATGG TGGAAAATTA  
360  
TTGAATGCGA ACATTAGTCA ATCGGTAAAG GTCAGTGACA ATAACTTAAA AGATTTGAAA  
420  
GATTATGTTA ACAAACGTGT GTTCAAAGGT TCAGAATATC AATTAAGTGA AATTAATTCT  
480  
GGTTCTGTAA AATACGAACA AACGTATGAT AATTTCCCGA TTTTGAACAA TAGTAAAGCG  
540  
ATGTTGAACT TTAATATAGA AGATAACAAA GCGGCTAGTT ATAAACAATC AATGATGGAT  
600  
GACATTAAGC CCACAGATGG TGCAGATAAG AAGCATCAAG TTATTGGAGT GAGAAAAGCA  
660  
ATCGAGGCAT TATAGTATAA TCGTTACTTG AAAAAAGGTG ATGAAGTCAT TAATGCTAGA  
720  
CTCGGTTACT ACTCAGTCGT GAACGAAACG AATGTTCAAT TGTTACAACC AAAC TGGGAA  
780  
ATTAAAGTGA AGCATGACGG TAAGGACAAA ACGAATACTT ACTATGTCGA AGCGACAAAT  
840  
AATAACCCTA AAATTATTAA TCATTAATAT GAATCGTAAT AAGCTAGTAT TGCAAGCTCG  
900  
TGCC  
904

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TTGTACCACC ACAGTTGTCA CGGAGACCAT AAAGATGCCG AGGAGTAAAA GTAAAAAGAA  
60  
CCAAATAGAA TTGATACCAG CGGCTGATAT GTTAAACTTG TTAGGGTTTG AATTACAACC  
120  
AACTAATGAT GGATTGATTA TTCATCCGTC AAGAATTTAA AACAAATGCA ACAGTTGATA  
180  
GTTTAACTGA TCATCGAATA GGAATGATGC TTGCAGTTGC TTCTCTACTT TCAAGCGAGC  
240  
CTGTCAAAAT CAAACAATTT GATGCTGTAA ATGTATCATT TCCAGGATTT TTACCAAAAC  
300  
TAAAGCTTTT AGAAAATGAG GGATAATATA AAATGGAAGA TATCTATAAA TTAATAGACG  
360

ATATCAATCT ACAAAACTA GAAAATTTAG ACTCTCGTGT TAATGAAGCA ATAACACTG  
 420  
 ACAACGATGA CGCATTATTT ATTCTAGGAG AGACACTTTA CAATTTTGGA TTAATGCCAC  
 480  
 AAGGTTTGGA AGTATTCCGC TCGTGCCATA TCNCAAATAT CCAGNCGANA GTGANGTGCT  
 540  
 GATTTATTTT ATTGAAGGTT TAATGTCTGA NAATCAACCT GCCGAAGCGT TAGAANANTT  
 600  
 AAGTTATGTT GATCCATCAC CTGCNNAGTT GATGTTNAAG AAATAGTTTT GCGANNTGAT  
 660  
 TATCTAAAC AGTATTCAGA ANTTATTTGG TAGAAAATA  
 699

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CCAAACAACC TATCCTTCAA ACAATTATCC AATATTTGTT GAACATGGTG CAATTGACCA  
 60  
 TATTAGCACG TATATTGATC AGTTTGATCA AAGTTTTATA TTAATTGACG AGCATGTAAA  
 120  
 TCAATATTNT GCTGAAAANT TTGATTGAAA TTTTAATCAA ATTGAAAATG TCCATAAAGT  
 180  
 TCATTAATCC NAACCTGGTG AAAAAGACGG AAAACATTTG ACCAATATCA AAGAAACATT  
 240  
 AGAATACATT NTGGTCACAT CATGTAACGC GTAATACAGC GATTATAGCT GTTGGTGGTG  
 300  
 GTGCGACAGG AGATTTTGCA GGATTTGTAG CAGCAACACT ATTAAGAGGT GTCCATTTTA  
 360  
 TACAAGTTCC TACAACGATT TTGGCGCATG ATTCTAGTGT TGGCGGTAAA GTGGGTATTA  
 420  
 ACTCAAAACA AGGTAAAAAC CTTATCGGTG CATTTTATCG TCCAAGTCT GTGATTTATG  
 480  
 ATTTAGACTT TTAAAGACG TTACCATTTG AGCAAATATT AAGTGGCTAT GCAGAAGTTT  
 540  
 ATAAGCATGC GTTATTGAAT GGTGAATCAA CGACGCAAGA AATCGAACAG CACTTTAAAG  
 600  
 ATAGAGAGAT ATTACAGCCA TTAAATGGTA TTGGATAAAT ATATTGCTAA AGGT  
 654

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTAACTTTTCG CTTTTTCTTT TTCTTCAATG TCTTGCACTT GTCTTTCAAC AATGTTAAAT

60  
 CTTTGGTTGTA AACCTGCTTT TTCTGTTTCT AGTTGTTTGA TGTCTTCCAT ATCAATATTT  
 120  
 GGATCTGTTG CTTTCTGACT CAATTCATCA TTTTATTTT TTAATTGNTG TCCAATCATA  
 180  
 CCTAAGGATT GTTTNAATTC ATATAATGTC GGCATNTCAT TTCCTCCTAA TAANTCATTG  
 240  
 TCATTTTTTAA AATTTGCGAT TCGAGCGTAC AATNTNNTCT CTNTNNTCTT NCTCTTCTAG  
 300  
 CGACATACTT TCTTTAGGTG GTTTCACCA ATCCAGATCG TATCTNACAT CATCAATTTT  
 360  
 AGTGATTTTN TCTACATCTT TCTTTAAATC TTCTGGGACN TTCTCNAAC GCCTACATTG  
 420  
 CTCTTTAGAG ATACTAGCAG CTATTTTCATT AGCTCCTAAA ATTTTCATCTA TCAAGCCGAA  
 480  
 AGACAAGGCT TCTTCTGCAG TAAGCCAAGT TTCTGCATCT AACATCTGTT TTAAGTGTTT  
 540  
 TTGATCTAAA TCTNTTGNTT TATCTAAATA AGCTGAATTA CTAACAGCAT CTGTTTTTTC  
 600  
 AAGTAAATCC GCTGTCTTTC TTAATTCTTC TGCATTACCT ACAGTCATAA CCCATGAATT  
 660  
 ATGAATCATT AAAAACTAT TNNTGGGGCA TAAAAATAGT GTCACCACTC ATAGGGATAA  
 720  
 CAACTAGCAA TTGGATGCCG CTAAGGCATC GACATAGATA TTANTTNNTG GAGGATGCAT  
 780  
 TTNTAGCATA TTGGNTTTTT GGATGNTCCN CAAATACANT GGCTCCAGAT GAATTTATAT  
 840  
 TGAACAACCT TTTCAACTGA TGTCTCCNNG GTCAACTTAG  
 880

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

AGTATTTTTT TGACCGAGAC ATGCAAGCCC TCCTGGTTGA TTATCATTTA CATATCGTAT  
 60  
 CATAACCAAT CATAACAAT AGTTTTATTA ACTTGTAGAC ACAATGTTTG CTAAAGTCAT  
 120  
 TTTTAAAAAA TATAGCCAAA AAATTAGCTA TATATTATAA AAGCGTGATA TAAATGTTTT  
 180  
 ATATAACAAA GAAATAAAAA TCATTTTTTA CAAATGGTTG TAAGAAAAAG ACATGCAGAT  
 240  
 GTTGTTAAAA TTTTAATAAG AATCAAGGAG GCTATATTAT ATGGCTAAAC TAAATGTAGA  
 300  
 AGTATTTGCG GACGGTGCAG ATATTGAAGA AATGAAAGCA GCTTATAAAA ACAACAAGT  
 360  
 GGATGGTTTT ACAACAAATC CTAGTTTAAT GCCGAAAGCG GCCGTAAGCA GATTACAAAG  
 420  
 CTTTTGCTGA AGAAGCTCGT GAAAGAAATT CCAGATGCTT CAATTTTCATT TGAAGTATTT  
 480  
 GCAGACGATT TAGAACTAT GGAAAAAGAA GCAGCAATTT TAAACAATA TGGCGAAAAT  
 540  
 GTATTTGTTA AAATTCCTAT TGTAATACA AAAGGTGAAT CAACGATTCC TTTAATTTAA

600  
AAACTTTTCAG CTGACAATGT GAGATTAAAC GTTNCGGCTG TTTACACAAT TGAACAAGGT  
660  
AAAGAAATAA CTGAAGCAGT AACTGAAGGT GTGCCCAACA TATGTTTCAG TATTTGCAGG  
720  
ACGTATTGCA GATACAGGCG TAGATCCATT ACCATTAATG AAAGAGGCTG TAAAAGTTAC  
780  
GCATAGTAAA GACGGCGTTA AATTATTATG GGCAAGTTGC CGCTCGTGCC  
830

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

NTTAATTTTA AAATGTACAA TGATATNTGT GAAAGCGCTT GCTTAGGAGG TGTATNTGAG  
60  
AGTGAATGAA ATGAATGCTA AAGAACNATT AGTGGACNAT TTAATGAAAA CATCATCGCA  
120  
ATTATTTTAAA TTNCACGGTG AAGTTGNCAT GCAGCTTNTC TTAAATGATG AATTAAAATT  
180  
ACCTTCTATT GNTGAAATAT GCGTGGAACG TAAGCGTTTA AGTGATATTG TGAAAGTTAT  
240  
TCCGCAATCA TATGCGTTAC TATACATAGA TAAGCAAGAT CAAGCAAGAG CTAAAGANNA  
300  
TTTATCACTT NCAAAAATTG CAAAAGTTTA TGTGCAATAT GATGATACAA CAATAATGAG  
360  
TATTTTTCGTT TATGATGTAG TAAACGATGA ATGGATTTTA AGATTGGATC CGAATATACG  
420  
TATACCTAAG AGTAACATAT ACTTCCATAG TTAAATTGG GATGTGGATT ATATTAAACC  
480  
GGAGATCGTT CTAATGTATG ATCTAATGCA ACACCATCAG TATCATCATT ATTCCAATTA  
540  
TAAACGAGTC ATAGATGCNT TAAGCTACTA TCAATTTTTT ATTTTAAAT TTGTAGTAGG  
600  
TGAGCNACGT ATTAAGGATG CAATCCAGAA GAACAATAAA TAATTAAGAA AAAGCAATTC  
660  
ATAACGCAGT TGAATACATG TGTTACGAAT TGCTTTTATA TTAGTTTTTA TCACACAAGT  
720  
TTTTTAATGC AACNCCGTGA TAGCAAACT CATATGTAGA TAATACAGCT TTTTCAGCAT  
780  
CATCTACAT  
789

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

ATATTCGAGA CGACCCCTAAN TAATTGTGTT GTCTGTCATA CTGGGNCANG ATTTGTGTGN  
60  
CTANATACNA CTNATCATTA GCANTAGATT GTTTATATGT TGTTGAGTGG CAAAATTGTT  
120  
GTGGTGCGTG TGGGGTTGCN TGCTGAGATG AGTGAGTATA TTGTTGAGTA TTATATGGCT  
180  
CTGGTGTTGG GTGTTGCGCC TGTGGCACGT TAGNCTCGAG CCGCTGGGTG TGTATTATCA  
240  
TCAGTTTTCT TCTGAGTATC ATCTGAGNTA TCTTGAGATG CATTGTCATC CTTATCTTTC  
300  
GACTCATCCT NTGATGCTTT ATCATCATTC TCNTCTTTAG CAGGACGTTG CTTTGTAGGT  
360  
GCTTGTTGCT GAGGTGGCAC ATATTGATAT TGATTCTGCT GTGGCAATTG CTGATATTGG  
420  
TTTGCTTG TG AATCTAGCTC AGCCTGCTTT TTTTCTCTT GTTGCTTTNN CTTTCTCTCT  
480  
TTATCTGCAA TTTCTTTTTG ACGCTTTTCT TTTTGTTTCT GCTTTTTGTT CGTTCAACAT  
540  
ACGTTCTTTA GCTTTATTCG AATGAATCTA CATATGCAAA AATTGCAAAT ACTAAATCCT  
600  
CCCGA  
605

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GGCAGGAGAC TGGTGGAGGT TCAGGTAACG CGCCGGCACG ATTAATGCCT GATAAAATAT  
60  
TGGATTTAAA GTATAAGTTG CGTGTTAATA ATGTACCGAC ACCAAGAACA GTAACATTTA  
120  
ATGATACATT AACATATAAA ACATATACAC AAGATTTTAT TAATTCACCT GCTGAAAGTC  
180  
ATACTGTAAG TACAAATCCA TATACAATCG ATATCATCAT GAATAAAGAT GCATTACAAG  
240  
CCGAGGTTGA TAGACGCATG GCAACAAGCT GATTATACAT TTGCATCATT AGATATCTTT  
300  
AATGATCTTA AAAGACGTGC ACNAACGATT TTAGATGAAA ATCGTAACAA TGTACCATTA  
360  
AATAAAAGAG TTTCTCAAGC ANATATTGAT TCATTAACTA ATCAAATGCA ACATACGTTA  
420  
ATTGGAAGTG TTGATGCTGA AAATGCNGTT AATAAAAAAG TTGACACAAA TGAAGATT  
480  
AGTTAATCAA AATGATGANT TGACAGATGA AGAAAAACAA GCNGCAATAC AAGTTATCGA  
540  
GGAACATAAA AATGAAATAA TTGGTAATAT TGGTGACCAA ACGACTGATG ATGGCGTTAC  
600  
TAGAATCACA AGATCAAGGT ATACAGACCT TAAGTGGGGA TACTGCAACA CCGGTTGTTA  
660  
AACCAAATGC TAGGAAAAGC AAT  
683



(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGATGATTAG ATAAATTGAA ACAACAACGT ATTGAGTTGA ATGAACAAAT CGATGCGCAG  
60  
GAAGCTACAT ACAAGTTTGT CACCAAGATA TTTTAGCTAT CGAAAATCAC TACCAAGATA  
120  
TTAAAGCTGA ACAATCAAAG TTAGGATGTA TTAATTCATC ATGCGATAGA TCATTTAAAT  
180  
GATGAATATC AATTGACTGT TGAACGTGCG AAATCTGAAT ATACGAGTGA TGAATCGATT  
240  
GACGCATTAC GTAAAAAAGT TAAGTTAATG AAGATGTCCG ATTGATGAAC TAGGTCCTGT  
300  
AAACTTAAAT GCAATTGAAC AATTTGAAGA GTTAAATGAA CGTTATACAT TTTTAAAGTGA  
360  
ACAACGTACA GATCTTCGTA AAGCTAAAGA AACATTAGAG CAAATTATAA GTGAAATGGA  
420  
TCAAGAGGTT ACTGAAAGAT TTAAAGAAAC TTTCCATGCT ATTCAAGGAC ATTTTACAGC  
480  
TCGTGCCCAA ACAATTGTTT GGTGGAGGCG ATGCAGAATT GCAATTAAC TGAAGCCGATT  
540  
ATTTAACAGC TGGTATTGAT ATTGTGGTAC AACCACCGGG TAAAAAGTTG CAACATTTAT  
600  
CGTTACTGAG TGGTGGTGAG CGTGCATTAA CTGCTATTGC TTTACTATTT GCAATTTTAA  
660  
AAGTAAGATC TGCACCTTTT GTTATATTAG ATGAGGTTGA AGCTGCACTA GATGAAGCAA  
720  
ATGTTATTAG ATACGCAAAA TATTTAAATG AGTTATCAGA CGAAACACAA TTCATTGTTA  
780  
TTACACACCG TAAAGGAACA ATGGAATTTG CAGATAGGTT ATACGGTGTA ACAATGCAAG  
840  
AATCAGGTGT TACTAACTT GTGAGTGTGA ATTTAAATAC AATAGATGAT GTGTTGAAGG  
900  
AGGAGCAATA ATGAGCGGCA CGAGCTCGTG CC  
932

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CGGTTAATCG GTAGTATTTT AGGTTCTGTT GTTATTAAGA TTTGGGAAGA TTTGATCTTC  
60  
CATCCCCCAA AGGGNTTAAC CGTATGGGGA TNCNTCANAA TCATTTGCCC AAGCTAAACC

120  
 ACCAAAGAAT GGATATTTGA ATCCGGTTGC ATTTAAGNTC AATTGGGATG ATTTTTAGCC  
 180  
 TCCAGTTATT AAGTTCAAGT GTTAAATACC CTGTTCTAAT TTTAATTAAT TCTATTAATT  
 240  
 TAAGATACTT AAAATGATAA GACACTAAGA AAGGGAGGCT ATTAGTAATA ATGCCCCAAA  
 300  
 ATAAAAGCAA ATGAAGCATT AGTTAAAGCA TTACAAGCAT GGGATATAGA TCACTTGTAT  
 360  
 GGTATTCCAG GAGACTCAAT CGACGCAGTT GTCGATTAGT TTAACGTACA GTGAGAGATC  
 420  
 AATTTAAATT TTATCATGTA CGTCATGAAG AAGTAGCAAG CTTAGCGGCT GCTGGTTACA  
 480  
 CAAAATTAAC TGGTNAAATC GGTGTGGCAT TAAGTATCGG TGNCCCTGGT TTAATTCATT  
 540  
 TATTAAATGG TATGTACGAT GCCAAAATGG ATAATGTACT CGTGCCAATT AATATTATCT  
 600  
 GGACAAACNG AATAGTACAG CACTTGGAAC GAAAGCATTT CAAGAAACAA ATTTACAAAA  
 660  
 ATTATGTGAA GATGTAGCCG TTTATAATCA CCAAATTGAA AAAGGTGACA ATGTGTTTGA  
 720  
 AATCGTTAAC GAAGCAATTC GTACGGCATA TGAACAAAAA GGTGTCGCTG TTGTTATTTG  
 780  
 TCCTAACGAC TTATTAAGT AAAAAATTAA AGATACAACG AATAAACCAG TAGATACATC  
 840  
 AAGACCAACA GTTGTATCAC CAAAATATAA AGACATCAAA AAAGCGGTTA AACTAATTAA  
 900  
 TAAAGTAAA AAGCCTGTCA TGTTAATTGG TGTAGGTGCA AAACATGCGA AAGATGAGCT  
 960  
 CGTGCC  
 966

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

CTGTGAAATT AAGTCGNTAT TACCCGCAAG GATTAAGAAG TTTGAATGGT GGTCGCATGG  
 60  
 CAAGATTTGG ACGTACACCA TTACTTGATG CAATGGAGAT GGCTAATGAG CATATTATGG  
 120  
 TGATTGCCAT GATAGAAGAT GTTGANGGGG TTATGGCCAT TGACGATATA GCTCAAGTCG  
 180  
 AAGGTTTAGA CATGATAGTC GAAGGTGCCG CAGGATTTAT CGCAGTCACT TGGCATACCA  
 240  
 TNGCAAACGA GCGTGATGAT CAAGTAACAT CACATNTTCA ACATATTTNT GNGGTTGTGA  
 300  
 ATGCACATGG TAAACATTTN TGTGCATTAC CACGTGAAGA TGAAGATATT GCAAAATGGC  
 360  
 AGGCACAAGG TGTACAAACA TTTATTTTAG GCACGAGCGG AAAAATATAT CGCCATTTAA  
 420  
 GTGCATCTCT AGCGACGTCT AAACAGAAAG GGGATGATGG CTAATGCGTA TAGTTCAACC  
 480  
 TGTTATTGAA CAATTAAAAG CACAATCTCA TCCAGTTTGT CATTATATCT ATGATTTAGT

540  
 CGGACTGGAA CATCATTTC AACATATTAC ATCGTCATTG CCGAGTAATT GTCAAATGTA  
 600  
 CTATGCAATG AAAGCAAATA GTGAACGAAC AATCCTAGAT ACAATTAGTC AGTATGTTGA  
 660  
 AGGATTGAA GTTGCACTC AAGGTGAAAT AGCAAAAGGT CTTGCTTTTA AACCAGCAAA  
 720  
 TCATATTATT TTTGGTGGCC CTGGTAAGAC AGACGAGGAA CTAAGATATG CAGTAAGTGA  
 780  
 AGGTGTTTCA CGTATTCATG TTGAAAGTAT GCATGAATTA CAACGGCTAA ATGCCATCTT  
 840  
 AGAAGATGAA GATAAGACAC AACACATTTT ATTGCGTGTT AATTTAGCAG GACCATTTCC  
 900  
 CAATGCAACG TTGCATATGG CAGGACGCCC AACACAATTT GGTATTTCTG AAGACGAAGT  
 960  
 TGATGATGTC ATTGAAGCTG CGCTAGTAAT GCCAAATATT CATCTAGATG GCTTTCATCT  
 1020  
 TCATTCCAT TTTCTAACAAT TTAGACTCGA ATTTACATGT CGATGTAGGG GAAACTTTAT  
 1080  
 TTTAAAAAG CAAAATCATG GCCTTGAAAA ACATCGATTT CCACTCAAAC ATATCAATCT  
 1140  
 TGGTGGGTGG CATAGGCGGT CAACTATGCA GATTTAACTA GGCCAACTNG AGTGGGATAA  
 1200  
 TTTTGNNGAA AATTTNAAAA CACTTATCGT TGAGCAAGAA ATGGAAGATG TGACATTGAA  
 1260  
 CTTTGAATGT GGGCGCTNTA TTGTGGCACA TTGGGGTTAC TATGTGACAG AAGTGCTAGA  
 1320  
 TATTANGAA GNGCATGGCG CTTGGTATGC CATTNNAAGA GGAGGTACGC AACACNTAG  
 1380  
 CCTGCCGNA TCTTGC  
 1396

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ACCAAAGCCA AATACTTGCA TTAANNCGGG GTAATTCCAA CAACTTAAGA ACNGTGCGAA  
 60  
 ACNAGCCTGC GGAACNACAA GCGATTACCA AATGCTTCGG GACNTTAAAA TACCACAACA  
 120  
 CAAAGAAGCA TTGTAAGCAC AAGTAACAAG TGCAGGACGC GTATCTGCAG CANATGGTGT  
 180  
 TGAACATACT GCGACTGAAT TAAATACTGC GATGACAGCT TTAAAACGTG CCATTGCTGA  
 240  
 TAAAGCTGAC ACACAAGCTA GTGGTAATTA TGTCAATGCT GATGCGAATA AACGCCAAGC  
 300  
 ATATGATGAA AAAGTGACAG CTGCAGAACA TATCGTTAGT GGTACACCAA CACCAACGTT  
 360  
 AACNCCATCA GATGTTACAA ATGCAGCAAC GCAAGTAACG AATGCGAAGA CGCAGTTANN  
 420  
 CGGTAATCAT AATTTAGAAG TAGCGACNCA AAATGCTAAC ACAGCAATTG ATGGTTTAAC  
 480  
 TTCTTTAAAT GGTCTCCAA AAACCCAAAA CTAAAGAAG AAGTGGGTCA AGCGACNGAC

540  
GTTNCCAAAT GTTCAAACCTG TTCGTGATAA TGCACAAACA TTAAACACTG CAATGAAAGG  
600  
TCTACGAGAT AGCATTGCGA ATGAAGCAAC GATTAAAGCA GGTCAAAACT ACACAGATGC  
660  
AAGTCAAAAC AAACAAAATG ACTACAACAA TGCAGTCACT GCAGCANAAG CAATCATTGG  
720  
TCAAACAACCT AGTCCATCAA TGATTGCGCA AGAAATTAAT CAAGCGAAAG ACCAAGTGAC  
780  
AGCTAAACAA CAAGCGTTAA ACGGTCAAAG AAAACTTAAG AACTNCGCAA ACCAAATGCG  
840  
AAGCAACAAT TGAATGGCTT AAGTGAAGTA ACTTAATGCC CCCCAGAGAT GNAGCGANAC  
900  
CNCCAAATCG AGGTGCAACG CATGTTAATG GAAGTAAACA CCCAAGCCCA CAATAATGGG  
960  
GACGGCATTAA AAATACAAGC TATGNCGGNA CTTGTNAAAT GGTAATTCAA AGACTCACAA  
1020  
TNCGGATTAA GCAAGGTGTT AACTTCACTT GATGCAGATG AAGCGAAACG TAATGCATAT  
1080  
ACAAATGCAG TGACGCAAGC TGANCAAATT TTAAATAAAG CACAAGGGCC AAATACTGCA  
1140  
AAAGACGGTG TCGAAACTGC GTTACAAAAT GTACAACGTG CTAAAAACGA ATTGAGCGGT  
1200  
AATCAAAATG TTGCGAACGC TAAGACAACCT GCGAAAAATG CATTGAATAA CCTTACATCA  
1260  
ATTAATAATG CACACAAAGC AGCATTGAAA TCACAAATTG AAGGTGCGAC AACAGTTGCA  
1320  
GGTGTAATC AAGTGTCTAC AATGGCATCT TGAATTAAAT ACCTGCAATT GAGCAACTTA  
1380  
CCAACGTGGT ATTAATGACG AAGCAGCTAC AAAAGCAGCT CAGAAATATA CTGAAGCAGA  
1440  
TAGAGATAAA CCCANCCTGC ATACAATGAT GCTGTAACAG CAGCTAAAAC GTTATTAGAT  
1500  
AAAACAGCTG GTTCAAATGA CAATAAAGTA GCCGTTGAAC AAGCATTACA ACGTGTGAAT  
1560  
ACTGCTAAAA CAGCATTAAA TGGTGACGCG CGATTAAATG AAGCGAAGAA CACAGCTAAA  
1620  
CAACAATTAG CGACAATGTC ACATTTAACT AATGCTCAAA AAGCAAACCTT AACAGAACAA  
1680  
ATTGAACGTG GTACAACCTG TGCTGGTGTT CAAGGCATCC AAGCAAATGC TGGTACTTTA  
1740  
AATCAAGCAA TGAATCAATT AAGACAAAGT ATTGCTTCTA AAGATGCGAC TAAATCAAGC  
1800  
GAAGATTATC AAGACGCGAA TGCAGATTTA CAAAATGCAT ACAATGATGC GGTAACATAAT  
1860  
GCTGGAGGTA TTATTAGTGC ANCGAATAAC CCTGAAATGA ATCCTGATAC AATTANCCAA  
1920  
AAAGCGAGCC AAGTGAACAG TGCGAAGTCT GCATTGANCG GTGATGAAAA ATTAGCAGCA  
1980  
GCAAAACAAA CTGCGAAATC AGATATCGGT CGTGTGACAG ACTTGAACAA TGCACAACGA  
2040  
ACTGCGNCAA ATGCTGAAGT GGATCAAGCA CCAANTCTTG CAGCTGTCAC AGCGGCTAAA  
2100  
AATAAAGCAA CATCGTTAAA CACAGCGATG GGTAATGTGA AACATGCACT TGCTGAAAAG  
2160  
GATAATACGA NACGTAGTGT CAATTACACA GATGCGGATC AACCAANACA ACAAGCGTNT  
2220  
GATACTGCAG GTACACAAGC AGAAGCAATT ACTAATGCAA ATGGCAGTNA CGCGAATGAA  
2280  
ACACAAGTTC AAGCAGCGCT TAACCAATTG AATCAAGCTA AAAACGACTT GGAATGGGTG  
2340

ATAATAAAGT TGCTCAAGCG AAAGAAACAA CAAAACGTGC ATTAGCTTCA TATAGTAACT  
 2400  
 TGAATAACGC GCAATCAACT GCAGCAACTA GTCAAATTGA CAATGCAACG ACAGTAGCAG  
 2460  
 ACGTAACTGC TGCACAAAAT ACTGCTAATG AATTAAATAC AGCAATGGGT CAACTTCAAA  
 2520  
 ATGGTATTAA TGACCAAAAC ACTGTTAAAC AACAAGTGAA CTTTACAGAT GCTGACCAAG  
 2580  
 GTAAGAAAGA TGCTTACACA AATGCTGTTA CGAATGCTCA AGGTATTTTA GATAAAGCAA  
 2640  
 CACGGTCCAA AATATGNCAA AAGCACAAGT TGAAGCTGCA TTAAATCNAG TANCNCTGC  
 2700  
 TAAGAATGCT TTAAACGGTG ATGCAAATGT NAGACAANCA AAATCAGATG CGAAAGCAAA  
 2760  
 CTTAGGTACA TTAACACACT TANATAATGC AAAAAACAA GATTTAACAT CACAAAGCGN  
 2820  
 NGGTGCAACA ACAGNCAACG GTGTAAATNG TGTTAAACG AAAGCACNAG ACTTAGATGG  
 2880  
 TGCAATGCAA CGATTAGAGT CAGCAATCGC AAATAAAGAC CAACTAAAG CGAGCGAAAA  
 2940  
 CTACATTGAC GCAGATCCAA CTAAGAAAAC AGCATTTGAT AATGCCATCA CACAAGCTGA  
 3000  
 ATCTTACTTA AATAAAGATC ATGGTACGAA TAAAGATAAG CAAGCTGTTG AACAAGCAAT  
 3060  
 TCAAAGTGTA ACGTCTACTG AAAATGCTTT GAACGGTGAC GCGAACTTAC AACGCGCTAA  
 3120  
 AACTGAAGCT ACACAAGCTA TCGATAACTT GACACAATTG AATACACCGC AAAAAACAGC  
 3180  
 ATTGAAACAA CAAGTGAATG CTGCACAACG CGTATCAGGT GTAAGTATGAT TGAAAAATAG  
 3240  
 TGCTACATCA CTTAATAATG CGATGGATCA ATTAAAACAA GCAATTGGTG ATCATGACAC  
 3300  
 AATTGTAGCT GGTGGTAATT AACTAACGC AAGTCCTGAT AAACAAGGTG CTTACTACTGA  
 3360  
 TGCATATAAT GCTGCGAAGA ATATCGTAAA TGGTTCACCT AATGTGATTA CAAATGCAGC  
 3420  
 AGATGTTACT GCGNCAACAC AACGTGTCAA TAATGCTGAA ACAAGTTTAA ATGGTGAGAC  
 3480  
 AAAGTTAGCA ACTGGCGAAG CAACAAGCTA AAGATGCATT ACGTCAAATG ACACATTTAT  
 3540  
 CTGATGCACA ANAAACAAAG TATTACTGGT CAAATTGATA GCGCGACACA AGTAACTGGT  
 3600  
 GTACAAAGTG TGAAAGACAA TGCAACAANT CTTGACAATG CAATGAATCA ACTTCGAAAT  
 3660  
 AGTATTGCGA ATAAAGATGA AGTAAAAGCG AGTCAACCAT ATGTTGATGC AGATACAGAT  
 3720  
 AAACAAAATG CATACAATAC AGCAGTTACA AGTGCTGAAA ATATCATTAA TGCAACGAGT  
 3780  
 CAGCCAACAC TTGATCCATC TGCAGTAACA CAAGCAGCTA ATCAAGTGAA CACTAACAAA  
 3840  
 ACTGCGCTTA ATGGTGCGCA AAAGTTAGCA NATAAAAAGC AAGAAACAAC TGCTAACATC  
 3900  
 ACCCGATTAA GTCATTTA  
 3918

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATGCGATACG CTTAACCAGC AATGCATGGT TTAAGACAGA GCATTCAAGA TAACGCAGCA  
60  
NCTAAACCGA ATAGCAAATA TATCAACGGA AGTCCACGAG AGCAACCAAA ACTATGATCA  
120  
AGCTGTTCAA GCCCCAAATA ATATTATCAA TGAACAAACT GCAACATTAG ATAATAATGC  
180  
GATTAATCAA GTAGCGGCAA CTGTGAATAC AACGAAAGCA GCATTACATG GTGATGTGAA  
240  
ATTACAAAAT GATAAAGATC ATGCTAAACA AACGGTTAGC CAATTAGCAC ATCTAAACAA  
300  
TGCACAAAAA CATATGGAAG ATACGTTAAT TGATAGTGAA ACAACTAGAA CAGCAGTTAA  
360  
GCAAGATTTG ACTGAAGTAC AAGCATTAGA TCAACTTATG GATGCATTAC AACAAAGTAT  
420  
TGCTGACAAA GATGCAACAC GTGCGAGCAG TGCATATGTC AATGCAGAAC CGAATAAAAA  
480  
ACAAGCCTAT GATGAAGCAG TTCAAAATGC TGAGTCTATC ATTGCAGGAT TAAATAATCC  
540  
AACTATCAAT AAAGGTAATG TATCAAGTGC GACTCAAGCA GTAATATCAT CTAAAAATGC  
600  
ATTAGATGGT GTTGAACGAT TAGCTCAAGA TAAGCAAACCT GCTGGAAATT CTCTAAATCA  
660  
TTTAGATCAA TTAACACCAG CTCAACAACA AGCGCTAGAA AATCAAATTA ATAATGCAAC  
720  
AACTCGTGAT AAAGTGGCTG AAATCATTGC ACAAGCGCAA GCATTAAATG AAGCGATGAA  
780  
AGCATTAATA NAAAGTATTA AGGATCAACC ACAAACTGAA GCAAGTAGTA AATTTATTAA  
840  
CGAGGATCAA GCGCAAAAAG ATGCATATAC GCAAGCAGTA CAACACGCTC GAAGATGCCT  
900  
TGNTTAACAA AACAACTGAT CCTACATTAG CTAAATCAAT CATTGATCAA GCGACACAGG  
960  
CAGTGACTGA TGCTAAAAAC AATTTACATG GTGGATCAA AACTAGCTCA AGATNAGCAA  
1020  
CGTGCAACAG AAACGTTAAA TAACTTGCTCT NACTTGAATA CACCACAACG TCAAGCACTT  
1080  
GANAATCAAC TCAATTCNTG CAGCAACTCG NCGNGANGTA GCACANAAAT TTAATGANGC  
1140  
ACANGCACNT TATCCACGCA ATGGANGCTT TNCGTCATAG CATTACGNN NCAACAAACA  
1200  
AAACAGATCT GGTNTGCAAN TTTTTTATTG AAGGTTNNNC CNCACCCCGG TGCTTCNCGC  
1260  
GCCAC  
1265

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TTCATTAGTG GTGTGGCAGC ATAGCTCAAN GATAACCAAA CTCCTGGAAA TTCTCTAAAT  
60  
TCATTTAGAT CAATTAACAC CAGCTCAACA ACAAGCGCTA GAAAATCAAA TTAATAATGC  
120  
AACAACTCGT GATAAAGTGG CTGAAATCAT TGCACAAGCG CAAGCATTAA ATGAAGCGAT  
180  
GAAAGCATT AAGAAAGTA TTAAGGATCA ACCACAAACT GAAGCAAGTA GTAAATTTAT  
240  
TAACGAGGAT CAAGCGCAAA AAGATGCATA TACGCAAGCA GTACAACACG AGCGAAAGAT  
300  
TTGATTAACA AAACAACTGA TCCTACATTA GCTAAATCAA TCATTGATCA AGCGACACAG  
360  
GCAGTGACTG ATGCTAAAA CAATTTACAT GGTGATCAAA AACTAGCTCA AGATAAGCAA  
420  
CGTGCAACAG AAACGTTAAA TAACTTGTCT AACTTGAATA CACCACAACG TCAAGCACTT  
480  
GAAAATCAAA TCAATAATGC AGCAACTCGT GGTGAAGTAG CACAAAAATT AACTGAAGCA  
540  
CAAGCACTTA ACCAAGCAAT GGAAGCTTTA CGTAATAGCA TTCAAGATCA ACAACAAACA  
600  
GAATCTGGTA GCAAGTTTAT TAATGAAGAT AAACCGCAAA AAGATGCTTA CCANGCAGCA  
660  
GTTCAANATG CAAAAGATTT AATTAACCAA ACAGGTANTC CAACGCTTGA TAAAGCACAA  
720  
GTTGAACAAT TGACACATGC TTTTAAACAA GCTAAAGATA ACCTACACGG TGATCAAAAA  
780  
CTTGCAGACG A  
791

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CTATTAAGGA ATCCTTGNN AATTCACATT AGCAAGTTGG ATTGTCCACC TTATTAATTG  
60  
ATAAAGTATG CAAATAATTT CACAGTGTTT CCAGCGGGGC CAANTTATGA TTGCAAGTAA  
120  
CCTATAGCAA TCGTATTCTT GTTCTTGCCA ACGCTATTTA AGTATCAGGT TTAACCAACA  
180  
GGTGCGACAA AAGGTTAGTT TGAAATTAGG GAGTGGGGCA GAATTGATAA AGAACCACTA  
240  
ATGACGATAA AGATTAAAAG GGAGGACGTT ATGATGACGG ATTAAAGTTG GAATCATTGG  
300  
GTGTGGTGGT ATTGCGAATG GCAAGCAACA TGCCAAGTTT ACNAAAAGTT GAAAATGTTG  
360  
AAATGATCGC ATTTTGTGAC GTAGACATTT CGAAAGCAGC GAGTGCGGCA GAAGCATACG  
420  
GAACTGACAA TGCAAAGGTT TATGATGATT ACAAAGCATT GTTAAAAGAT GACACGATTG  
480  
ATGTTATCCA TGTTTGTACG CCAAATGACT CGCATTGTGA AATTACTGTA GCAGGGTTGC  
540

ATGCCGGTAA GCATGTGATG TGTGAAAAAC CAATGGCTAA AACGACAGCA GAAGCTCAAA  
 600  
 AAATGATAGA TACAGCTAAA TCAACAGGTA AAAAATTAAC AATAGGTTAT CAAAATCGCT  
 660  
 TCAGACCAGA TAGTCAATTT TTACATCAAG CAGCGCAACG TGGCGACTTA GGAGACATTT  
 720  
 ACTTCGGAAA GGCACATGCC ATTCGTCGTC GTGCAGTACC GACATGGGGT GTCTTTCTAA  
 780  
 ACGAAGAAGC CCAAGGTGGA GGACCTTTAA TCGATATTGG TACGCACGCA TTAGATTTAA  
 840  
 CGTTATGGAT GATGGATAAT TATGAACCAG AATCAGTGAT GGGTTCAACA TTCCATAAAT  
 900  
 TAAATAAGCA GCATGATGCG CCAAACGCTT GGGGTTTCATG GAATCCAGAT GAATTAACAG  
 960  
 TTGAAGACTC TGC GTTTGGC TTTATTAAAT GAAGAACGGA GCGACGATCA TTTTAGATCC  
 1020  
 GCTTGGGCGA TTAATTCTTT AGAAGTGGAT GAGGCAAAAT GTTCATTATT AGGAACGAAA  
 1080  
 GCAGGTGCTG ATATGAAAGA TGTTCTACGT ATTCATGGTG AAGATATGGG CACACTTTAT  
 1140  
 ACCAAACACG TTGAATTNGA AAACAAAGGC GTCGACTTTT ATGAAGGTAA TGAAGTGGAT  
 1200  
 GAAGCTGAAG AAGAANCAAA AGCTTGGATT GATGCAGTTG TAAATGATAC TGAACCAAGT  
 1260  
 GTGAAACCGG AACAAGCAAT GGTAGTTACA AAAATTCTTG AAGCGATTTA TCAGTCTGCA  
 1320  
 AAATCAGGCA AAGCAATTTA CTTTGAATAA CATCATACGG TAAGGAGGCA CATCATGACA  
 1380  
 AAATTAATAAG TTGGTGTGAT AGGTGTTGGT GGCATTGCAC AAGACCGTCA TATTCCAGCA  
 1440  
 TTGCTGAAAC TCAAAGACAC AGTCTCATTA GTTGCAGTAC AAGATATTAA TACAGTGCAG  
 1500  
 ATGATTGATG TTGCGAAGCG CTTTAATATA CCTCAGGCAG TTGAGACACC TAGCGAGCTG  
 1560  
 TTTAAACTTG TTGATGCGGT GGTCATTTGT ACACCCAATA AATTCCATGC TGATCTTTCT  
 1620  
 ATAGAAGCAT TGAACCATGG TGTCCATGTC TTATGCGAAA AGCCAATGNC AATGACGACG  
 1680  
 GAAGAGTGTG ATCGCATGAT TGAAGCGGCT AATAAAAAATC ACAAATTATT AACTGTGCGT  
 1740  
 TATCATTATC GTCACACAGA TGTCGCTATG ACTGCTAAAA AAGCAATTGA AGCAGGTGTG  
 1800  
 GTTGGTAAAC CATTAGTAGC ACCGTTGTCC AANCGATGCG TAGGCGTAAA GNACCTGGGT  
 1860  
 GGGGCGTTTT TACCCAATAA AACCGTTGCA AGGTGGCGGT AGTTTAATCG ATTATGGTTT  
 1920  
 CCCACTTGTT AAGACTTATC TTTGTGGCTA TTAGGTAAAG ATATGGTGCC GCATGAAGTG  
 1980  
 CTAGGAAAAA CATATAATCA ATTGAGCAAA CAACCGAATC AAATTAATGA TTGGGGAACA  
 2040  
 TTTGATCACA CTAAATTTGA TGTCGATGAT CATGTTACTA GTTATATGAC ATTTGCCAAT  
 2100  
 CGAGCAAGCA TGCAGTTTGA ATGTTCTGGT TCTGCAAATA TAAAGGAAGA TAAGGTACAC  
 2160  
 GTTAGTTTAT CAGGAGAAGA TGGCGGTATC AATTTATTTT CATTTGAAAT ATATGAGCCC  
 2220  
 CGCTTTGGAA CTATTTTGA AAGCAAAGCT AATGTTGAGC ATAACGAAGA CATTGCTGGT  
 2280  
 GAGAGACAGG CGCGTAACTT TGTCAATGCG TGTTTAGGTA TAGAAGAGAT TGTGGTGAAA  
 2340  
 CCGGAAGAAG CACGCAATGT AAATGCCCTT ATAGAAGCGA TTTATCGTAG CGATCTTGAT



2400  
 AACAAAGAGCA TACAACCTTTA ATGATTATTA TATATAATAC AAAATTCTCA ATATAAAAAG  
 2460  
 ANGGAGTGCT TTTCAATGAA AATAGGTGTA TTTTCAGTAT TATTTTACGA TAAAAATTTT  
 2520  
 GAAGATATGT TAGATTATGT CGCAGAATCT GGATTGGATA TGATTGAAGT TGGAACAGGT  
 2580  
 GGTAACCCAG GAGATAAATT TTGTAAGTTA GATGAGTTGT TAGAAAATGA AGACAAGCGA  
 2640  
 CAAGCATTTA TGAAGTCAAT CACAGACAGA GGCTTACAAA TAAGTGGTTT CAGTTGTCAT  
 2700  
 AACAAATCCAA TTTCTCCAGA TCCGATAGAA GCGAAAGAAG CCGATGAAAC GTTACGTAAA  
 2760  
 ACAATCCGTT TAGCAAATCT ATTAGACGTG CCAGTTGTGA ATACATTTTC TGNCATTGCA  
 2820  
 GGGTCAGATG ATACCGCTAA AAAGCCTAAT TGGCCTGTGA CACCTTGGCC AACAGCCTAC  
 2880  
 TCTGAAATTT ATGATTATCA GTGGAATGAA AAGTTGATAC CATATTGGCA AGATTTAGCT  
 2940  
 GAGTTTCCNC AAGAGCAAGA TGTNNAAATT GCCATNGAGT TACATNCAGG ATTTTTAGCT  
 3000  
 CANACACCAA ATACGATGTT NAAGTTACGT GAGCCAACAA ATGAATATAT CGGTGCTAAC  
 3060  
 TTAGATCCTA GTCATTTATG GTGNCAAGGT ATTGACCCAA NTCCTGCGAN TCGCATATTA  
 3120  
 GGCCCNANCA AATNCAATTC ATCACTTCCA TGAATTCCG AAGAAACGTA TGTTANTCNA  
 3180  
 GGGNATGTAA ANATGTATGG TCTAGCTGAT NTCCAGCCAT ATGGTNACGT TGCGACANGN  
 3240  
 GCATGGACAT TCCNTACAGN TGGNTATGGA CATAGTCCAT ATGNATGGGC AGATNTCATA  
 3300  
 AGTCAACTTA NTATTAGATG GAG  
 3323

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TCCATTTAAT TCCACCTTGC CCCGACAGGT TTTNCCGACC TGGAAAGCGG TCAGTGAGCC  
 60  
 CNAACNCAAT TAATGTGAGT TAGCTCCACT TCATTAGGCC ACCCCAGGCC TTTACACTTT  
 120  
 ATGCTTCCGG CTCCGTATGT TGTGTGGAAT TTGTGAGCGG ATAACAATTT CACACAGGAA  
 180  
 ACAGCTATGN CCATGATTAC NCCAAGCTCG AAATTAACCC TCACTAAAGG GAACACAAGC  
 240  
 TGGAGCTCCC ACCGCGGTGG CGGCCGCTCT AGAACTAGTG GATCCCCCGG GCTGCAGGAA  
 300  
 TTCGACGAGA ACGCGTGCAG CGTTTACAGT TGCGTCTATT GATTTAGGTG CGCATCCAGA  
 360  
 ATTTTtaggg AAAAATGATA TTCAATTAGN CAAAAAGAA TCTGTAGAGG ATACTNCNAA  
 420  
 AGTATTAGGT AGAATGTTCG ATGGTATTGA ATTCAAACCTT TAACTGAGCT TCATGGGGCA

480  
 CCAGGTTTTG AAGAAGAAGT AAAAAATTAT ATGACTCAGC AAATGGCGCC GTATGTAGAT  
 540  
 GGAATTTATT GAAAATCGTA TGGGTGGATT TTTTGGGTGT GAAAAAATCT AAAAAATCCAA  
 600  
 ATGCAAAACG TGTAATGATT GCAGNACATA TGGATGAAAT C  
 641

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CTGCTTAAAT TCGAACGTGT CATTGACATT TTCAATAAGA AAAACAACGG AGCATGGAAT  
 60  
 TTCTGTCCGC AAAACGCCGG TTATTGGGAA CATATCCCTA AGAGTATTAC AAAATTATCA  
 120  
 GATTTAAAAA TCGTTGGTTT AGATTTCTAT ATCACTACTG AAGAATCAAA ACGATTTACT  
 180  
 GATTTTCCTA AAGACTTTAA AGGTATTGCA GGTTCGATAT TAGAAGTAAA ATCGAATACA  
 240  
 CCAGGTAACA CAACACAAGT ATTAAGACGT AATAACTTCC CGTCTGCACA TCAATTTNTA  
 300  
 GTTAGAAACT TTGGCACGAG ACTGGTGGCG TTGGTAAATG GGAGTTTATT CGAAGGAAAG  
 360  
 GTGGTTGAAT AATGATAGTA GATAATTTTT CAAAAGACGA TAACTTAATC GAGTTACAAA  
 420  
 CAACATCACA ATATAATCCA ATTATTGACA CAAACATCAG TTTCTATGAA TCAGATAGAG  
 480  
 GAACTGGTGT TTAAATTTT GCAGTAACTA AGAATAACAG ACCGTTATCT ATAAGTTCTG  
 540  
 AACATGTTAA GACATCTATC GTGTAAAAAC CCGATGATTA TAACGTAGAT AGAGGCGCTT  
 600  
 ATATTACAGA CGAATTAACG ATAGTAGACG CAATTAATGG GCGTTTGCAG TATGTGATAC  
 660  
 CGAATGAATT TTAAACAT TCAGGCAAGG TGCATGCTCA GGCATTCTTT ACACAAAACG  
 720  
 GGAGTAATAA TGTGTTGTT GAACGTCAAT TTAGCTTCAA TATTGAAAAT GATTTAGTTA  
 780  
 GTGGGTNTGA TGGTATAACA AAGCTTGTTT ATATCAAATC TATTCAAGAT ACTATCGAAG  
 840  
 CTGTCGGTAA AGACTTTAAC CAATTAAAGC AAAATATGGC TGATACACAA ACGTTAATAG  
 900  
 CAAAAGTGAA TGATAGTGCG ACAAAGGCA TTCAACAAAT CGAAATCAAG CAAAACGAAG  
 960  
 CTATACAAGC TATTACTGCG ACGCAAACTA GTGCAACACA AGCTGTTACA GCTGAAGTCG  
 1020  
 GATAAANTAG GTGGGAAAAA GAGCAAGCGA TTGGGGACCG TTTTAACGAA GTNGGACAAC  
 1080  
 AAATCAATGC GCCTGGCCTT GTNAAGGTAA TNCAACAACA AATTGGGAAA  
 1130

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
CCTCAGCATA TGGTTGAACC CTTTCTTGAT AACCCATATC TGTTAGTTTT CCCCAATGAT
60
TGCTCGCATA GCTAATTGTG CCAATTGGAAT ATCAAGTAAT TTTACTTAGG CACGAGAATG
120
GTNCCGTTCT ACTAGAACGG TGGGTTTACT TCTAAAACAA TATACACCAT CGTGAGCTAT
180
AACGAATTGA ATGTTGATTA AGCCAATGAT GTTTAAACCT TTAGCTAATT TTATAGTATA
240
GTCCTCAAGT GTTGCTAACT CGTCTTCTGT CAAAGTTTGT GCGGATATA CAGCGATTGA
300
GTCACCACTA TGTACACCAG CAGTTTCAAT ATGTTCCATG ATTCCTGGAA TAATGACCGT
360
TTCTCCATCA CAAATCGCAT CAACTTCAAT TTCTTTACCA GTTAAATATC TATCGACTAG
420
TACCGGATGT TCCGGACTCG CTTTTACAGC CTGGGTCATA TAGTTTTCTA ACTCTTTGTC
480
ATTGTCTACA ATTTCCATTG CGCGACCACC TAATACATAA GAAGGTCTTA CTACAACCGG
540
ATATCCGATT TCTGCAGCAT TCGCTAATGC TTCCTCAGGT GATGTAGCTG ATTTCCCTTG
600
TGGCTGTGGC ACGTTAATTT TTCTTAATAG TGCTTCAAAT TCTTTTCTAT CTTCAGCACG
660
ATTTAGATTT TCTAGTGAAG TACCAAGTAT TTAAACACCA TGTTTAGCCA ATTTGTCTGC
720
TAAATTAATC GCTGTTTGTC CTCCAATTG TACAACGACA CCTTTAGGTT TTTCTAAATT
780
AATGATATTC ATCACATCTT CTTCAAGTAA AGGTTCAAAG TATAATTTGT CAGAAATTGA
840
AGAAGTCTGT TGAAACTGTT TCTGGATTGT TATTCACAAT TATCGCTTCG TACCCTGCTT
900
TTTGAATTGC CCAAACGGCG TGAAGTGTG CATAGTCAAA TTCTACACCT TGGCCGATTC
960
GAATTGGTCC AGAGCCTAAT ACTAAGATTT CTCTTTGTCA GTAACATATG ATTCATTTTC
1020
AGTTTCGTAT GTACCATAAT AATATGGTGT TGAGATCAAA TCAGCTGCGC AGTATCAACA
1080
TCTGTAACAG GTTAATATCA TTTC
1104
```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CTATCATAAA AACATAAAGT ATTGTAAGCT TTTTATCGAT ATTTTTTATT TATAAAAAATA  
 60  
 AAATGAGATA ACTNTGTGAA TTTTATTGA GATAAATTAG ATAGTGNTGT TTTTGTGATG  
 120  
 TTTAATAATA TCTTGGGTGT GTTAATACTA GTAATGCTTT CAACTGATGC ATTAAGACTG  
 180  
 TGACATCATA ACTCATTTAA GAACTTCGCT TATTAATTTT CTACCAATAC AATCCCTTCT  
 240  
 AAGTGCACATA AAAAATCCTT ACTGCTAAGT GATTAAACTT AACAATAAGG ATTTATTTAT  
 300  
 CGCTAATGCA TGATTATTAA CGGAATCTCA TACCACCATC TACAATAATT GTTTGTCCAG  
 360  
 TAATGTAATC AGAGTCTTTA CCAGCTAAGA AGCTCACTAC ATTTGAAACA TCTTCTGGTT  
 420  
 GAGAACTCT GCCCAAAGCA ATCTGACTTG TAAATTGTTT CCAACCCCAT GCTTCAGGTT  
 480  
 TACCTGCTTC TTCGGCTGTT GCCACTGCGA TACTTTCCAT CATTTGGTGTT TGAACGATAC  
 540  
 CAGGTGCGAA TGCATTCACA GTAATACCTT CAGACGCTAA ATCTTGTGCG GCTACTTGTG  
 600  
 TTAAACCTCG CACTGCGAAT TTTGTACTGC AATATAAAGA CAAGCCTGGG TTACCCCTCAA  
 660  
 CGCCTGCTTG AGATGTTGCA TTGATAATTT TACCGCCATG ATTGAATTTT TTAAATTGTT  
 720  
 CATGTGCGGC TTGAATACCC CATAGCACAC CTGCAACGTT CACGCCATAT ACTGTTTTAA  
 780  
 ACTGTTCTTC AGTAATTGTA TCGATTGGTG TTGTTGGTCC AAGGCCGGCA TTGTTAACCA  
 840  
 TGACATGGAA ATCGCCAAAT TGCCTCGGA GTTGCTGTC TTAGTGCCTT AAATACATCA  
 900  
 TCACGGTTTG ATACATCTGC TTTGATAGCA ATAGCTTTTG TACCATCACT TGATAATTTA  
 960  
 AGTGCAGCTG CTTTTGCCCC TTCTTCATTG AAATCAACAA CTGCTACTTT GAAACCATCT  
 1020  
 TCCACTAAAC GTTCTGCAAT TTTAAAACCA ATCCCTTGTG CTCCGCCAGT TACTAATGCT  
 1080  
 ACTTTGTTGT TTGTCATAAA GATCACTCCT CAAATTTCTT TCCTTTAATT ACATTTTACT  
 1140  
 CCTCTTCATT TGAATAGTAC AACAAAGGTA GCTCCATTTA ACAAATATT CAGATATTTA  
 1200  
 AGGTATAGTT AAACGCACTA CCATTAGTGA TTGGCAATGC GTTTAAATGT CGTTTTAAAA  
 1260  
 GTTCTTATGT TGAATATTAT TTTTAAAGT CTCTCGATTA GTTTGTCATC AATCTTTTTT  
 1320  
 CGAGACATGG GCCTTTTGAT TCAATCGGCG GNTTCCGTGT TATCACTGAC AACTTTAGTT  
 1380  
 GTAGCTTCAT CTTTATGTAT TTCTTCGCTA AATCCTTCAA GGTTTTTAGT CGTGGGATTT  
 1440  
 TTAACCTCAG GATGTTCCAT CATGTCTTTG ACTATCAAGT TCCTTTTTAC ACGTGTCTTT  
 1500  
 ATGGTGATGC TTGATTGGC GTTCCCTTTT ACTTTTTTTG AATAGTGGGT AGGTATCTGC  
 1560  
 TGCAGCTACT AATTTNCTTC TTACCCTTAA AATAGATATT GGCTTGGAAG CAAAACCAGA  
 1620  
 GTATTTGCAG ATACAAAGTT GCATTAATAC TTAAAGCAAT AATAGCCAAT ACAAATTAAT  
 1680  
 ATTGACACCT NTTGAAATCC CTTCTTTTAA ATTAAGTCAG ATGCCAATAC GATGACAGGG  
 1740  
 TACGGATTGA AAGTATAATT ACAAATATAG AAATTATTGC CGATATAACT ATTGTTACTA  
 1800  
 TTAAATAATC AGCTCTGCTA CCTGATAATA AATAGAAAAG GCGAAAATTA GTCCATAGCA

1860  
AATTACAAAC CCACATAAAG TTATAGCCAT GAGTACTATA TAAGCTATTT GAAAATATAA  
1920  
ACCTATCTTT ATGAATGATT TTCTACATTT TTTCCATGTC TATCCCCATT ATTAATATTA  
1980  
TACTTACCTA ATATA  
1995

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGTACTTGAA CACTGTACTG CGGATGAGTT TTTTATTGAC ACGGAATTAT TAGGGTTCAA  
60  
CGGTGACTTA CCACGTTTCG TAATTACCTC CAAACGACAG CTAGTACGTT TATAAGATGG  
120  
TGTATCCGTG TATTGATCAA CATCACTATT AGTTAATAAG TTAATTGCAC CTAGATCTCC  
180  
ATTTTCCATC GCATCATTAT TTAATGGAAT ATAGATTTCT TTACCTTTAA CACGATCTGT  
240  
CACGTGAACT TGTAATACCG CTTCTCCTGT TTCAGAAATC AGCTTAACTT CTGCACCTTC  
300  
ATGAATGCCT CTATCTTCAG CAAGCTCTGG AGAAATTTCA ACAAATGCAC GTGGCACTTT  
360  
GTATTTAATC ATTGGTGTTT GATAAGTCAT ATTACCTTCA TGGAAGTGCT CTAACAATCG  
420  
ACCATTGTTT ACATGAATAT CATAAATTC ATCTTGCTTA AAGTAATTAT CAAATGATAA  
480  
TGGGAATAAT TTTGCTTTAC CATTATCAAA ATTGAATCCT TCTAAGTATA GAATAGGCTC  
540  
ATCAGTNCCA TCCNGNTTGT ACTTGNCCAT TGTAAACTAT TGAATCCTTC TANNCGATTC  
600  
ATAACTTACC CCAGCATATA GAGGTGTAA GCGTCCTACC TTCAATCCAT AATTTCACTA  
660  
GGATGCTTGT AATTCCAATC CAAATCCCTA ATCTATTAGC AATTGCTTGG AAAATTTTCC  
720  
AGTCAGGTTT TGAATACCA AGAGGTTCTA ATGCTTGGTA TAAACGTTGA ATACGACGTT  
780  
CGGTATTTGT AAAAGTACCG TCTTTTTCOA GTGAAGGACT TGCTGGCAAT ACAACATCTG  
840  
CGTATGTTGC TGTGAATGTT AAAAATTCAT CTTGGACTAC CATGAAATCT AATTTTTCAA  
900  
ACGCAGCTTG TACAAAATTA ATATTTGAAT CCACAATACC CGTATCTTCA CCATATAAGT  
960  
ACAATGAGTG TACTTCTCCG TCATGTATAC CTTCTACCAT TTCATGATTA TCTTTACCAG  
1020  
CTTTTGGATT CAATTTAACG CCATATTCTT TTTCAAATTT AGCACGAGCG AATATCATCC  
1080  
GCTTCAATAC TTTGATAACC AGTAATCTTA TCAGGCATAC TTCCCATATC ACTACATCCT  
1140  
TGAACATTAT TATGTCCACG TAATGGATAC GCACCAGTAC CAGGACGACG ATAATTACCT  
1200  
GTTACTAATA ATAAGTTTGA AATCGCTGTA CTTGAGTCAC TACCAATGTC TTGTTGTGTA

1260  
 ATACCCATTG CCCAACAAAT TACAACAGAT TCAGCTTTAG CACATTCTTC AGCAAATTTA  
 1320  
 ATCAATTCTG ATTCAGGAAT ACCTGTTGCT TCTTCAGCAA AAGCCATTGT AAATGTTTCT  
 1380  
 AATGATTTGT AATATTCATC AAAATCATCT ACCCACTCAT CAATAAATGC TTTATCGTGT  
 1440  
 AAATCATGAT CAATAATATA CTTAGTCACT GCACTTAACC ACGCTAAATC CGTACCTGGT  
 1500  
 TTAGGTTGAT AAAAACGATC CGCACGTTCT GCCATTTTCAT GTTTTCTAAT ATCAAATACA  
 1560  
 TGTATTTTTT GTCCAAATAA TTTTGTAGCA CGTTTCATGC GTGATGCGAT AACTGGATGA  
 1620  
 GCTTCGGCTG TATTGGTACC TATCAATACA GACATTGCCG CTTTTTCTAA ATCTTCAATA  
 1680  
 CTACCTGAGT CACCGCCGTG TCCAACCGTT CTAAATAAGC CTTTTGTTGC AGGTGCTTGG  
 1740  
 CAATATCTTG AACAGNTATC AACGTTATTT GTGNCAATAA CTTGGTCTTG CTTAATTTNN  
 1800  
 GGGATGNAAA TACGATTCTT CCATTCCGGC CGGTTTTAGA AGAAGGAAAT GAATTGATAG  
 1860  
 TGCATCTTGG GCCAATACTT NNNCTTTNAA TAGATGTAAA ATTATCTGCA AATGACAATT  
 1920  
 TAAAGGTTCC ATCCCATCTT  
 1940

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GATTCAACAT AACGTCGTGT CCTTCAGCAT ATATAGTATC GAATGCTATG GACGATTAAC  
 60  
 CTGACCCAGA TAAACCTGTC ATAACAATTA ATTTATTTTT AGGTAGTTCG GATATCAATA  
 120  
 TCTTTCAAGT TATGCGCAGC AGCACCTTTT ACTACTATGG ATGGNTCTTT CATTTACTTG  
 180  
 TCACCCNTCT GCTTTTAATT CAAATAACAT ATCTCTTAAT TCNGTAGCTT TCTCGAAATC  
 240  
 TAAATCTTTC GCTGCTTGTT TCATTTCTTT TTCTATATTG TCGATTGTCT TTNGACGTGC  
 300  
 TCTTTTCGGC ATCTTCTTAG GTATCACAGT TTGTGCTTNG TCATNATTTT CGTCATTTTC  
 360  
 AACAGTAGCA CTAATTAAAT CATGTACTTN TTTATTAATT GTTTTAGGTG TAATACCATG  
 420  
 TTTTTCATTA TGTTTCATCT GTATTTCTCG ACGACGTTGT GTCTCATCAA TTGCATACTT  
 480  
 CATNGAATCA GTCATATTAT CGGCATACAT AATGANTTCA CATTTATCGN TACGCTCGTG  
 540  
 CCGAATCGGC ACGAGCTCGT ACCTATTGTT TGAATTAATG AGCGGNTAGA ACGTAAAAAT  
 600  
 CCTTCTTTAT CTGCATCTAA TATGACAAGT AGAGAACTT CTGGTATATC AATACCCTCT  
 660  
 ACTTAATAAA TTAATACCTA CGATAACATC ATATGTACCC ATTGTAAGT CTCTAATTAT

720  
TTCGATTCGT TCGTAATGTC TTGATTTCTG AATGCAGATA ATTAACTTTA ATACCCGCTT  
780  
CTTTCATGTA TGTGGTTAAA TCTTCACTCA TCTTTTtagT GAGCGTTGTA ACAAGTACGC  
840  
TCGTGCC  
847

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CCGCTTCGCA CGAGCNAAGG CTTTTATTGC ANCCCTCGCA TCTTCTTTAG CTTACACTAA  
60  
ATCTTTGATG TCTTGTAATG CTTGTGCAAG TTGTGCTTTG GCTTGTTCAA TTTCTTCTTT  
120  
AGTCATCGCA TTGTTAATGT CGTTATGACC TTGTTGAAGT ATTTGANTAA TTCGATCTTT  
180  
AAGCGCTTGT TTNTCCTTAT CTGTTAGATT TGGATTGTGA TCGATTTCGN CAATTAATGC  
240  
TTGAACTTGT TTATCAACAT CTTGTTTCGC ATCTTCTTTA GCTTACACTA AATCTTTAAT  
300  
GTCTTGTAAT GCTTGCGCAA GTTGTGCTTT AGCTTGTTCA ATTTCTTCTT TAGTCAGCGC  
360  
ATTGTTAATG TCGTTATGAC CTTGTTGAAG TATTTGATTA ATACGATCTT TTAAGTGCTT  
420  
GTTTTTCCTT ATCTGTTAGA TTTGGATTTT GATCAATTTT GTCAATTAAT GCTTGAACCT  
480  
GCTTATCAAC GTCTTTATTG GCATCAATTT TNGCTTTNGG TATTTCATTA GCANGCACTN  
540  
GTTCAATCGC GTGGTTGCCT GCTGTTTGAA CTTGAGATAC AGCCTGATTA CTTGTTGCTT  
600  
TATTAATGTT GTTGATGATG CTGGTTTGCC AATTCTTCTT GCTTTATTTT TTCGGCAATA  
660  
AGCTTGCTTT GATCCGTCGC ATTTGAAGCT TCGATTCTT TTAGCTTATT AGCTAAAGCT  
720  
TGATTAATTG ATTGAATTGC CTTGTCTTTA GCATCTTGTA GTCGTTGATC ACCATTAAGA  
780  
TTATGGATTG CATCATTGAC TGCTTGGATT GCGCCATTGA TATCATTAC ATTTGTGTTA  
840  
TCACTATTTA GCAATGTATT TGCTAGACGT TTGGCATCAT CGAAGTTTGT TTTAGCATTA  
900  
TCGTCAGCGT TTTGGTAATT GACAGTTTGC TCTGCATTTG GAATTTTCATT GTCAACTAAA  
960  
TGTTTCAATG TTTCCATTGC ATCATTTAAG TCAATTTGAT TATTAACAAT ATCTGTTACA  
1020  
TCTGATACAG TATCGGCATT GTTAATTGCT TTATGTGCAA GATCTTGTTG CTGTTGATTT  
1080  
AATCCATTTA ACGAATTAAC AAACGCATTT GCTTTATCCT TTGGCATTTG CAAGGTTTTG  
1140  
GTCTCCATTT AATGCATTTT GAGCATCGAT AATATTTTGT TTCAATTGCT CTGCTTCAGC  
1200  
TTTTGCAATT GCATTACTTG CACTTTATCT AACTCATGTG CTGCATTGCG AATGCATATC

1260  
ATAATTTGCT TTCAATGTCA TCTGCATGAT GTATTGTGCT  
1300

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CTTTTCATCT CTTGACCTG TGTAATACCT TTGATCAGCT GCACAAATAG ACAAGTATAA  
60  
AGGTCTTACG ATGACATGAT TACCATAAAT ATCAACATTA TTATATGTGA CGTCGAACTG  
120  
TCTCGGTGCA ACGAGTTGAT ATACTTGATT AATCATCGGC AATATCACCT TGAATAATGG  
180  
NATTTGCTAC TTTNAANTCA TNCGGGGTTG TCACTTTAAT GTTGTATAGT TCTCCACGTA  
240  
CCAATTTAAC TGCATGTCCA GATTGACAA TTATTTTACA TGCATCTGAT AAGATTTCTT  
300  
TNTGGTTCAC TACTTAAGGC GCGATAACTA TCTTGTAATA ATTTAATATT AAATGATTGT  
360  
GGTGTGTTGGC CTTGATACAT TTCATTCTT ACAGGGATAC TGTGTATGTT CTGTTTATCT  
420  
TTAGACATTA CAATCGTATC AATTGCTTCA ATGACTGTAT CTACTGCACC ATATTNNGCT  
480  
GCTACTTCAA TGTTCTCTTT AATAATACGT TGAGTTAAAA ATGGTCTTAC GGCATCATGA  
540  
GTTACAATCA CATCATCATT ATTAATTCCA TTTACATTGC GAATATGGTC GATAATGTTC  
600  
ATAATTGTTT CGTTTCGATC CGNACCACCT GCAACTACTT TGACACGTTG ATCTGTAATG  
660  
TTATATTTTTT TTAAAATATC CTGTGTATGG GAAATCCACT GTGCTGGCGT TGCGATAATA  
720  
ATCTCATTAA ATTCACTCAC TAAAATGAAC TTCTCAATTG TATGGATTAA AATCGGTTTA  
780  
TTATCAATAT CTAAAAATTG TTTTGGGTAA TGGCACGTTC CCCATTCTCG AACCAATACC  
840  
TCCTGCTAAA ATACCTGCAT AAATCATGTT GGCCTCCATC CTGTCATTAC ATCATTTCCA  
900  
TTTATACATT ACTGACCTAT GCCCGCACAT AAGCCTAACC TATTGCTCAC TNGNCTCTTN  
960  
TATTAATCCA AAGATAGTTG TCACAATAGT GTGATAATTN TTTATAAAAA TGTATTTNTG  
1020  
NNACTGACCA NTCTAAGTTG TTTTGGCATG CAGCTAATCA TTAACCTCTGA CGATATTAAA  
1080  
TTGTAAAGG TATTAATGTT TACTCTTTCA CAAATTCATT ATTACTGCCA TCATTTNNCC  
1140  
ATATATTATA ATAAATTTAT CTTATTAAGT GGCTGNACTT GATTTTCACT TTAAAAATTA  
1200  
TCAAATATTG CCATCTCATT TTAAGNATAC AAAATGCAAA ACAACCGATT CACAAGCATA  
1260  
TTTCACACAA GTAAACCGGC TATTTATCAA CGTATATTCG AAGATGAATT ATTTGATAG  
1320  
TATCTTGTAG ACCAGNCGGC ATTCGCACTT TCAATAGCNT ATTAACCTAT ACCAGNGGTT



1380

TCGTCCTCNA NGGTGCATAC TAATAAATCG TAAACNTGAC TTTAG

1425

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TTTCTTACCT TTAATAATTG GTAATTCATC TTCCATCCTC TTGTTTGATC TGTGTCGCAT  
60  
AAGCTTCATC AAATAGTACA TCAGTACGTG GAACACCTGT AGGCACTACA TTTTCTCTT  
120  
TAATACCAA TGCTTCAGCG TAGAATGGAA TATCGGTTTC AGATGATACA TAAGCTTTGG  
180  
CACGAGCTAC GATGATTTAA TGAATCAATA AATGGTCCAC CCTTTTACC AGTACGACTA  
240  
AAGCCAACTG TTTTAAAGGC ACCAACGGCA TGCCATACTT GAATAACTTC TTGAGAACGT  
300  
CTAAAACGCA CTGTATAAAT CAAGGGGTGA AAGTCATCAA CAAAGATGTA GTCTGCCTTC  
360  
CCAAGTAAAT ATGGCAATCT AAACCTGTCTG ATGATGCCAC GTCTATCTGT AATATTCGCT  
420  
TTAAAACAG TGTGAATATC ATACTTTTTA TCTAAATTTT GACGTAACAT TTCGTTATAG  
480  
ATGTATTCAA AGTTTCCAGA CATCGTTGGT CTAGAGTCTG ATGTGAACAA CACCGTATTC  
540  
CCTTTTTTCA AGGGTGAAAA ATTTGTCGTG ATTAATATC GCNTNAAAAA TAAATTGTCT  
600  
TTGTTATTAA ATGAATGTTT GCGGAAATAC NTACGTAATT CTTTAATATT TACGAACGAA  
660  
AATAAATACT TTTAACCTCC GGAGTCGTTA CNACCAACAT CAAGGACAAA TTCATTAAAC  
720  
TTTCGNAGAA ATTTCAGGGT GTAACAGTAT AAACCGTTTT CTTCGAAATG CCGCCTTTTC  
780  
TAAATTCTTT TAGGTAAGTC TGCAATAAGA AATTGATTTT ACCATTTTGT GTTTCTAATT  
840  
CGTTGTATTG TTCTTCTTGT TCTGGCTTTA GATTTTGATA TGCATCATTG ATCACATCTG  
900  
GGTTTANCTG TGCAATATAA TCAAGTTCTT GCTCATTAC TAATAAGTAC TTATCTTCAG  
960  
GTAAGTAATA ACCATTATCT AAGATAGCTA CATTGAAACG ACAAACGAAT TGATTCCCAT  
1020  
CTATTTTGAC ATCATTCGCC TTCATTGTAC GTGTCTCAGT TAAATTTCTT AATACAAAAT  
1080  
TACTATCTTC TAAATCTAGG TTTTCACTAT GTCCTTCAAC GAATAACTGA ACACGTTCCC  
1140  
AATAGATTTT ATCTATATAT ATCTTACTTT TANCCAACGT TAATTCATCC TTTTCTATTT  
1200  
ACATAATCCA TTTTAATACT GTTTTACCCC AAGATGTAGA CAGGTCTGCT TCAAAGCTT  
1260  
CTGTAAGATC ATNAATTGTT GCAATTTTCA ATTCTTGACC TTTTAACAAC GCTAATTTAT  
1320  
CTACAATATC TGGGTATTGA ATGTATAAGT CTACAACATC TTGGAAATCT TGTGACCCAC

1380  
TTCGACTACT ACCAATCAAC GTTAGTCCTT TTTCCAATAC TAGACGTGTA TTAAC TTCTA  
1440  
CTGGGAACTC ACTTACACCT AACAGTGCAA TGCTTCCTTC TGGTGAAATA TANTCAATCA  
1500  
TTTGATTTAT TGCTGATTGG NTACCACGCC CACCAACGCA CTCAAATGCA TGATCANATG  
1560  
TTAAGCCTTC AGGTATTTTA TTAATAAAGA AGACATCATC AACAAATGAG AAGTGA CTCA  
1620  
ATTTATAATC TTGGTNNACC AAAGACATAT ATGGNAGACT TCTGGATATT AATNGACGGA  
1680  
ATAAAATGGC TGTAATGTAA CCTAAGTTAC CATCACCCCA AATACCAAAT GTATTTTTAT  
1740  
TTGAAATAGA TTTCTTTTCA ACAACGACGA ATAGCATGCA AACTTACTGT TACAAGCTCT  
1800  
GTAGATGAAA TAATACTTAA ATCAATATCA TCAGGTAGTG GTACAGCTCT ATCATGATTT  
1860  
AGCAACACAA AATCTTGCAT AAACCCATCA TGTCCACTTG ATCTGAAGTA GCTCGATTTT  
1920  
AAATAGTTTT CAGCAATGAC ATCGTCTTTT TCTGTCGGCG TATTCGGTAC CATAACTACT  
1980  
TTTGTACCTT TATTAAACAC ACCTTTACTG TCAAATACGA CCTCACCAAC ACCTTCATGA  
2040  
ATTAAAGACA TTGGCAATTT CTGAGATAAG ACATTCTCAT CACGGCTACC AGTATAATAT  
2100  
CTTTGATCGG CAGCACAAAT TGACATATAT AAAGGACGTA CAATGACATA GTCACTGTAA  
2160  
ATATCTACGT TGTTATACGT AACTTCAAAT TGTCTAGGTG CAACTAATTG ATATACTTGA  
2220  
TTAATCATCG GCCAATACCA CCTCGAATAA TAGCATTTCG TACTTTTTAA TCGTAAGGTG  
2280  
TTGTTACTTT AATGTTATAT AACTCACCTT TTACAAGTCG AACCGGTTTG TTTGTTTCTA  
2340  
CAATAATCTT ACAAGCATCA GATAAAATAC TCTTTTGCTC ATCACTCAAC TGTGCATAGC  
2400  
TTTCTTTTAA TAAATTAATA TTAAACGATT GAGGTGTTTG ACCTTGGTAC ATTTCAATTAC  
2460  
GCACTGGAAT TGCATCAATC GTTTGATTAT CTTTAGATGT AACAATCGTA TCTATAGCAT  
2520  
CAATCACTGT ATCTACTGCA CCGTACTCTA AAGCAGCTTG AATATTTTCT TTAATAATAC  
2580  
GATGCGTTAA AAATGGTCTA ACTGCATCAT GTGTCACAAT GACATCGTCA TCGTTAATAC  
2640  
CATTTGTTGA TTCAATATGT TTAACGATAT TCATAATTGT ATCGTTACGA TCGCTACCAC  
2700  
CTTGAATGAC TTCAATTCTT TCATCAGAAA TTTTGAATTT TCTAAGTGTA TCTTTCGTAT  
2760  
GCGTCATCCA TTGTTGTGGC GTCGCGATAA TAATTTTTTC AAAATCATTAA ATTAAAATAA  
2820  
ATTTTTCTTA ATGTATGGAT TAAAATCGGN TTGTTGTCTA AATCTAAAAA TNGTTTAGGT  
2880  
AAAGGGTACG GTTACCCATT CCTTGAGCCT ATACCTCCAG CTAGAATACC AGCGTATTTT  
2940  
ATAAAATACT TCCTCCATTC AACTATATCT ATATTTAATT ATTTAAATTT CGTTGCATTT  
3000  
TCCAATTGAA AACTCATTTT AAAATCAAAA CTCTAAATGT CTGTGTATTA CTTAAAATTA  
3060  
TACATATTTT GCTTATATTT TAGCATATTT TGTTTAAACC TATATTACAT TATATCAGAC  
3120  
GTTTTCATAC ACAAATAATA ACATACAAGC AAACATTTTCG  
3160

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
AAAAAACAA TTTANCCCAT NACNACTTGT CGTTAATTAT TCATACGAAA TACATGATTA
60
ATGTACCACT TTAACATAAC AAAAAATCGT TATCCATTCA TAACGTATGT GTTTACACAT
120
TTATGAATTA GATAACGATT GGATCGATTA TTTTATTTTA CAAAATGACA ATTCAGTTGG
180
AAGGTGATTG CTTTTGATTG AATCGCCTTA TGCATGAAAA ATCAAAAGGT TATTCTCATT
240
GTATAGTCCT GCTTCTCATC ATGACATGTT GCTCACTTCA TTGTCAGAAC CCTTCTTGAA
300
AACTATGCCT TATGACTCAT TTGCATGGCA AGTAATATAT GCCAACATTA GCGTCTAAAC
360
AAATCTTNGA CTAAACGTTT ACTNGAGCGA CCATCTGGAT ATTTAAAANG TTTAGCTAAG
420
AATGGTACAA CTTTTTCAAC CTCATAATCT TCAGTGTCCTA AAGCATCCAT TAATGCATCA
480
AAGGATTGTA CAATTTTACC TGGAACAAAT GATCCATATG GTTCATAGAA ATCACGCGTC
540
GTAATGTAAT CTTCTAAGTC AAATGCATAG AAAATCATCG GCTTTTTTAAA TACTGCATAT
600
TCATATATTA AAGATGAATA ATCACTAATC AACAAGTCTG TAACAAAGAG AATATCGTTA
660
ACTTCACGAT GATCTGACAC ATCGATAAAG TATTGTCTAT GTTCACGTGA AATATTAAGT
720
CTATTTTTTA CGAACGGATG NATTTTGAAT AACACAACTG NATTATGCTT CTCGCAGGAT
780
CTTGCTAAAC GTTCAAAATC AATTTTAAAA AATGGATAAT GTGCCGTACC GTGACCATTA
840
CCTCTAAATG TCGGTGCGAA TAGAATAACT TTCTTACCTT TTATAATTGG CAATTCATCT
900
TCCATCTCTT GTTTAATTTG TGTTGCATAA GCTTCATCAA ATAGTACATC AGTACGTGGT
960
ACACCTGTTG GTACAACATT TTCTTCTCTA ATTCCAAATG CTTCAGCATA AAATGGAATA
1020
TCGGGTTTCT GATGAAACAT ATGCTTTCGG TGTAACCTACG ATGGGTTTTA ATGAATCGAT
1080
AAACGGACCA CCTTTTTNAC CTGTACGACT AAAGCCAACT GTTTTAAAGG CACCAACAGC
1140
ATGNCACACT TGAATAATTT CTTGTGATGG TCTAAAGCGA ACCGTATAAA TTAATGGATG
1200
GAAATCATCA ACAAAAATAT AATCGGCCTT ACCAAGTAAA TATGGCAATC TAACTTGTC
1260
TCTCCATTTG CGTCTATCCG TAATATTCGC CTTAAATACC GTTTTAATAT CATAATCAAA
1320
ATCTACTTTG TGGCGTAGTA ACTCATCATA TACATACTTG AAATTCCCTG ATAAATTCGG
1380
ACGCGAATCT GATGTGAATA ATATTGTTNT GCTTCTTTTA ATATGTAGTA ACTTTGTAAT
1440
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ATTAAAAATA GCTTTAAATA AGAAACTTCT ACTTTCAAAT GAAGCTTTAT GACCTTGTTT  
 1500  
 ATGAAGCCAG TGTGCACTTG GCGCAATGAC CCTGATTTCT CTTGAGGTAA GGTGATTTCA  
 1560  
 ATATCAAATA CAAATTCGGN TAACCGTCAC TTGGCTATCT CCGGAGTAAT GGTATTAGAC  
 1620  
 CGTATGTTGT GATACGCCAC CTTTACGGAA AACTTTAGCA TCATACGCTA ATAAAG  
 1676

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GATTTCGAGCT CGGTACCGGG GATCCTCTAG AGTCGACCTG CAAGCTATAC CAAGCTAGAG  
 60  
 TACTGCGACG CAAACTAGTG CAACACCTAA GGCTGTTACA GCTTGGAAGT CGATAAAATA  
 120  
 GTTGAAAAAG AGCAAGCGAT TTTTGAACGT GTTAACGAAG TTGAACAACA AATCAATGGC  
 180  
 GCTGACCTTG TTAAAGGTAA TTCAACAACA AATTGGCAAA AGTCTAAACT TACAGATGAT  
 240  
 TACGGTAAAG CAATCGAATC GTCTGAGCAG TCCATAGATA GCGTTTTAAG CACAGTTAAC  
 300  
 ACATCTAGGA TTATTCATAT TACTAATGCA ACAGATGCGC CAGAAAAGAC GGATATAGGC  
 360  
 ACGTTAGAGA AGCCTGGACA AGATGGTGTT GATGACGGTT CTTGTTCTGA TGAATCAACT  
 420  
 TATACATCAA GCAAATCTGG TGTGTTAGTT GTTTATGTTG TTGATAATAA TACTGCTCGG  
 480  
 TGCAACATGG TACCCAGACG ATTCAAACGA TGAGTTCACA AAATACAAAN TCTTACGGCA  
 540  
 CATGGTACCC GTTTTATTAA AAAGAATGAT GGAAACTTAA CTAGCAATTT GGTGAGGA  
 600  
 ACGTCTTACA ACGCTTTAAA TCAAGCTAAG CAGTATGTAG ATGATAAATT CGGAACAACG  
 660  
 AGCTGGCAAC AACATAAGAT GACAGAGCCG AACGGTCAAT CAATTCAAGT TAACTTAAAT  
 720  
 AATGCGCAAG GCGATTTGGG ATATTTAACT GCTGGTAATT ACTATGCAAC AAGAGTGCCG  
 780  
 GATTTACCAG GTAGCGTTGA AAGTTATGAG GGTTATTTAT CCGTATTCGT TAAAGATGAT  
 840  
 ACAACAAGC TATTTAACTT CACACCTTAT AACTCTAAAA AGATTTACAC ACGATCAATC  
 900  
 ACAAACGGAA GACTTGAGCA ACAGTGGACA GTTCCTAATG AACATAAGTC AACGGTATTG  
 960  
 TTCGACGGTG GAGCAAATGG TGTAGGTACA ACAATCAATC TAACTGAACC GTACACAAAC  
 1020  
 TATTCTATTT TGTTGGTAAG TGGAACCTAT CCAGGTGGCG TTATTGAGGG ATTCGGACTA  
 1080  
 ACCGCATTAC CTAATGCAAT TCAATTAACC AAACCGAATG TAGTTGACTC AGACGGTANC  
 1140  
 GGTGGCGGTA TTTATGAGTG TTTACTATCA AAAACAAGTA GTACCCACTT TAAGAATAGA  
 1200

CAACGATGTG TATTTTCGATT TAGGCAAAAC ATCAGGTTCT GGAACGAATG CCAACAAAAGT  
 1260  
 TACTATAACT AAAATTATGG GGTGGAAATA ATGAAAATAA CAGTAAACGA TAAAAACGAA  
 1320  
 GTTATCGGAT ACGTTAATAC TGGCGGTTTA CGCAATAGTT TAGATGTAGA TGATAACAAT  
 1380  
 GTGCCTATCA AATTCAAAGA AGAGTTTGAA CCTAGAAAAGT TTGTTTTTCAC TAACGGCGAA  
 1440  
 ATTAAATATA ACAGCAATTT TGAAAAAGAA GACGTACCGA ATGCATCAAG CCAACAAAAGT  
 1500  
 GAATCAGATT TGAGTGATGA AGAACTTCGC GGAATGGTTG CGAGTATGCA AATGCAGGTG  
 1560  
 GCACAAGTAA ACGTATTAAC AATGGAATTA GCTCAACAAA ACGCTATGTT AACACAACAG  
 1620  
 TTGACTGAAC TGAAAACTAA CAAAACAAGT ACTGAGGGGG ACGTTTAATG ATGAAGATGA  
 1680  
 TTTATCCGAC TTTTAAAGAC ATCAAAACTT TTTATGTTTG GGGTACTAT AAAAACGAGC  
 1740  
 AAATTAAGTG GTACGTAGAC AAGGGTTTAA TCGATAAAGA AGAATACGCT TTAATCACTG  
 1800  
 GAGAAAAATA TCCAGAAACA AAAGATGAAA AGTCACAGGT GTAATGCTTG TGGCTTTTTA  
 1860  
 ATTTAACAAA AAGTAGGTGG CGTAATGTTT GGTTTTACCA AACGACATGA ACAAGATTGG  
 1920  
 CGTTTAACGC GATTAGAAGA AAATGATAAG ACTATGTTTG AAAAATTCGA CAGAATAGAA  
 1980  
 GATAGCTTA GAGCGCAAGA AAAGATTTAT GACAAATTAG ATAGAAATTT TGAAGAATT  
 2040  
 AAAGCGCGAC AAGGTAGAAG ATGAAAAGAA TAAAGAAAAG AATGCCAAGA ATATTAGAGA  
 2100  
 CATAAAAATG TGGATTCTCG GTTTGATAGG GACTATCTTC AGTACGATTG TCATAGCTTT  
 2160  
 ACTAAGAACT ATTTTTGGTA TTTAAAGGAG GTGATTACCA TGCTTAAAGG GGATTTTAGG  
 2220  
 ATATAGCTNC TGGGCGGTCC TCCTGGTTGG GGGTAAATGT AAATAACAGT TAAGAGTCAG  
 2280  
 TGCTCCGGCA CTGGCTTTTT ATTTTGATTG AAATGAGGTG CATACTGGG ATTACCTAAT  
 2340  
 CCAAAGACTA GAAAGCCTAC AGCTAGTGAA GTGGTGGAGT GGGCAAAGTC GAATATTGGT  
 2400  
 AAGAGGATTA ATATAGATAA TTATCGGGGC AGTCAATGTT GGGATACACC TAACTTTATT  
 2460  
 TTTAAAAGAT ATTGGGGTTT TGTAAACATG GGCAATGCTA AGGATATGGC TAATTACAGA  
 2520  
 TATCCTAAGG GTTTCCGATT CTATCGTTAT TCATCTGGAT TTGTTCCGGA ACCCGGAGAC  
 2580  
 ATAGCAGTTT GGCACCCTGG CAACGGAATA GGTTCGGACG GACACACCGC AATAGTAGTA  
 2640  
 GGACCATCTA ATAAAAGTTA TTTTATAGC GTTGACCAAA ACTGGGTAA TTCTAATAGT  
 2700  
 TGGACAGGTT CTCCAGGAAG ATTAGTAAGA CACCCTTATG TAAGTGTTAC AGGCTTTGTT  
 2760  
 AGGCCTCCGT ACTCAAAAGA TACTAGCAAA CCTAGTAGTA CTGATACAAG TTCAGCATCA  
 2820  
 AAAAGCCAAT GACTCAACAA TTACTGGCGA AGCGAAGAAA CCGCAATTTA AAGAAGTTAA  
 2880  
 AACAGTAAAA TACACTGCTT ACAGCAATGT TTAGATAAAG AAGAGCACTT CATTGATCAT  
 2940  
 ATAGTTGTAA TGGGTGATGA ACGCTCAGAT ATTCAAGGAT TATATATAAA AGAATCAATG  
 3000  
 CATATGCGTT CTGTAGACGA ACTTTATACG CAAAGAAAATA AGTTTATAAG CGATTATGAA

3060  
ATACCGCATT TATATGTCGA TAGAGAGGCT ACAGGAATTC CGGAATTCCG  
3110

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AAATTATATA TAATAACGTC GTTTTAACTA AGGCAACATA AGGAGGTGCG TCAATTGGCT  
60  
CAAGCAAAAA AGAAATCGAC AGCTAAGAAA AAAACAGCAT CAAAAAAAAG AACAAATTCA  
120  
AGGAAAAAGA AGAATGATAA TCCGATACGT TATGTCATAG CTATTTTAGT AGTTGTATTA  
180  
ATGGTGTTGG GTGTTTTCCA ATTAGGAATA ATCGGTCGTC TAATTGACAG CTTCTTTAAT  
240  
TATTTATTTG GGTACAGTAG ATATTTAACA TATATTTTAG TACTCTTAGC AACTGGTTTT  
300  
ATTACATACT CTAAACGTAT TCCTAAAACT AGACGAACGG CTGGTTCGAT TGTATTGCAA  
360  
ATTGCATTGC TATTTGTATC ACAGTTAGTT TTTCATTTTA ATAGTGGTAT CAAAGCTGAA  
420  
AGAGAACCTG TACTTTCTTA TGTATATCAG TCATACCAAC ACAGTCATTT TCCAAATTTT  
480  
GGTGGCGGTG TATTAGGTTT TTATTTATTA GAGTTAAGCG TACCTTTAAT TTCATTATTT  
540  
GGTGATGTA TTATTACTAT TTTATTATTA TGCTCAAGTG TTATTTTATT AACAAACCAT  
600  
CAACATCGTG ATGTTGCAAA AGTTGCACTG GAAAATATAA AAGCTTGGTT TGGTTCATTT  
660  
AATGAAAAAA TGTCGAAAG AAACCAAGAA AAACAATTGA AGCGTGAAGA AAAAGCGAGA  
720  
CTTAAAGAAG AACAAAAGGC ACGTCAAAAT GAACAGCCAC AAATAAAAAGA TGTGAGTGAT  
780  
TTTACGGAAG TGCTCAAGA AAGAGATATT CCAATTTATG GGCATACTGA AAATGAAAGT  
840  
AAAAGCCAGT GTCAACCAAG TCGAAAAAAA CGAGTGTTTG ATGCAGAGAA TAGTTCGAAT  
900  
AACATCGTAA ATCATCAAGC AGATCAGCAA GAGCAATTAA CAGAACAAAC TCATAACAGT  
960  
GTTGAAAGTG AAAACACTAT TGAAGAAGCT GGTGAAGTTA CGAATGTATC GTATGTTGTT  
1020  
CCACCGTTAA CTTTACTTAA TCAACCTGCA AAACAAAAAG CAACATCTAA AGCTGAAGTA  
1080  
CAACGTAAAG GACAAGTACC AAAGAGATAC ATNAAAAGAT TTTGGGGTNA AATCCNAAAG  
1140  
TNGACACAAA TNAAATTGTC CTNCAGTAAC TCAATATGAA ATCCCACCCA GCTCAANGGG  
1200  
GGTTNAAAGT GAGTAAAAAT GTAAACTTTG CATAATGATA TTGCATTAGC TTTAGCACCA  
1260  
AAAGATGTTA GAATCGAAGC ACCAATACCT GGTGCTCTG CAGTAGGTAT TGAAGTGCCA  
1320  
AATGAGAAAA TTTCATTAGT TTTACTAAAA GAAGTTTTAG ATGAAAAATT CCCGTCTAAT

1380  
 AATAAACTAG AAGTTGGATT AGGAAGAGAT ATATCAGGTG ATCCAATTAC TGTTCCACTA  
 1440  
 AATGAAATGC CACACTTATT GGTGGCAGGA TCGACGGGTA GTGGTAAATC TGTTTGTATA  
 1500  
 AATGGTATTA TTACAAGTAT TTTATTAAAT GCTAAGCCGC ATGAAGTTAA ACTTATGTTA  
 1560  
 ATCGATCCGA AAATGGTTGA ACTAAATGTT TATAACGNNN NNNCACATTT ATTAATTCCG  
 1620  
 GTTGTTACAA ATCCTCATAA AGCTGCTCAA GCTTTAGAAA AAATTGTAGC TGAGATGGAA  
 1680  
 AGACGTTATG ATTTATTCCA ACATTCATCA ACTAGAAATA TTAAAGGTTA TAACGAATTA  
 1740  
 ATCCGTAAGC AAAATCAAGA ATTAGATGAG AAGCAACCAG AATTACCTTA TATCGTTGTT  
 1800  
 ATTGTAGATG AGCTTGCAGA TTTAATGATG GTAGCTGGTA AAGAAGTTGA AAATGCGATT  
 1860  
 CAACGTATCA CACAAATGGC ACGTGCAGCA GGTATACATT TGATTGTAGC AACACAAAGA  
 1920  
 CCTTCTGTGG ATGTAATTAC AGGTATCATT AAAAATAACA TTCCATCTAG AATTGCTTTT  
 1980  
 GCTGTGAGTT CTCAAACAGA TTCAAGAACT ATTATTGGTA CTGGCGGCGC AGAAAAGTTA  
 2040  
 CTTGGTAAAG GGTGACATGT TATACGTTGG AAATGGTGAT TCATCACAAA CACGTATTCC  
 2100  
 AAGGGGCGTT TTTAAGTGAC CAAGAGGTGC AAGATGTTGT AAATTATGTA GTAGAACAAC  
 2160  
 AACAGGCAAA TTATGTAAAA GAAATGGAAC CAGATGCACC AGTGGATAAA TCGGAAATGA  
 2220  
 AAAGTGAAGA TGCTTTATAT GATGAAGCGT ATTTGTTTGT TGTTGAACAA CAAAAGGCAA  
 2280  
 GTACATCATT GTTACAACGC CAATTTAGAA TTGGTTATAA TAGAGCATCT AGGTTGATGG  
 2340  
 ATGATTTAGA ACGCAATCAG GTAATCGGTC CACAAAAAGG AAGCAAGCCT AGACAAGTTT  
 2400  
 TAATAGATCT TAATAATGAC GAGGTGTAAA AAATTTGATT AAGCAAATA AATTGGAATA  
 2460  
 TGGTGACCAA CTATCCAAGT AATTTATCAA TTGCCAGAGA ATTAAATGTA AAAACCGACG  
 2520  
 ATGTTTATGA AGCAATTCAG GCATTGATTA CTG  
 2553

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCGTACATTA ACAACCTGGA TTAATTACAG ATTACGTTTT GTCTCATCTA AAAATTGTTG  
 60  
 ATAATCTTTG ATCAATTTCC AAATCTGTAC GTATGTATTA TCTTAGTAGT AGTTTAATAT  
 120  
 GCACTAAATA CTTGCAATTG ATATTTACCA TATTTATTGT CAAATCCAAT TATCTTGTGT  
 180  
 TTTTCATAAA ACGATTGCTT TAAATAATCT TCTAACACAT CAAACATCGT ATTATCACCG

240  
 ACATGGTGCC CGTATAAAAT AGTATTATGA TTTAAATTCT NCAATTCATT TCTAAAATCC  
 300  
 ATAAAAATAC TACCTTTACG TCGATGTTCT CGCTCAAAAT CTAAATTTAA ATAATCGTGA  
 360  
 TTTGTCTTAC CTTGTAGTAC TGGATAANTT AATGATGTTT CTGATAATTT TATCCATCCA  
 420  
 ACAATGTCTT TATTTATTTT TTCAAGTGAT TCAAATTGTG GTCTCACATG TTCTTGATGT  
 480  
 TTGNTCATCA GCATNTGAAA TTTNTGTTGT AATTTCTCAT AANTTGCGCG TTCTTGCTTG  
 540  
 TCTTCAATAT ATGTTTGAAC AATTTTGTAA CCAAAAATGA TAATAATTAC AACCAATAAA  
 600  
 ATTTGTACAA TAGTTAAAAA TCGCTTCATT CTCATAAAAA CCCTCTTTAA TAAACAANTT  
 660  
 TCTTCAGTCA TCACTAAACC AGTTGTTGTA CCGTTTTAGA TTCGATTTCTG TTGACTTTGA  
 720  
 CAAATTAAGT AAATTAGCAT TGGACCACCG ACAATCATTAA AAATAGCATT GGCTGGAATT  
 780  
 TCTAAAGGAG GCTGTATCAC TCGTCCTAAT AAATCAGCCA CTAACAATAG CCATGCACCA  
 840  
 ATAAGTGTAG AAAACGGAAT AAGTACTCTG TAATTGCCCC CAACTAGCTT TCTAACCACA  
 900  
 TGTGGCACAA TAATACCTAA AAAGGCTAGT TGTCCAACAA TCGCAACAGT TGCACTTGCT  
 960  
 AAAAATACTG CTAATAAACC TGTTAACCAT CTGTAACGAT CAATATTAAA ACCGATACTT  
 1020  
 CGCGCTTGTA TGTCGTCTAA ATTTAGTAAA TTCAATTTAG GGGACAATAG TAATGTTAAT  
 1080  
 ATTAATCCCA ATAATGCTGA TACTGCTAAT ATGTATACGT CGCTCCATAT TTTCATTGTT  
 1140  
 AAGCCTTGAG GAATTTTCAT TAAAGGGTTT TGAGTTAAAA TTTCTAAAC ACCATTTAAT  
 1200  
 AATACGNATA ACGCAACACC TACTAATATC ATACTTACAG CATTGAATCT AAATTTAGAA  
 1260  
 TGCAACAATA TAATTATTAA AAATGGTATT AAACCTCCAA TAAAACTTAA TAATGGTAAG  
 1320  
 TAAAAGTACA ATTGTGGAAT AAACAACATA CCAAGTGCTC TCATTATAAG TGCACCTGAG  
 1380  
 GAAACGCCAA TGATATTCGC CTCTGCCAAA GGATTTTGTA GTCCTGCTTG TAATAATGCT  
 1440  
 CCAGAACTG CTAACATTGC GCCANCCATC AATGCAANTA ATAGACGTGC CAATCCCCAA  
 1500  
 TCAATGATTG AATCCACTGC TTCATTGCTA CCAGTTGTAA ATTTTGTAAG TAGGTCATTA  
 1560  
 AATGACAATT TAATTGTACC GGTTACAAAC GAAATATAAG CAGTTGCGAT TAAAATGACT  
 1620  
 AACAAACATA AAAATAGTAG TTTCTTTTAA TTTTATCA TCAG  
 1664

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:



Val	Leu	His	Xaa	Ile	Arg	Glu	Ile	Leu	Leu	Gln	Leu	Val	His	His	Ser
1				5					10					15	
Asp	Xaa	Gly	Xaa	Gly	Ile	Gln	Pro	Pro	Lys	Phe	Phe	Gln	Pro	Gly	Asp
		20					25					30			
Xaa	Xaa	Lys	Val	Thr	Ile	Asp	Asn	Ile	Gly	Thr	Leu	Thr	Thr	Tyr	Ile
		35				40						45			
Xaa	Lys														
	50														

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Val	Pro	Ile	Lys	Ala	Val	Ile	Ala	Gln	Thr	Met	Thr	Thr	Leu	Pro	Arg
1				5				10						15	
Val	Ile	Asn	Ile	Lys	Arg	Leu	Thr	Ser	Gly	Leu	Asn	Lys	Pro	Leu	Ser
		20					25					30			
Phe	Met	Met	Pro	Lys	Lys	Ile	Met	Ala	Xaa	Ile	Asn	Ile	Ile	Thr	Thr
		35				40						45			
Xaa	Met	Xaa													
	50														

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Val	Ile	Lys	Phe	Lys	Asn	Val	Thr	Lys	Arg	Tyr	Gly	Lys	His	Val	Ala
1				5				10					15		
Val	Asp	Asn	Ile	Ser	Phe	Asn	Ile	Asn	Glu	Gly	Glu	Phe	Phe	Val	Leu
		20					25					30			
Ile	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Thr	Thr	Thr	Leu	Lys	Met	Ile	Asn
		35				40					45				
Arg	Leu	Ile	His	Leu	Ser	Glu	Gly	Tyr	Ile	Tyr	Phe	Lys	Asp	Lys	Pro
	50				55					60					
Ile	Ser	Asp	Tyr	Pro	Val	Leu	Arg	Asn	Ala	Leu	Gly	Tyr	Trp	Xaa	Arg
65				70				75						80	
Xaa	Gly	Xaa	Arg	Leu	Glu	Leu	Xaa	Pro	Ile						
			85					90							

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Val	Cys	Cys	Phe	Gly	Ala	Ser	Thr	Met	Leu	Ser	His	Ile	Thr	Ala	Tyr
1				5					10					15	
Glu	Ile	Leu	Ser	Glu	Ile	Xaa	Lys	Lys	Leu	Ala	Gln	Lys	Leu	Met	Arg
			20				25						30		
Leu	Pro	Leu	Xaa	Val	Val	Glu	Ser	Lys	Lys	Ile	Gly	Glu	Leu	Lys	Asn
		35					40					45			
Ile	Phe	Xaa	Asp	Lys	Val	Glu	Thr	Ile	Glu	Leu	Pro	Leu	Ala	His	Met
	50				55						60				
Ile	Pro	Glu	Val	Xaa	Gly	Asn	Leu	Leu	Val	Ala	Ala	Ile	Phe	Leu	
65					70				75					80	
Tyr	Ile	Met	Xaa	Xaa	Asp	Trp	Arg	Ile	Gly						
				85					90						

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Val	Thr	Ser	Phe	Ile	Tyr	Lys	Ile	Leu	Tyr	Val	Val	Lys	Ile	Asn	Ala
1				5					10					15	
Tyr	Thr	Tyr	Asp	Ile	Met	Thr	Glu	Asp	Ile	Met	Xaa	Leu	Ser	Ile	Leu
			20				25						30		
Leu	Ile	Phe	Leu	Cys	Ile	Arg	Leu	Val	Ser	Leu	Lys	Ile	Cys	Ile	Xaa
		35				40						45			
His	Ser	Lys	Gln	Leu	Lys	Ala	Asp	Gly	Ala	Val	Glu	Tyr	Gly	Val	Lys
	50				55						60				
Asn	Ser	Lys	Phe	Leu	Ala	Ile	Thr	His	Val	Leu	Ile	Tyr	Val	Leu	Ala
65					70				75					80	
Gly	Val	Glu	Ala	Phe	Ile	Asn	Lys	Asp	Thr	Phe	Ser	Phe	Ala	Asn	Gly
				85				90						95	
Ile	Gly	Leu	Val	Ile	Leu	Ile	Phe	Ala	Tyr	Ile	Met	Leu	Phe	Met	Val
			100				105						110		
Ile	Lys	Thr	Leu	Gly	Gly	Ile	Trp	Thr	Leu	Lys	Leu	Phe	Ile	Leu	Pro
	115					120						125			
Asn	His	Pro	Ile	Ile	Lys	Ser	Gly	Leu	Tyr	Lys	Ile	Thr	Lys	Thr	Pro
	130				135						140				
Lys	Leu	Leu	Leu	Lys	His	His	Ser								
145					150										

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
Val Arg Val Thr Gly Ile Xaa Pro Tyr Gly Ala Phe Val Glu Thr Pro
 1          5          10          15
Asn His Thr Glu Gly Leu Ile His Ile Ser Glu Ile Met Asp Asp Tyr
      20          25          30
Val His Asn Leu Lys Lys Phe Leu Ser Glu Gly Gln Ile Val Lys Ala
      35          40          45
Lys Ile Xaa Ser Ile Asp Asp Glu Gly Lys Leu Asn Leu Ser Leu Xaa
      50          55          60
Asp Asn Asp Tyr Phe Lys Asn Tyr Glu Arg Lys Lys Glu Lys Gln Ser
      65          70          75          80
Val Leu Asp Glu Ile Arg Xaa Thr Glu Lys Tyr Gly Xaa Gln Thr Leu
      85          90          95
Lys Arg Thr Leu Thr Asn Leu Gly
      100
```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```
Val Thr Xaa Gly Val Xaa Glu Leu Ile Ile Xaa Ser Gly Glu Glu Glu
 1          5          10          15
Ser Ser Ser Gln Leu Cys His Pro His Ser Val Lys Asp Val Thr Gly
      20          25          30
Ala Gly Asp Ser Phe Cys Ala Ala Val Val Tyr Ser Trp Xaa Asn Gly
      35          40          45
Met Ser Thr Val Asp Ile Leu Ile Ala Gly Met Val Asn Ala Xaa Lys
      50          55          60
Thr Ile Glu Thr Lys Tyr Thr Val Arg His Asn Leu Asp Gln Gln Gln
      65          70          75          80
Leu Tyr His Asp Met Glu Asp Tyr Lys Asn Gly Lys Phe Thr Gln Val
      85          90          95
Tyr
```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```
Val Asn Lys Asn Xaa Thr Thr Met Ser His Ile Thr Xaa Xaa Gln Ser
 1          5          10          15
Ala Ile Leu Ala Ser Lys Val Asn Ala Pro Ser Val Tyr Asn Xaa Asn
```

	20					25						30							
Asn	Met	Ser	Glu	Asn	Phe	Thr	Gln	Arg	Val	Lys	His	Xaa	Leu	Arg	Lys				
		35					40					45							
Asn	Glu	Ala	Thr	Thr	Xaa	Tyr	Gln												
	50						55												

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Val	Ser	Ser	Arg	Asp	Ile	Gly	Glu	His	Val	Met	Asn	Leu	Leu	Met	His				
1				5					10					15					
Val	Asp	Gln	Val	Ser	Tyr	Val	Arg	Phe	Ala	Ser	Val	Tyr	Lys	Glu	Phe				
		20					25					30							
Lys	Asp	Val	Asp	Gln	Leu	Leu	Ala	Ser	Met	Gln	Gly	Ile	Leu	Ser	Glu				
		35					40					45							
Asn	Lys	Arg	Ser	Asp	Ala														
	50																		

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Val	Ala	Xaa	Val	Xaa	Ile	Ile	Xaa	Phe	Met	Met	Leu	Xaa	Pro	Xaa	Gly				
1			5					10					15						
Gly	Phe	Ile	Ala	Leu	Glu	Gln	Ile	Gly	Glu	Arg	Met	Asn	Ile	Ala	Ala				
		20					25					30							
Ile	Glu	Val	Asp	Lys	Ser	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Ser	Ser	Ala				
		35					40					45							
Leu	Arg	Gln	Leu	Pro	Thr	Tyr	Leu	Arg	Lys	Asn	Tyr	Asp	Asn	Leu	Asn				
	50					55					60								
Val	Ile	Thr	Met	Ile	Leu	Phe	Gly	Glu	Asn	Asn	Asp	Phe	Lys	Pro	Leu				
65				70				75						80					
Cys	Leu	Asn	Ser	Asn	Phe	Val	Glu	Ile	Glu	Gln	Thr	Asp	Asp	Tyr	Val				
			85					90						95					
Val	Phe	Glu	Lys	Tyr	Leu	Asn	Tyr												
			100																

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Val	Glu	Ile	Lys	Val	His	Ala	Leu	His	Ser	Gly	Ile	Thr	Leu	Ile	Lys
1				5					10					15	
Asp	Lys	Gly	Lys	Ile	Ile	Asp	Ile	His	Leu	Ser	Val	Lys	Ala	Thr	Glu
			20					25					30		
Asn	Ile	Asp	Gly	Glu	Val	Leu	Phe	Lys	Ala	Thr	Gln	Pro	Leu	Gly	Arg
		35					40					45			
Thr	Met	Lys	Val	Gly	Val	Gln	Asn	Asn	Ala	Met	Thr	Ile	Thr	Leu	Thr
	50					55					60				
Lys	Gln	Asn	Gln	Trp	Leu	Asp	Ser	Leu	Lys	Phe	Leu	Val	Lys	Cys	Ile
65					70					75					80
Glu	Glu	Ser	Met	Arg	Ile	Ser	Asp	Glu	Ala						
				85					90						

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Val	Glu	Tyr	Phe	Val	Ser	Tyr	Tyr	Asp	Tyr	Tyr	Gln	Pro	Glu	Ala	Tyr
1				5					10					15	
Val	Pro	Ser	Thr	Asp	Thr	Phe	Ile	Glu	Lys	Asp	Ala	Ser	Ile	Asn	Asp
			20					25					30		
Glu	Ile	Asp	Xaa	Xaa	Arg	His	Ser	Ala	Thr	Ser	Ala	Leu	Phe	Glu	Arg
		35					40					45			
Asp	Asp	Val	Ile	Ile	Ile	Ala	Ser	Val	Ser	Cys	Ile	Tyr	Gly	Leu	Gly
	50					55				60					
Asn	Pro	Glu	Glu	Tyr	Lys	Asp	Leu	Val	Val	Ser	Val	Arg	Val	Gly	Met
65					70					75					80
Glu	Met	Asp	Arg	Ser	Glu	Leu	Leu	Arg	Lys	Leu	Val	Asp	Val	Gln	Tyr
				85					90					95	
Thr	Arg	Asn	Asp	Ile	Asp	Phe	Pro	Thr	Arg	Asn	Arg	Phe	Glu	Cys	Val
			100					105					110		
Val	Met														

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Val	Gly	His	Ile	Leu	Ile	Glu	Ile	Ser	Xaa	Asp	Gly	Pro	Gly	Phe	Met
1				5					10					15	

Glu Asp Xaa Pro Tyr Glu Thr Leu Gly Xaa Gly Leu Ser Leu Pro Pro  
                   20                  25                  30  
 Phe Leu Glu Asn Lys Arg Glu Tyr Ile Glu Ser Glu Ile Arg Pro Phe  
                   35                  40                  45  
 Asn Thr Lys Arg  
                   50

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Val Ser Ile Thr Leu Xaa Pro Ala Leu Ala Ala Thr Leu Phe Lys Lys  
   1                  5                  10                  15  
 Gly Val Lys Arg Arg Asn Lys Gln His Gln Glu Gly Leu Gly Val Val  
                   20                  25                  30  
 Ser Thr Thr Tyr Lys Xaa Val Xaa His Trp Val Thr Lys Ser  
                   35                  40                  45

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Val Val Gln Glu Thr Leu Asn Met Ser Lys Ala Arg Gly Tyr Glu Val  
   1                  5                  10                  15  
 Gly Gly Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr  
                   20                  25                  30  
 Ser Asn Pro Leu Asp Ala Arg Ser Tyr Ala Val Leu Tyr  
                   35                  40                  45

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Val Glu Gly Asn Phe Gly Leu Ala Ile Asn Asn His Gln Asn Ile Val  
   1                  5                  10                  15  
 Gly Thr Ile Gly Leu Ile Arg Leu Asp Asn Asn Met Ser Ala Leu Lys  
                   20                  25                  30

Lys Met Phe Val Asp Lys Gly Tyr Arg Asn Leu Lys Ile Gly Lys Lys  
35 40 45  
Leu, Leu Asp Lys Val Ile Met Thr Cys Lys Glu Gln Asn Ile Asp Xaa  
50 55 60  
Xaa Tyr Leu Gly Thr Xaa Asp Lys Xaa Xaa Ser Ala Gln Tyr Xaa Tyr  
65 70 75 80  
Xaa Asn Xaa Gly Phe Arg Xaa Asn  
85

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Val Ile Gly Leu Lys Ser Lys Thr Ile Ile Ser Asn Glu Trp Gly Ala  
1 5 10 15  
Ile Met Ile Gln Ser Met Trp Phe Asn Leu His Val Gln Asp Leu Glu  
20 25 30  
Lys Ser Ala Gln Phe Tyr Lys Ala Leu Gly Phe Lys Ile Asn Arg Asn  
35 40 45  
Pro Gln Met Leu Asp Lys Met Val Gly Ile Gln Ile Gly Gln Thr Thr  
50 55 60  
Ala Ile Leu Ile Glu Asn Lys His Phe Gln Asn Val Ser Gln Gln Ser  
65 70 75 80  
Leu Asn Thr Glu Pro Asn Glu Val Met Ile Ser Leu Gly Val Thr Gln  
85 90 95

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Val Ser Leu Met Thr Thr Phe Ser Glu Lys Glu Lys Ile Gln Leu Leu  
1 5 10 15  
Ala Asp Ile Val Glu Leu Gln Thr Glu Asn Asn Asn Glu Ile Asp Val  
20 25 30  
Cys Asn Tyr Leu Lys Asp Leu Phe Asp Lys Tyr Asp Ile Lys Ser Glu  
35 40 45  
Ile Leu Lys Val Asn Glu His Arg Ala Asn Ile Val Ala Glu Ile Gly  
50 55 60  
Asn Xaa Ser Pro Ile Leu Ala Leu Ser Gly His Met Asp Val Val Gly  
65 70 75 80  
Cys Arg Lys Ser Arg  
85

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Val	Glu	Xaa	Met	Asn	Lys	His	Tyr	Xaa	Ile	Val	Ile	Ile	Gly	Gly	Gly	
1				5					10					15		
Thr	Ala	Gly	Val	Thr	Val	Ala	Ser	Arg	Leu	Leu	Arg	Lys	Asn	Xaa	Asn	
			20					25					30			
Leu	Lys	Glu	Lys	Ile	Ala	Ile	Ile	Asp	Pro	Ala	Asp	His	His	Tyr	Tyr	
		35				40						45				
Gln	Pro	Leu	Trp	Thr	Leu	Val	Gly	Ala	Gly	Val	Ser	Ser	Leu	Lys	Ser	
	50				55					60						
Xaa	Ser															
65																

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Val	Leu	Arg	Asn	Lys	Ile	Lys	Arg	Ala	Ile	Arg	Glu	Asn	Phe	Lys	Val	
1				5					10					15		
His	Lys	Ser	Xaa	Ile	Leu	Xaa	Lys	Asp	Ile	Ile	Xaa	Ile	Xaa	Arg	Gln	
			20					25					30			
Ala	Ala	Lys	Asp	Met	Thr	Thr	Leu	Gln	Ile	Gln	Xaa	Ser	Leu	Glu	His	
		35				40						45				
Xaa	Leu	Lys	Ile	Gly	Lys	Val	Phe	Asn	Lys	Lys	Ile	Lys				
	50				55					60						

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Val	Asp	Gly	Val	Ser	Leu	Ala	Val	Phe	Asp	Lys	His	Asp	Asn	Ser	Phe	
1				5				10					15			
Asp	Ile	His	Leu	Ile	Pro	Glu	Thr	Arg	Arg	Ser	Thr	Ile	Leu	Ser	Ser	
			20					25					30			
Thr	Lys	Leu	Gly	Asp	Lys	Val	His	Leu	Glu	Thr	Asp	Val	Leu	Phe	Lys	
		35				40					45					
Tyr	Val	Glu	Asn	Ile	Leu	Asn	Lys	Asp	Lys	Asp	Gln	Leu	Ser	Val	Asp	



50 55 60  
Lys Leu Arg Ala Phe Xaa Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val 1	Xaa	Gln	Ser	Leu 5	Tyr	Glu	Phe	Leu	Glu 10	Glu	Asn	Ile	Asn	Tyr 15	Leu
Lys	Glu	Asn	Gly 20	Xaa	Tyr	Asn	Glu	Ile 25	Asp	Thr	Ile	Glu	Gly 30	Ala	Asn
Gly	Pro	Glu 35	Ile	Lys	Ile	Asn	Gly 40	Lys	Ser	Tyr	Ile	Asn	Leu 45	Ser	Ser
Xaa	Asn 50	Tyr	Leu	Gly	Leu	Ala 55	Thr	Asn	Glu	Asp	Xaa 60	Arg	Ser	Ala	Ala
Lys 65	Ala	Ala	Ile	Asp	Thr 70	His	Gly	Val	Gly	Ala 75	Gly	Ala	Xaa	Arg	Thr 80
Xaa	Asn	Gly	Thr 85	Leu	Asp	Leu	His	Asp 90	Glu	Leu	Glu	Glu	Thr 95	Leu	Ala
Lys	Phe	Xaa	Gly 100	Thr	Glu	Ala	Ala	Ile 105	Ala	Tyr	Gln	Xaa	Arg 110	Ile	Xaa
Leu	Xaa	Ile 115	Trp	Leu	Leu	Xaa	Gln 120	Leu	Val	Xaa	Glu	Xaa 125	Lys		

(2) INFORMATION FOR SEQ ID NO:282:

- ```
(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 51 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

[illegible]

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```
Val Lys Glu Asn Asp Val Lys Lys Phe Lys Tyr Lys Asn Phe Xaa Asp
 1           5           10           15
Glu Ile Glu Ile Asp Phe Thr Asp Ser Asn His Leu Ala Ala His Arg
          20           25           30
```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```
Val Thr Pro Asp Ala Asn Gly Lys Val Ala Phe Asp Gly Leu Glu Leu
 1           5           10           15
Thr Phe Thr Gly Thr Pro Ala Val Asn Asp Ser Phe Thr Leu Lys Pro
          20           25           30
Val Ser Asp Ala Ile Val Asn Met Asp Val Leu Ile Thr Asp Glu Ala
          35           40           45
Lys Ile Ala Met Ala Ser Glu Glu Asp Ala Gly Asp Ser Asp Asn Arg
          50           55           60
Asn Gly Gln Ala Leu Leu Asp Leu Ala Lys Gln Gln
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```
Val Leu Leu Pro Leu Val Phe Ile Ser Val Leu Ile Gly Ile Phe Asn
 1           5           10           15
Tyr Ile Lys Val Leu Pro Phe Ile Ile Lys Tyr Val Gly Ile Ala Ile
          20           25           30
Asn Lys Ile Thr Arg Met Gly Arg Leu Glu Ser Tyr Phe Ala Ile Ser
          35           40           45
Thr Ala Met Phe Gly Gln Pro Glu Val Tyr Leu Thr Ile Lys Asp Ile
          50           55           60
Ile Pro Arg Leu Ser Arg Ala Lys Leu
65           70
```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
Val Ile Ile Ser Asn Asn Val Gly Asp Met Ser Ile Gly Phe Ser Ser
 1           5           10           15
Asp Asp Asn Glu Leu Thr Met His Phe Arg Asn Asn Glu Lys Val Asn
      20           25           30
Ile Lys Lys Gly Lys Lys Val Val Leu Ala Ala Gln Ile Leu Asp Glu
      35           40           45
Leu Glu Thr Arg Trp Gln
50
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
Val Thr Tyr Xaa His Met Ser His Arg His Thr Leu Ile Ser His Ser
 1           5           10           15
Phe Lys Phe Xaa Arg Leu Pro Gln Asp Ile Asn Phe Phe Ser Trp Xaa
      20           25           30
Gln His Val Lys Asp Ser Asp Lys Thr Asp Glu Leu Thr Tyr Ser Glu
      35           40           45
Ser Leu Xaa Pro Glu Gly His Pro Thr His Pro Leu Thr Pro Thr Lys
      50           55           60
Leu Pro Xaa Thr Met Glu Glu Xaa Arg Ala Tyr Ala Pro Glu Phe Asp
      65           70           75           80
Xaa Arg Asn Pro Phe Ala Thr Leu
                        85
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
Val Ile Ser Leu Leu Lys Asp Ala Lys Leu Pro Ser Ser Val Thr Arg
 1           5           10           15
Gly Asp Tyr Leu Ala Ile Leu Ser Xaa Gly Ala Tyr His Tyr Ser Met
      20           25           30
Xaa Ser Asn Tyr Asn His Met His Lys Pro Ser Val Phe Phe Leu Lys
      35           40           45
Asp Val Thr Ala Arg Val Val Ile Lys Arg Gln Ser Leu Arg Gln Leu
      50           55           60
```

Ile Ile Asn Xaa Thr Gln  
65 70

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Phe | Val | Asn | Lys | Leu | Phe | Asn | Val | Ser | Ser | Ala | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | Tyr | Asp | Gly | Val | Val | His | Ile | Gly | Tyr | Asp | Asn | Asn | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Thr | Glu | Gln | Phe | Lys | Met | Ser | Lys | Ser | Arg | Asn | Leu | Leu | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Arg | Ser | Gln | Asn | Xaa | Val | Leu | Ile | Arg | Leu | Leu | Asn | Trp | Leu | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Thr | Thr | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Leu | Gly | Leu | Thr | Asn | Ser | Val | Val | Ala | Ile | Ile | Ile | Ile | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | Xaa | Ala | Val | Thr | Gly | Leu | Arg | Leu | Leu | Gln | Ile | Glu | Gln | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Gly | Lys | Cys | Ser | Trp | Xaa | Ile | Arg |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Val | Asp | Asn | Met | Ser | Asp | Tyr | Lys | Leu | Lys | Ile | Ile | Xaa | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Xaa | Ser | Asp | Ile | Thr | Gly | Tyr | Gln | Ile | Pro | Asn | Gln | Xaa | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ala Gln Tyr Val Ile Ser Gln Leu Ser Gln Gly Lys Arg Glu Val Asp  
           35                          40                          45  
 Asn Leu Thr Leu Asn Xaa Xaa Glu Xaa Leu Tyr Ser Tyr Xaa Arg Gln  
           50                          55                          60  
 Val Leu  
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Val Lys Gln Thr Xaa Val Glu Glu Ile Xaa Ala Ser Ile Asn Xaa Ala  
   1                          5                          10                          15  
 Gly Leu Xaa Xaa Glu Ile Pro Asp Phe Lys Xaa Glu Val Xaa Xaa Xaa  
           20                          25                          30  
 Xaa Lys Lys Trp Arg Leu Cys Tyr  
           35                          40

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Val Ser Thr Asp Phe Ile Leu Cys Lys Leu Gln Ala Phe His Ile Ile  
   1                          5                          10                          15  
 Lys Phe Glu Lys Arg Tyr Ile Glu Val Glu Lys Asn Glu Tyr Thr Ala  
           20                          25                          30  
 Lys Tyr Asn Glu Tyr Ser Gln Leu Asp Ala Thr Tyr Ser Gln Ala  
           35                          40                          45  
 Val Ala Tyr Leu Leu Asn Lys Tyr Gly Ala Val Thr Asp Asp Tyr Tyr  
           50                          55                          60  
 Lys Glu Lys Ser Tyr Thr Arg Phe Leu Asn Gly Glu Ile Lys Ser Ile  
   65                          70                          75                          80  
 Ser Lys Gly Lys Tyr Thr Arg Ala Ser Glu Gly Leu Tyr Cys His His  
           85                          90                          95  
 Ile Ser Glu Asp Lys Phe Gln Asn Leu Ser  
           100                          105

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```
Val Ile Leu Ser Ser Ile Xaa Phe Tyr Met Gln Leu Leu Gln Lys Asn
 1             5             10             15
Pro Met Ala Ile Gly Val Trp Ala Gly Leu Cys Gln Met Ile Lys Pro
      20             25             30
Thr Val Ile Asp Trp Asp Ile Ser Glu Tyr Thr Pro Lys Pro Ala Trp
      35             40             45
Met Gln Ala Thr Lys Ala Arg Ala Tyr Val Pro Arg Ile Leu Val Glu
      50             55             60
Lys Leu Leu Ile Xaa Ile Asp Asp Met Leu Glu Gly Ile Glu Ile Tyr
65             70             75             80
Asp Xaa Xaa Glu Ser Arg
      85
```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```
Val Xaa Thr Tyr Val Asn Asp Tyr Leu Asn Glu Ala His Ile Thr Asn
 1             5             10             15
Lys Trp Ser Glu Met Met Leu Trp Ser Ser Gln Gln Arg Ser Gln Tyr
      20             25             30
Thr Val Gln Leu Ile Asn Lys Ile Glu Thr Asp Asp Ser Tyr Ile His
      35             40             45
Ile Ser Lys Gly Glu Leu Gly Ile Ser Leu Met Pro His Ile Gln Leu
      50             55             60
Lys Lys Ala Met Ser Asn Thr Ala Ser His Ile Glu Asp Leu Ser Cys
65             70             75             80
Gly Leu
```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```
Val Cys Lys Lys Tyr Val Leu Gly Gln Phe Lys Pro Gly Met Thr Ala
 1             5             10             15
Pro Gln Cys Ala Gly Ile Ile His Thr Asp Phe Xaa Arg Gly Phe Ile
      20             25             30
Arg Ala Gly Ser Asn Lys Leu Leu Met Thr Met Tyr Asn Met Ala Ala
      35             40             45
Lys Val Ala Leu Lys Lys Arg Ala Asp Thr Asp
```

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Val Leu Thr Leu Ala Glu Met Lys Arg Thr Ile His Asp Ile Leu Asp
 1           5           10           15
Phe Arg Asp Glu Asp Ile Trp Xaa Cys Tyr Leu Gly Thr Leu Ala Val
      20           25           30
Ser Pro Xaa Leu Xaa Asp Asp Xaa Gly Xaa Xaa Leu Leu Ser Arg Xaa
      35           40           45
Xaa Asn Ala Tyr Asn Xaa Tyr Xaa
 50           55

```

## (2) INFORMATION FOR SEQ ID NO:298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Val Phe Asn Tyr Gly Gln Ser Val Phe Glu Gly Leu Lys Ala Tyr Lys
 1           5           10           15
Arg Asp Gly Glu Gly Cys Thr Xaa Pro Xaa Pro Glu Glu Asn Phe Lys
      20           25           30
Arg Leu Asn Asn Ser Leu Ala Arg Leu Glu Met Pro Gln Val Asp Asp
      35           40           45
Ala Glu Leu Leu Glu Gly Leu Lys Xaa Leu Val Asp Ile Glu Arg Asp
      50           55           60
Xaa Xaa Pro Glu Gly Glu Gly Gln Ser Leu Tyr Xaa Xaa Pro Phe Gly
      65           70           75           80
Xaa Ala Thr Glu Gly Ala Xaa Gly Val Gly Ala Ser His Gln Tyr Xaa
      85           90           95
Ile Tyr

```

## (2) INFORMATION FOR SEQ ID NO:299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | Ile | Leu | Glu | Asp | Pro | Pro | Arg | Asp | Leu | Asp | Ile | Tyr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ile | Ala | Glu | Arg | Ala | Gly | Gln | His | Pro | Xaa | Val | Glu | Arg | Ile | Xaa |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Gly | Xaa | Gln | Arg | Arg | Ile | Asp | Ile | Xaa | Thr | Val | Glu | Ser | Cys |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Lys | Thr | Arg | Ile | Leu | Lys | Val | Asp | Asn | Pro | Glu | Ile | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Lys | Pro | Thr | Gly | Ser | His | Phe | Gln | Gln | Cys | Val | Trp | Asn | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Arg | Gln | Val | Pro | Tyr | Gly | Thr | Leu | Thr | Thr | Tyr | Gly | Ala | Ile | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Lys | Val | Gly | Lys | Val | Leu | Asp | Lys | Pro | Gln | Met | Ser | Ala | Gln | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Gly | Gly | Ala | Val | Gly | Ser | Asn | Pro | Leu | Ser | Ile | Ile | Val | Pro | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Arg | Val | Val | Gly | Lys | Thr | Gly | Ser | Leu | Thr | Gly | Phe | Gly | Gly | Thr |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Ile | Asn | Asn | Lys | Ile | Lys | Leu | Leu | Glu | Leu | Glu | Asn | Ile | Asp | Met | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Leu | Tyr | Ile | Pro | Lys | His | Ser | Thr | Lys | Pro |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Leu | Val | Glu | Cys | Met | Met | Ala | Leu | Asn | Thr | Ala | Gly | Xaa | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Thr | Val | Glu | Thr | Leu | Ala | Glu | Tyr | Ser | Gly | Val | Pro | Val | Trp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asn | Gly | Leu | Thr | Asp | Glu | Asp | His | Pro | Thr | Gln | Xaa | Leu | Ala | Asp | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Ala | Lys | Glu | Val | Phe | Lys | Lys | Arg | Leu | Cys | Arg | Tyr |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Val Asn Leu Pro Asp Phe Pro Pro Lys Ile Gly Val Asn Lys Ser Thr
 1          5          10          15
Leu Ser Arg Tyr Xaa Xaa Gly Ser Arg Xaa Ile Pro Met Glu Asp Ile
          20          25          30
Ala Glu Ile Ala Asn Ala Leu Lys Val Thr Pro Glu Tyr Leu Leu Leu
          35          40          45
Xaa Asn Arg Gln Pro Glu Xaa Glu Val Gln His Arg Ala Ala His Leu
          50          55          60
Glu Gly Glu Leu Thr Asp Asp Glu Cys Gln Arg Val Leu Asp Tyr Ala
65          70          75          80
Asp Tyr Ile Arg Ser Lys Arg Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Val Lys Pro Xaa Cys Ala Lys Lys Asp Arg Tyr Pro Ile Asp Pro Met
 1          5          10          15
Arg Arg Leu Asn Gln Glu Ile Ile Asp Tyr Ile Asp Thr Leu Asn Tyr
          20          25          30
Ile Asp Gln Tyr Ser Ser Ala Gly Ser Phe Arg Arg Phe Lys Glu Met
          35          40          45
Ser Lys Asp Leu Asp Phe Ile Ile Ser Thr Asp Asn Pro Gln Ala Val
          50          55          60
Gln Gln Gln Leu Leu Asn Ile Pro Asn Lys Val Lys Glu Val Ala Val
65          70          75          80
Gly Asn Thr Gln Val Ser Leu Glu Leu Ala Tyr Asp Asp Glu Thr Ile
          85          90          95
Gly Val Asp Phe Arg Leu Ile Glu Pro Arg Ala Phe Tyr His Thr Leu
          100          105          110
Gln His Phe Thr Gly Ser Asn Arg Thr
          115          120

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Asp | Ile | Tyr | Ser | Glu | Xaa | Asp | Leu | Ile | Glu | Ile | Thr | Asp | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Xaa | Ser | Ile | Ser | Phe | Asn | Phe | Ala | Ser | Tyr | Met | Ser | Ala | Ser | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Phe | Lys | Asp | Tyr | Ala | Leu | Xaa | Thr | Asn | Asp | Lys | Ser | Gln | Tyr | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Asp | Tyr | Asn | Gln | His | Val | Ala | Ile | Val | Ala | Leu | Tyr | Leu | Ala | Xaa |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Asn | Lys | Ala | Gln | Ala | Lys | Gln | Phe | Ile | Ser | Ala | Met | Val | Glu | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Arg | Tyr | Xaa | Pro | Ala | Thr | Pro | Thr | Phe | Leu | Asn | Ala | Xaa | Arg | Ala | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Gly | Glu | Leu | Val | Ser | Cys | Phe | Xaa | Xaa | Lys | Lys | Trp | Val | Xaa | Xaa |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Asn | Ser | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Met | Glu | Val | Thr | Cys | Leu | Lys | Gln | Ile | Thr | Trp | His | Asp | Leu | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Ile | Ile | Lys | Asp | Gly | Asp | Val | Ile | Gly | Leu | Pro | Ala | Leu | Ala | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Asn | Leu | Pro | Ala | Glu | Val | Leu | Arg | Ala | Val | Leu | Ala | Gln | His | Asp |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Tyr | His | Thr | Pro | Lys | Asp | Leu | Thr | Phe | Ile | Leu | Ala | Asn | Asp | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Ser | Leu | Gly | Ala | Ala | Pro | Asp | Leu | Asp | Asp | Phe | Ile | Glu | Arg | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Met | Ile | Lys | Arg | Val | Ile | Met | Ser | Ile | Leu | Thr | Ala | Ser | Ser | Lys | Thr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Gln | Ala | Met | Lys | Asn | Asn | Asp | Ile | Glu | Ala | Tyr | Phe | Leu | Pro | Gln |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Gly | Ile | Ile | Ala | Thr | His | Tyr | Arg | Gln | Ser | Asn | Gln | Leu | Leu | Pro | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Val | Ile | Thr | Lys | Ile | Gly | Leu | Asn | Thr | Ala | Val | Asp | Pro | Arg | Tyr | Gly |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Gly | Lys | Val | Asn | Thr | Arg | Thr | Thr | Asp | Asp | Leu | Val | Ser | Leu | Val |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Thr | Ile | Asn | Asp | Glu | Thr | Tyr | Leu | His | Tyr | Thr | Phe | Pro | Ser | Val | Asp |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Ala | Leu | Leu | Arg | Gly | Thr | Tyr | Ala | Asp | Gln | Gln | Gly | Asn | Ile | Tyr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Xaa | Gln | Glu | Ala | Tyr | Leu | Ser | Glu | Cys | Tyr | His | Val | Ala | Leu | Asn |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ala | Lys | Ala | Asn | His | Gly | Lys | Val | Ile | Xaa | Gln | Val | Lys | Ala | Leu | Val |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Asp | Tyr | His | Leu | Lys | Pro | Asn | Glu | Val | Val | Ile | Pro | Gly | Asn | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |

Val Asp Tyr Val Phe Val Thr Glu Asp Glu Lys Asn His Arg Gln Val  
245 250 255  
Ile Gln Ser His Tyr Leu Pro Ala Leu Ser  
260 265

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Val Val Lys Ile Val Xaa His Gln Lys Asp Ser Asn Xaa Glu Lys Asp  
1 5 10 15  
Asp Lys Ala Arg Thr Xaa Gln Gln Asp Xaa Lys Xaa Xaa Asp Ser Ser  
20 25 30  
Xaa Asp Lys Lys Asp Asn Xaa Asp Asp Ser Xaa Asp Val Xaa Lys Asp  
35 40 45  
Asn Lys Asp Asn Ser Ala Asn Asp Asn Gln Gln Gln Ser Asn Ser Lys  
50 55 60  
Cys Asn Lys Gln  
65

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Val Arg Arg Phe Pro Asp Ile Glu Arg Arg Val Gln Thr His Asp Phe  
1 5 10 15  
Thr Trp Gln Ala Glu Ile Met Ser Lys Pro Val Lys Asn Met Thr Val  
20 25 30  
Ala Ile Ile Gly Thr Gly Arg Ile Gly Ala Ala Thr Ala Lys Ile Tyr  
35 40 45  
Ala Gly Phe Gly Ala Thr Ile Thr Ala Tyr Asp Ala Tyr Pro Asn Lys  
50 55 60  
Asp Leu Asp Phe Leu Thr Tyr Lys Asp Ser Val Lys Glu Ala Ile Lys  
65 70 75 80  
Asp Ala Asp Ile Ile Ser Leu His Val Pro Ala Asn Lys Glu Ser Tyr  
85 90 95  
His Leu Phe Asp Lys Ala Met Phe Asp His Val Lys Lys Gly Ala Ile  
100 105 110  
Leu Val Asn Ala Ala Arg Gly Ala Val Ile Asn Thr Pro Asp Leu Xaa  
115 120 125  
Ala Ala Val Asn Asp Gly Thr Leu Leu Gly Ala Ala Ile Asp Thr Tyr  
130 135 140  
Glu Asn Glu Ala Ala Tyr Phe Thr Asn Asp Trp Thr Asn Lys Asp Ile  
145 150 155 160  
Asp Asp Lys Thr Leu Leu Glu Leu Ile Gly Thr

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```

Val Val Val Leu Met Cys Cys Leu Lys Tyr Glu Asn Asp Tyr Tyr Glu
 1          5          10          15
Glu Val Arg Ala Gln Leu Pro Asp Ile Gly Glu Ala Ile Glu Thr Pro
 20          25          30
Asp Gly Asn Arg Glu Ser Ser Cys Phe Lys Tyr Ile Arg His Phe Tyr
 35          40          45
Ala Gly Glu Ala
 50

```

## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Val Asn Thr Xaa Leu Leu Asn Xaa Arg Val Glu Pro Ala Ile Val Lys
 1          5          10          15
Ile Pro Val Ser Val Asp Glu Asn Ile Asp Asn Val Glu Lys Lys Leu
 20          25          30
Asn Thr Leu Phe Thr Ile Leu Cys Val Val Asn Xaa Xaa Leu Phe Val
 35          40          45
Ser Asp Pro Val Val Ile Gly Ile Asp Ala Phe Glu Asp Thr Arg Val
 50          55          60
Ile Leu Xaa Val Ser Ala Glu Thr Ile Pro Gly Xaa Gly Phe Ser Gly
 65          70          75          80
Ala Arg Ile Ile Arg Lys Glu Val His Lys Met Phe Leu Gln Glu Gly
 85          90          95
Ile Lys Thr Pro Xaa Pro Ile Met Thr Pro Phe Asn His Ser Glu Xaa
100          105          110
Gly Val

```

## (2) INFORMATION FOR SEQ ID NO:310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```
Val Thr Gln Leu Leu Lys Asn Ala Xaa Lys Lys Xaa Asn Asp Leu Ile
 1           5           10           15
Lys Glu Glu Ala Glu Ile Val Lys Asn Asp Asp Leu Pro Xaa Xaa Leu
      20           25           30
Ile Ile Xaa Gly Xaa Gln Tyr Asp Xaa Arg Trp Arg
      35           40
```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```
Val Arg Phe His Asp Gly Xaa Thr Phe Asp Ala Asp Ala Val Lys Lys
 1           5           10           15
Asn Ile Asp Ala Xaa Gln Gln Asn Lys Lys Leu His Ser Trp Leu Lys
      20           25           30
Ile Ser Thr Leu Ile Asp Asn Val Lys Val Lys Asp Lys Tyr Thr Val
      35           40           45
Glu Leu Asn Leu Lys Glu Ala Tyr Gln Pro Ala Leu Ala Glu Leu Ala
      50           55           60
Met Pro Arg Pro Tyr Val Phe Val Ser Pro Lys Asp Phe Lys Asn Gly
      65           70           75           80
Thr Thr Lys Asp Gly Val Lys Lys Phe Asp Gly Thr Gly Pro Phe Lys
      85           90           95
Leu Gly Glu His Lys Lys Asp Glu Ser Ala Asp Phe Asn Lys Asn Asp
      100           105           110
Gln Tyr Trp Gly Glu Lys Ser
      115
```

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```
Val Pro Ile Asp Tyr Ile Xaa Gln Thr Gly Asp Ile Val Glu Ile Arg
 1           5           10           15
Thr Ser Lys His Ser Tyr Gly Pro Ser Arg Asp Trp Leu Xaa Ile Val
      20           25           30
Lys Ser Ser Ser Ala Lys Gly Lys Ile Lys Ser Phe Phe Xaa Xaa Gln
      35           40           45
Asp Arg Ser Ser Asn Ile Glu Lys Ala Arg Met Met Val Glu Val Glu
      50           55           60
Ile Lys Asp Gln Gly Phe Arg Val Glu Asp Ile Leu Thr Glu Lys Asn
      65           70           75           80
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Val | Val | Asn | Xaa | Lys | Tyr | Asn | Phe | Xaa | Asn | Glu | Asp | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ala | Ala | Val | Gly | Phe | Gly | Gly | Val | Thr | Ser | Leu | Gln | Ile | Val | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Thr | Glu | Arg | Gln | Arg | Ile | Leu | Asp | Lys | Gln | Arg | Ala | Leu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Ala | Gln | Glu | Val | Thr | Lys | Ser | Leu | Pro | Ile | Lys | Asp | Asn | Ile | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asp | Ser | Gly | Val | Tyr | Val | Glu | Gly | Leu | Glu | Asn | Val | Leu | Ile | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Xaa | Lys | Cys | Cys | Asn | Pro | Ile | Pro | Gly | Asp | Asp | Ile | Val | Gly | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Thr | Lys | Gly | His | Gly | Thr | Lys | Val | His | Arg | Thr | Asp | Cys | Pro | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Lys | Asn | Glu | Thr | Glu | Arg | Leu | Ile | Asn | Val | Glu | Trp | Val | Lys | Xaa |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Asp | Ala | Thr | Gln | Lys | Tyr | Gln | Val | Asp | Leu | Glu | Val | Thr | Ala | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Arg | Asn | Gly | Leu | Leu | Asn | Glu | Val | Leu | Gln | Ala | Val | Ser | Ser | Thr |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Xaa | Gly | Asn | Leu | Ile | Lys | Val | Ser | Gly | Arg | Ser | Asp | Ile | Asp | Xaa | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Xaa | Ile | Ile | Asn | Ile | Ser | Val | Met | Val | Lys | Asn | Val | Asn | Asp | Val | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Val | Val | Glu | Lys | Thr | Lys | Gln | Leu | Gly | Asp | Val | Tyr | Thr | Gly | Asn |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Leu | Gly | Thr | Arg | Gly | Ser | Lys | Asn | Ile | Glu | Ser | Arg | Trp | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Thr | Val | His | Pro | Ile | Arg | Ile | Pro | Pro | Gly | Asp | Pro | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Asp | Ile | Val | Ile | Gly | Arg | Val | Ala | Gln | Val | His | Ile | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Val | Ile | Leu | Asp | Asn | Gly | Lys | Leu | Asp | Ile | Lys | Ser | Ile | Lys | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Arg | Leu | Gly | Tyr | Ser | Asp | Tyr | Thr | Val | Val | Asn | Glu | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Met | Lys | Ala | Pro | Xaa | Ala | Ser | Lys | Glu | Glu | Leu | Ala | Gly | Leu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Arg | Asn | Phe | Asp | Asn | Gln | Ser | Asp | Glu | Lys | Arg |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     | 90  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Thr | Arg | Leu | Lys | Thr | Met | Gly | Lys | Leu | Ala | Met | Leu | Met | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Lys | Asp | Leu | Asp | Gln | Ala | Phe | Lys | Lys | Lys | Asp | Thr | Val | Leu | Ile | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ile | Ile | Glu | Arg | Asp | Glu | Asp | Ile | Asp | Asp | Leu | Tyr | Ser | His | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asn | Ala | Thr | Tyr | Leu | Ile | Asp | Asn | Asp | Pro | Phe | Val | Ala | Ala | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | His | Leu | Ala | Ala | Arg | His | Leu | Glu | Arg | Ile | Gly | Asp | His | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Ile | Ala | Glu | Ser | Val | Tyr | Phe | Tyr | Leu | Thr | Gly | Thr | His | Tyr | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ile | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Asn | Lys | Ile | Leu | Ser | Gln | Phe | Leu | Asn | Ile | Lys | Pro | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Ser | Glu | Met | Val | Gly | Arg | Leu | Glu | Lys | Ala | Gly | Tyr | Val | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Tyr | Lys | Gly | Val | Arg | Leu | Thr | Glu | Asp | Gly | Leu | Thr | His | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Ile | Ile | Lys | Arg | His | Arg | Leu | Leu | Glu | Leu | Phe | Leu | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Lys | Tyr | Asn | Trp | Glu | Glu | Val | His | Gln | Glu | Ala | Glu | Ile | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | His | Arg | Ile | Ser | Asp | Leu | Phe | Val | Glu | Arg | Leu | Asp | Ser | Cys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Gly | Asn | Xaa | Xaa | Gln | Ala | Asp | Leu | Ile | Gly | Tyr | Ser | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Phe Asp Gly Ala Ile Xaa Arg Gln Glu Ala Ser Xaa Asp Val His Ala  
20 25 30  
Val Ile Leu Ser Asn Lys Thr Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Val Val Ser Met Lys Tyr Asn Thr Asn Val Lys His Thr Thr Leu Glu  
1 5 10 15  
Ala Phe Val Thr Thr Val Asn Asp Leu Gly Ile Glu Leu Ile Ile Asn  
20 25 30  
Glu Ala Leu Arg Glu Val Arg Lys Arg Gln Leu Ile Glu Leu Ile Asp  
35 40 45  
Asp Ala Leu Val Asn Lys Asp Glu Ala Ala Phe Asn Gln Tyr Thr Ala  
50 55 60  
Glu Tyr Lys Asn Leu Glu Ala Phe Leu Gly Xaa  
65 70 75

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Tyr Lys Val Lys Val Ala Val Ile Met Gly Ser Ser Ser Asp Trp  
1 5 10 15  
Lys Ile Met Gln Glu Ser Cys Asn Met Leu Asp Tyr Leu Glu Ile Pro  
20 25 30  
Tyr Glu Lys Gln Val Val Ser Ala His Arg Thr Pro Lys Met Met Val  
35 40 45  
Gln Phe Ala Ser Glu Ala Arg Glu Arg Gly Ile Asn Ile Ile Ile Ala  
50 55 60  
Gly Ala Gly Gly Ala Xaa His Leu Pro Gly Met Val Ala Ser Leu Thr  
65 70 75 80  
Thr Leu Pro Val Ile Gly Val Pro Ile Glu Thr Xaa Lys Phe Lys Gly  
85 90 95  
Tyr

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
Val Lys Lys Ile Asp Cys Ser Xaa Ile Gly Ile Cys Gly Tyr Glu Tyr
 1           5           10           15
Arg Gln Leu Lys Gln Glu Thr Xaa Leu Xaa Leu Phe Xaa Lys Leu His
      20           25           30
Pro Ser Phe Xaa Gly Gln Gly Val Arg Met
      35           40
```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
Val Leu Gly Leu Ile Glu Gly Lys Ser Gln Arg Lys Ala Tyr Ile Asp
 1           5           10           15
Ala Gly Tyr Ser Thr Lys Gly Lys Ser Asp Asn Tyr Ile Asp Ser Arg
      20           25           30
Ala Phe Glu Leu Ser Lys Asn Ser Ala Gly Leu Asp Arg Tyr Glu Glu
      35           40           45
Leu Arg Gln Glu Ala Gly
      50
```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```
Val Lys Asp Leu Leu Gln Ala Gln Gln Lys Leu Ile Pro Asp Leu Ile
 1           5           10           15
Asp Lys Met Tyr Lys Arg Phe Ser Ile Leu Thr Thr Ile Ser Lys Asn
      20           25           30
Gln Pro Val Gly Arg Arg Ser Leu Ser Glu His Met Asp Met Thr Glu
      35           40           45
Arg Val Leu Arg Ser Glu Thr Asp Met Leu Lys Lys Gln Asp Val Ile
      50           55           60
Lys Val Lys Pro Thr Gly Met Glu Ile Thr Ala Glu Gly Glu Gln Leu
      65           70           75           80
Ile Ser Gln Leu Lys Gly Tyr Xaa Asp Ile Tyr Gly Asp Asp Asn Arg
      85           90           95
Leu Val Lys Lys Gly Ile
      100
```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ile | Met | Arg | Lys | Glu | Ile | Glu | Ala | Leu | Ile | Phe | Ser | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Tyr | Asp | Ile | Tyr | Val | Asn | Thr | Gly | Val | Asn | Gln | Gly | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ile | Lys | Asp | Gly | Tyr | Leu | Thr | Ile | Asp | Ser | Met | Pro | Tyr | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Glu | Arg | Leu | Tyr | His | Phe | Ala | Tyr | Gly | Thr |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Cys | Ile | Val | Leu | Val | Lys | Val | Val | Glu | Asn | Ala | Glu | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ile | Glu | Ile | Phe | Asn | Ser | Val | Asp | Asn | Asn | Asn | Lys | Lys | Ile | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Asp | Gly | Asn | Val | Val | Gly | Ala | Val | Ser | Cys | Gln | Tyr | Gly | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asp | Asp | Gly | Ser | Arg | Phe | Tyr | Asn | Met | Met | Lys | Lys | Gly | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Glu | Asp | Tyr | Thr | Leu | Val | Ser | Leu | Leu | Thr | Lys | Gly | Gly | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ser | Leu | Ser | Ile | Ala | Asp | Met | Ala | Asp | Asp | Glu | Thr | Ile | Cys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Asn | Gly | Val | Asp | Lys | Gly | Thr | Ile | Val | Asn | Ala | Ile | Thr | Glu | Asn |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Phe | Thr | Thr | Val | Glu | Glu | Val | Thr | Ala | Lys | Thr | Lys | Ala | Gly | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Cys | Gly | Lys | Cys | Lys | Pro | Gln | Ile | Ala | Gln | Ile | Leu | Gln | His | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Asp | Asp | Phe | Val | Ala | Ala | Lys | Pro | Ala | Gly | Ile | Cys | Gly | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Asp | Leu | Thr | Arg | Asp | Gln | Ile | Val | Thr | Gln | Ile | Arg | Ala | Lys | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Lys | Thr | Ser | Lys | Glu | Val | Arg | His | Val | Leu | Asn | Phe | Lys | Asn | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gly | Cys | Pro | Lys | Cys | Arg | Pro | Ala | Ile | Asn | Tyr | Tyr | Leu | Asn | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Tyr | Pro | His | Asp | His | Glu | Asp | Glu | Arg | Glu | Ser | Arg | Phe | Ala | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Tyr | His | Ala | Asn | Ile | Gln | Asn | Asp | Gly | Thr | Phe | Ser | Val | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Gln | Met | Arg | Gly | Gly | Val | Thr | Asp | Ala | Asp | Gln | Leu | Ile | Arg | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Glu | Val | Ala | Lys | Lys | Tyr | His | Val | Pro | Leu | Val | Lys | Val | Thr | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Gln | Arg | Val | Gly | Leu | Tyr | Gly | Gly |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Met | Thr | Pro | Leu | Val | Glu | Pro | Xaa | Pro | Xaa | Thr | Val | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asn | Lys | Ser | Asn | Ser | Asn | Ser | Ser | Thr | Leu | Xaa | Tyr | Leu | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Asn | Arg | Gly | Trp | Asp | Phe | Asp | Gly | Ser | Tyr | Gly | Trp | Gln | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Asp | Leu | Xaa | Asn | Val | Phe | Trp | Xaa | Ser | Ser | Ser | Met | Gly | Met | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Gly | Phe | Trp | Arg |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Gln | Leu | Ile | Thr | Gln | Ile | Tyr | Gly | Ala | Glu | Lys | Arg | Val | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Val | Asn | Gln | Leu | Val | Ser | Xaa | Ser | Phe | Asn | Lys | Lys | Ile | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Thr | Xaa | Ser | Asp | Trp | Ile | Ser | Ser | Asn | Pro | Ile | Glu | Val | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Phe | Ile | Lys | Asp | Pro | Tyr | Ser | Gly | Phe | Asn | Val | Ser | Xaa | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Tyr | His | Thr | Ala | Tyr | Tyr | Met | Leu | His | Thr | Ser | Gln | Leu | Lys | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Lys | Met | Leu | Asn | His | Ala | Met | Pro | Ile | Leu | Leu | Val | Ser | Gly | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Asp | Ser | Leu | Gly | Asp | Tyr | Gly | Lys | Gly | Ile | Leu | Lys | Leu | Ala | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Tyr | Arg | Glu | Ala | Gly | Ile | Lys | Asn | Cys |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```
Val Thr Leu Glu Val Ala Glu Met Xaa Asn Ser Xaa Lys Asp Xaa Lys
 1          5          10          15
Lys Phe Glu Ile Ile Asp Arg Xaa Lys Ser Phe Tyr Asp Glu Glu Gln
          20          25          30
Xaa Ile Asp Leu Val Phe Val Val Asn Gln Ile Asn Gly Trp Asn Arg
          35          40          45
Leu Asn Ile Ile Ser Asp Arg Leu
50          55
```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```
Val Asp Ser Val Thr Ile Lys Val Leu Asn Glu Pro Ser Pro Lys Leu
 1          5          10          15
Leu Thr Thr Trp Tyr Ala Glu Gln Val Thr Gln Gly Lys Ile Lys Thr
          20          25          30
Ser Lys Tyr Val Lys Lys Glu Cys Glu Arg His Leu Arg Tyr Leu Glu
          35          40          45
Asn Gly Gly Lys Trp Val Phe Asp Glu Glu Leu Ala His Arg Pro Ile
          50          55          60
Arg Phe Ile Glu Lys Phe Cys Lys Xaa Ser Lys Gly Ser Lys Arg Gln
          65          70          75          80
Leu Ala Leu Gln Pro Trp Gln His Phe Ile Ile Gly Ser Leu Phe Gly
          85          90          95
Trp Val His Lys Glu Thr Lys Leu Arg Arg Phe Lys Glu Ala Leu Ile
          100          105          110
Phe Met Gly Ala Lys Lys Trp
          115
```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Xaa | Xaa | Val | Ile | Lys | Glu | Lys | Pro | Xaa | Ala | Arg | Trp | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Xaa | Ser | Pro | Xaa | Xaa | Ala | Ile | Asp | Gly | Asp | Thr | Leu | Val | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Xaa | Xaa | Ala | Ser | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asn | Leu | Ser | Ile | Ser | Leu | Thr | Ser | Leu | Ala | Thr | Gly | Ile | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Val | Ala | Ala | Gly | Asp | Ile | Ala | Asp | Lys | Ile | Gly | Gln | Xaa | Arg | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Tyr | Met | Gly | Leu | Ile | Ile | Xaa | Met | Phe | Xaa | Ser | Leu | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Asp | Ile | Thr | Ala | Leu | Leu | Ile | Ile | Xaa | Arg | Asn | Phe | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ile | Ser | Xaa | Tyr | Leu | Gly | Tyr | Pro | Pro | Thr | Val | Gly | Val | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Gln | Phe | Lys | Gly | Glu | His | Leu | Arg | Arg | Ala | Ile | Ser | Tyr | Leu | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Ser | Thr | Val | Gly | Gly | Ile | Gly | Leu | Ala | Gly | Val | Ile | Gly | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ala | Thr | Asn | Phe | Gly | Trp | Gln | Met | Asn | Phe | Ile | Ile | Ser | Ile | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Xaa | Phe | Ile | Ala | Ile | Leu | Leu | Leu | Lys | Gly | Thr | Pro | Glu | Lys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gln | His | Xaa | His | Arg | His | Pro | Phe | Asp | Tyr | Lys | Gly | Met | Ser | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Ala | Val | Met | Ile | Gly | Ser | Phe | Thr | Leu | Leu | Leu | Thr | Gln | Gly | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gln | Gly | Trp | Phe | Ser | Thr | Phe | Ser | Phe | Ile | Cys | Leu | Ser | Ile | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ile | Thr | Thr | Leu | Ile | Phe | Ile | Ile | Ile | Glu | Arg | Arg | His | Glu | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Phe | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Val Ala Pro Phe Leu Tyr Leu Xaa Ile Asn Asp Glu Xaa Xaa Asp Met  
 1 5 10 15  
 Lys Ile Ala Gly Asp Leu Asn Ala Tyr Asn Ala Leu Xaa Ala Tyr Thr  
 20 25 30  
 Val Xaa Arg Glu Leu Gly Leu Asn Glu Gln Xaa Asn  
 35 40

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Val Tyr Val Ile Ser Leu Asn Asp Asn Ala Ala Asp Gly Arg Asp Thr  
 1 5 10 15  
 Ser Trp Ile Tyr Asp Ala Asp Phe Gly Lys Ile Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Val Met Ser Lys Leu Arg Pro Leu Leu His Tyr Ala Arg Ala Lys Asp  
 1 5 10 15  
 Ile Asp Asn Tyr Arg Thr Val Glu Glu Ser Tyr Arg Gln Gly Gln Tyr  
 20 25 30  
 Tyr Arg Xaa Xaa Ile Val Asp Gly Lys Leu Asn Ile Gln Phe Asn Glu  
 35 40 45  
 Gly Glu Pro Tyr Phe Gly Arg His  
 50 55

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Val His Pro Asp Val Leu Leu Thr Arg Tyr Val Glu Gly Lys Glu Asp  
 1 5 10 15  
 Gln Val Glu Lys Val Leu Tyr Gln Leu Ala Asp Ile Asp Ile Ser Glu  
 20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Lys | Asp | Phe | Ile | Leu | Leu | Pro | Thr | His | Pro | Tyr | Gln | Xaa | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Xaa | Gln | Tyr | Pro | Gln | Tyr | Met | Gln | Tyr | Ser | Glu | Gln | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Asp | Leu | Gly | Val | Ser | Gly | Asp | Leu | Val | Ser | Pro | Thr | Ser | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Arg | Thr | Val | Phe | Ser | Lys | Ala | Leu | Asn | Ile | Tyr | Leu | Xaa | Xaa | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | His | Val | Xaa | Ile | Thr | Asn | Phe | Xaa | Arg | Thr | Asn | Asp | Leu | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ile | Xaa | Arg | Thr | Ser | Cys | Met | Pro | Arg | Met | Ser | Ser | Ser | Ser | Asp | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Arg

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Asn | Lys | Glu | Leu | Ile | Gln | His | Ala | Ala | Tyr | Ala | Ala | Ile | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ile | Leu | Asn | Glu | Tyr | Phe | Arg | Glu | Glu | Asn | Leu | Tyr | Gln | Val | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Pro | Gln | Asn | His | Gln | Trp | Ser | Ile | Gln | Leu | Ser | Glu | Leu | Glu | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Glu | Phe | Arg | Tyr | Trp | Ser | Ala | Met | Gly | His | His | Met | Tyr | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Glu | Val | Trp | Leu | Ile | Asp | Gly | Lys | Ser | Lys | Lys | Ile | Thr | Thr | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Glu | Ala | Ile | Ala | Arg | Ile | Leu | Pro | His | Met | Ala | Gln | Ser | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gln | Thr | Ala | Val | Gln | Pro | Thr | Tyr | Gly | Xaa | Asn | Tyr | Val | Xaa | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Arg

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Val | Ser | Phe | Leu | Thr | Ser | Arg | Asp | Ile | Pro | Xaa | Asp | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Lys | Met | Asp | Val | Asp | Pro | Pro | Xaa | Tyr | Leu |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
Val Lys Asn Val Lys Thr Gln Ser Ile Gln Asn Ala Ser Ile Val Thr
 1          5          10          15
Val Glu Tyr Glu Asn Asn Thr Asp Met Asp Lys Ala Glu Glu Gln Leu
 20          25          30
Lys Lys Glu Ile Asp Lys Ile Lys Phe Lys Asp Glu Val Gly Gln Pro
 35          40          45
Glu Leu Arg Arg Asn Ser Met Asp Ala Phe Pro Val Leu Ala Tyr Ser
 50          55          60
Phe Gln Ile Lys Arg
65
```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
Val Met His Xaa Ile Phe Pro Val Val Ser Xaa Thr Phe Ala Ser Phe
 1          5          10          15
Lys Ser Met Tyr Gly Gly Ile Pro Gln Asp Phe Ile Asp Tyr Leu Phe
 20          25          30
Ile Asp Glu Ala Gly Gln Ala Ile Pro Gln Ala Ala Val Gly Ala Leu
 35          40          45
Tyr Arg Ser Lys Lys Val Val Ala Val Gly Asp Pro Ile Gln Ile Glu
 50          55          60
Pro Val Val Thr Leu Glu Ser His Leu Ile Asp Asn Ile Arg Lys Asn
 65          70          75          80
Tyr His Val Pro Glu Tyr Leu Val Ser Lys Glu Ala Ser Val Gln Ser
 85          90          95
Val Ala Asp Asn Ala Asn Gln Tyr Gly Phe Trp Lys Ser Asp Ala Thr
100          105          110
Asp Ser Asn Gln Lys Thr Trp Ile Gly Ile Pro Leu Trp Val His Arg
115          120          125
Arg Cys Leu Lys Pro Met Phe Thr Ile Ala Asn Gln Ile Ala Tyr Asn
130          135          140
Asn Lys Met Val Leu Ala Ser Asn Ile Thr Lys Val Gly Lys Thr Gly
145          150          155          160
Trp Tyr Asp Val Lys Gly Asn Ala Val Gln Asn Ile Xaa Glu Arg Ala
165          170          175
Trp Val Lys Lys
180
```

(2) INFORMATION FOR SEQ ID NO:338:



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Phe | Phe | Asp | Tyr | Thr | Phe | Ala | Ser | Val | Gly | Val | Lys | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Lys | Gln | Phe | Asp | Tyr | Lys | Met | Val | Glu | Val | Thr | Gln | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | Asn | Tyr | Tyr | Pro | Gly | Asn | Ser | Pro | Leu | His | Leu | Arg | Val | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Asp | Thr | Ser | Asn | Arg | Gln | Ile | Leu | Arg | Ala | Ala | Ala | Val | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Ala | Asp | Lys | Arg | Ile | Asp | Val | Leu | Ser | Met | Ala | Met | Met | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Leu | Thr | Val | Asp | Glu | Leu | Thr | Glu | Phe | Xaa | Val | Xaa | Tyr | Ala | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Tyr | Trp | His | Pro | Lys | Asp | Leu | Xaa | Asn | Met | Ile | Gly | Leu | Gln | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Gln | Ser | Ser | Lys | Trp | Asn | Ala | Met | Ser | Leu | Leu | Met | Asp | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Thr | Lys | Gln | Ala | Glu | Val | Leu | Arg | Thr | Ala | Ile | Asp | Glu | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Val | Ile | Gly | Ile | Gly | Ala | Gly | Met | Ser | Ala | Ser | Asp | Gly | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Tyr | Val | Gly | Glu | Arg | Phe | Thr | Glu | Asn | Phe | Pro | Asp | Phe | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Tyr | Arg | Phe | Phe | Asp | Met | Leu | Gln | Ala | Ser | Leu | His | Pro | Tyr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Trp | Gln | Glu | Tyr | Trp | Ala | Phe | Glu | Ser | Arg | Phe | Ile | Thr | Xaa | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Tyr

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Pro | Ile | Lys | Ala | Ile | Ile | Asp | Ser | Leu | Thr | Thr | Phe | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Glu | His | Arg | Leu | Gln | Tyr | Val | Gly | Thr | Asn | Arg | Thr | Asn | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Asn | Asp | Ser | Xaa | Ala | Thr | Asn | Thr | Leu | Ala | Thr | Gln | Phe | Ala | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ser | Phe | Asn | Gln | Pro | Ile | Ile | Trp | Leu | Leu | Trp | Trp | Tyr | Trp | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Asp | Glu | Phe | Asp | Glu | Leu | Ile | Pro | Tyr | Met | Glu | Asn | Val | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Asp | Gly | Cys | Ile | Arg | Thr | Asn | Glu | Ser | Xaa | Val | Cys |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Gly | Thr | Asp | Lys | Arg | Val | Ser | Pro | Asp | Leu | Phe | Ile | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Asn | Phe | Tyr | Asp | Tyr | Leu | Leu | Leu | Asn | Ser | Asp | Gly | Leu | Thr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Val | Lys | Asp | Asn | Glu | Ile | Lys | Arg | Leu | Leu | Val | Lys | Glu | Gly | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Glu | Asp | His | Gly | Asp | Gln | Leu | Met | Gln | Leu | Ala | Leu | Asp | Asn | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Lys | Asp | Asn | Val | Thr | Phe | Ile | Leu | Ala | Ala | Ile | Xaa | Gly | Asp | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Leu | Lys | Gly | Met | Arg | Lys | Gln | Tyr | Glu | Val | Gly | Glu | Gln | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Ile | Glu | Phe | Val | Thr | Gly | Arg | Val | Asn | Pro | His | Arg |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Val | Gln | Val | Met | Lys | Phe | Gly | Lys | Thr | Ile | Ala | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Ser | Val | Leu | Leu | Xaa | Gly | Cys | Thr | Thr | Asp | Lys | Lys | Glu | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Lys | Ala | Tyr | Leu | Lys | Gln | Val | Asp | Lys | Ile | Lys | Asp | Asp | Glu | Glu | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Xaa | Thr | Val | Xaa | Lys | Lys | Ile | Ala | Glu | Leu | Asp | Glu | Lys | Lys | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Leu | Thr | Glu | Asp | Val | Asn | Ser | Lys | Asp | Thr | Ala | Gly | Ser | Arg | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gln | Ser | Ser | Ser | Leu | Leu | Asn | Xaa | Phe | Lys | Val | Phe | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ser | Asp | Thr | Val | Ile | His | Gly | Ser | Asp | Val | Asp | Leu | Val | Asn | Trp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Glu | Asn | Ala | Leu | Gln | Ser | Gly | Leu | Ala | Ala | Lys | Glu | Arg | Lys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Ala | Val | Ser | Pro | Lys | Ser | Gly | Leu | Glu | His | Met | Ser | Phe | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Gly | Ser | Val | Lys | Glu | Val | Xaa | Gly | Ala | Asp | Met | Tyr | Asp | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Asn | Ala | Leu | Ala | Asp | Leu | His | Glu | Asp | Tyr | Arg | Asp | Asn | Ala | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ile | Tyr | Met | Arg | Tyr | Ala | Asp | Tyr | Val | Lys | Ile | Ile | Ser | Val | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Gly | Thr | Thr | Asn | Phe | Phe | Asp | Thr | Pro | Ala | Glu | Lys | Val | Xaa | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Pro | Val | Gly | Ile | Tyr | Arg | Cys | Arg | Xaa | Leu | Pro | Leu | Leu | Trp | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Phe | Asn | Tyr | Cys | Gly | Xaa | Tyr | Leu | Leu | Met | Gly | Gln | Pro | Tyr | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Thr | Asp | Leu | Tyr | Xaa | Gln | Xaa | Xaa | Lys | Ile | Asp | Thr | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Val | Ile | Lys | Glu | Val | Glu | Leu | Lys | Lys | Pro | Ile | Thr | Tyr | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Thr | Ser | Asp | Ser | Lys | Leu | Xaa | Lys | Glu | Trp | Met | Asp | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Pro | Arg | Tyr | Lys | Xaa | Thr | Leu | Leu | His | Arg | Arg | Leu | His | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Leu | Xaa | Lys | Met | Leu | Glu | Asp | Leu | Ser | Phe | Glu | Ala | Pro | Ser | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Ala | Val | Val | Asp | Ile | Thr | Pro | Gln | Tyr | Val | Asp | Asp | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ser | Ile | Ser | Thr | Xaa | Lys | Asp | Leu | Ser | Ala | Phe | Ile | Leu |     |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Ile | Leu | Lys | Asp | Thr | Asn | Leu | Met | Tyr | Leu | Glu | Trp | Asn | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Val | Xaa | Arg | Val | Val | Ala | Val | Val | Glu | Xaa | Gln | Gly | Thr | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Val | Asn | Lys | Ala | Leu | Gln | Tyr | Trp | Val | Ser | His | Val | Asp | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | His | Tyr | Leu | Leu | Gly | Ser | Ala | Leu | Gly | Pro | Asp | Pro | Phe | Pro | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Val | Arg | Asp | Phe | Gln | Ser | Val | Ile | Gly | Lys | Glu | Xaa | Lys | Ser | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Leu | Lys | Lys | Glu | Gly | Arg | Leu | Pro | Asp | Ala | Ile | Val | Ala | Cys | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Gly Gly Gly Ser Asn Ala Ile Gly Leu Val Pro Phe Ile His Leu Leu  
100 105 110  
Lys Met Met Leu His  
115

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Val Gly Arg Leu Pro Lys Lys Ile Gln Asn Ile Glu Gln Arg Pro Xaa  
1 5 10 15  
Gly Val Ser Xaa Thr Thr Phe Thr Ile Ala Val Asn Arg Thr Phe Thr  
20 25 30  
Asn Ala Gln Gly Glu Arg Glu Ala Asp Phe Ile Asn Cys Val Thr Phe  
35 40 45  
Arg Lys Gln Ala Glu Asn Val Asn Asn Tyr Leu Ser Lys Gly Ser Leu  
50 55 60  
Ala Gly Val Asp Gly Arg Leu Gln Ser Arg Ser Tyr Asp Asn Lys Glu  
65 70 75 80  
Gly Arg Arg Val Phe Val Thr Glu Val Val Ala Asp Ser Val Gln Phe  
85 90 95  
Leu Glu Pro Lys Asn Asn Asn Gln Xaa Gln Asn Asn Asn Tyr Gln Gln  
100 105 110  
Gln Gly Gln Ala Gln Thr Gly Asn Asn Pro Phe Asp Asn Ser Glu Glu  
115 120 125  
Asp Phe Ser Asp Leu Pro Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Val Val Ser Gln Ser Ile Leu Leu Thr Leu Ser Thr Xaa Leu Thr Asn  
1 5 10 15  
Val Thr Xaa Leu Thr Ser Xaa Ala Gln Xaa Pro Ala Asp Tyr Val Lys  
20 25 30  
Asn Met Ile Thr Gly Ala Ala Gln Met Asp Gly Gly Ile Leu Val Val  
35 40 45  
Ser Ala Ala Asp Gly Pro Met Pro Gln Thr Arg Glu His Ile Leu Leu  
50 55 60  
Ser Arg Asn Val Gly Val Pro Ala Leu Val Val Phe Leu Asn Lys Val  
65 70 75 80  
Asp Met Val Asp Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val  
85 90 95  
Arg Asp Leu Leu Ser Glu Tyr Asp Phe Pro Gly Asp Asp Val Pro Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ile | Ala | Gly | Ser | Ala | Leu | Lys | Ala | Leu | Glu | Gly | Asp | Ala | Gln | Tyr | Glu |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Glu | Lys | Ile | Leu | Glu | Leu | Met | Glu | Ala | Val | Asp | Thr | Tyr | Ile | Pro | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Gln | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Lys | Val | Ser | Gly | Cys | Ser | Asp | Leu | Val | Gln | Cys | Ala | Ile | His | Asp |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Cys | Gln | Tyr | Tyr | Glu | Val | Gln | Met | Pro | Gln | Ala | His | Arg | Val | Val | Pro |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Thr | Thr | Ile | Asn | Met | Gly | Asn | His | Ser | Trp | Lys | Ala | Leu | Glu | Ile | Ile |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Tyr | Glu | Thr | Tyr | Cys | Thr | Leu | Cys | Asp | Ser | Xaa | Leu | Asn | Lys | Xaa | Thr |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Xaa | Val | Asn | Ile | Asn | Cys | Ala | Asn | Pro | Glu | Cys | Asn | Lys | Gln | Ile |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Val | Ser | Glu | Glu | Xaa | Glu | Thr | Lys | Tyr | Leu | Gly | Ala | Cys | Ser | Tyr |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Glu | Cys | Ala | Lys | His | Glu | Arg | Asn | Arg | Tyr | Val | Gln | Ala | Asn | Asn | Ile |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Ser | Asp | Asn | Glu | Trp | Gln | Gln | Arg | Leu | Thr | Asn | Phe | Asp | Asp | Leu | His |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| Gln | His | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```
Val Thr Arg Ser Lys Met Ile Val Val Glu Ser Tyr Asp Val Asn Gly
 1      5      10      15
Asn Lys Val Glu Leu Thr Ala His Glu Asp Val Ala Arg Met Ile Leu
      20      25      30
His Ile Ile Asp Gln Met Asn Gly Leu Pro Phe Xaa Glu Arg Ala Asp
      35      40      45
Arg Ile Leu Thr Asp Lys Glu Val Glu Ala Tyr Phe Ile Asn Asp
 50      55      60
```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```
Val Thr Lys Asn Ala Gly Asn His Glu Ile Glu Ile Asp Arg Pro Ile
 1      5      10      15
Val Asn Pro Ile Lys Lys Leu Pro Thr Arg Phe Thr Ile Asn Val Ala
      20      25      30
Ile Gly Asn Phe Glu Val Asn Leu
      35      40
```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```
Val Lys Gly Gln Asn Leu Thr His Gly Thr Asn Ala Ile Asp Tyr Ile
 1      5      10      15
Thr Phe Asp Pro Asn Thr Asn Thr Asn Gly Ile Thr Ala Ala Trp Ala
      20      25      30
Asn Arg Gln Gln Pro Asn Asn Gln Ala Gly Val Gln His Leu Asn
      35      40      45
Val Asp Val Thr Tyr Pro Gly Ile Ser Ala Ala Lys Arg Val Pro Val
      50      55      60
Thr Val Asn Val Tyr Gln Phe Gly Ile Pro Ser Asn Tyr Leu Tyr Asn
      65      70      75      80
Asn Ser Trp Trp His Phe Ser Lys Trp Tyr Ala Ser Ile Arg Ile Cys
      85      90      95
Thr Tyr Ala Lys Arg Phe Arg Phe Thr Asn Arg Trp Ile Tyr Val
      100      105      110
```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Thr | Thr | Gln | Asn | Gln | Ala | Ile | Asp | Asn | Thr | Thr | Gly | Ala | Thr | Thr |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Glu | Glu | Lys | Asn | Ala | Ala | Lys | Asp | Leu | Val | Leu | Xaa | Ala | Lys | Glu | Lys |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ala | Xaa | Gln | Asp | Ile | Leu | Xaa | Ala | Gln | Xaa | Thr | Asn | Asp | Val | Thr | Gln |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ile | Asn | Asp | Gln | Ala | Val | Ala | Asp | Ile | Gln | Gly | Ile | Thr | Gly | Asp | Thr |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Thr | Ile | Xaa | Asp | Val | Ala | Ile | Asp | Xaa | Xaa | Ala | Thr | Pro | Ala | Thr | Xaa |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Xaa | Xaa | Ala | Leu | Xaa | Gly | His | Xaa | Ala | Xaa | Ala | Thr | Xaa | Glu | Xaa | Xaa |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Xaa | Gln | Xaa | Xaa | Xaa | Thr | Lys | Xaa | Xaa | Ala | Gln | Xaa | Xaa | Thr | Xaa | Val |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Phe | Thr | Xaa | Leu | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Val | Xaa |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |
| Xaa | Leu | Ala | Xaa | Xaa | Xaa | Arg | Thr | Leu | Xaa | Ser | Arg | Xaa | Xaa | Xaa | His |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Xaa | Xaa | Xaa | Xaa | Xaa | Asn | Arg | Phe |     |     |     |     |     |     |     |     |  |  |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Val | Ser | Leu | Ile | Asp | Asp | Glu | Asp | Asp | Asn | Xaa | Asn | Asp | Arg | Gln |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Val | Val | Ser | Ala | Pro | Ser | Lys | Lys | Pro | Thr | Thr | Pro | Thr | Thr | Tyr |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Thr | Glu | Thr | Thr | Thr | Gln | Val | Xaa | Met | Pro | Thr | Val | Glu | Arg | Gln | Thr |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gln | Gln | Gln | Ile | Val | Tyr | Lys | Thr | Pro | Lys | Thr | Ile | Ser | Trp | Ile | Lys |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
Val Lys Ile Met Glu Met Ser Val Thr Glu Val Ile Phe Ser Phe Leu
 1          5          10          15
Gly Gly Leu Gly Ile Phe Leu Tyr Gly Leu Lys Ile Met Gly Asp Gly
 20          25          30
Leu Gln Ala Ser Ala Gly Asp Arg Leu Arg Asp Ile Leu Asn Lys Phe
 35          40          45
Thr Ser Asn Pro Val Leu Gly Val Ile Ala Gly Ile Val Val Thr Ile
 50          55          60
Leu Ile Gln Ser Ser Ser Gly Thr Thr Val Ile Thr Ile Gly Leu Val
 65          70          75          80
Thr Ala Gly Phe Met Thr Leu Lys Gln Ala Ile Gly Val Ile Met Gly
 85          90          95
Ala Asn Ile Gly Thr Thr Val Thr Ala Phe Ile Ile Xaa Ile Arg Phe
100          105          110
Arg Arg Ile Cys Lys Cys Gln Phe
115          120
```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
Val Leu Cys Asp Ala Asp Val Leu Ala Leu Ile Asp Ile Asp Val Asp
 1          5          10          15
Ile Asp Val Leu Lys Glu Pro Asp Ala Leu Val Leu Val Asp Cys Leu
 20          25          30
Val Thr Leu Asn His Xaa Met Met
 35          40
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
Val Leu Val Glu Leu Glu Ser Leu Thr Leu Val Glu Pro Asp Ile Glu
 1          5          10          15
Ser Leu Lys Leu Val Asp Val Glu Thr Asp Thr Leu Pro Leu Ile Glu
 20          25          30
Ser Asp Val Glu Ser Asp Val Leu Val Glu Phe Asp Pro Leu Met Leu
 35          40          45
Asp Glu Ser Leu Val Asp Ile Glu Ser Leu Ser Asp Ala Leu Met Leu
```

50  
Ile Glu Ser Asn  
65

55

60

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ile | Ser | Lys | Xaa | Gln | Trp | Val | Val | Val | His | Phe | Tyr | Pro | Ser | Trp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Asp | Ala | Glu | Gly | His | Phe | Glu | Asn | Asn | Gly | Arg | Cys | Asn | Leu | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Xaa | Thr | Leu | Asn | Leu | Pro | Arg | Met | Ala | Leu | Glu | Ser | Ala | Gly | Asn |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Thr | Lys | Phe | Trp | Glu | Ile | Phe | Tyr | Glu | Arg | Ile | Asp | Val | Leu | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Ala | Leu | Leu | Tyr | Arg | Ile | Asn | Arg | Leu | Lys | Asp | Xaa | Val | Pro | Asn |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asn | Ala | Pro | Ile | Leu | Tyr | Lys | Ser | Gly | Ala | Phe | Asn | Tyr | Lys | Leu | Lys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Thr | Asp | Asp | Val | Ala | Glu | Leu | Phe | Lys | Asn | Lys | Arg | Ala | Thr | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Met | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Xaa | Ser | Thr | Lys | Thr | Ala | Leu | Xaa | Gly | Asp | Ala | Lys | Leu | Asn | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Lys | Ala | Ala | Ala | Lys | Gln | Thr | Leu | Gly | Thr | Leu | Thr | His | Ile | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Ala | Gln | Arg | Asn | Ala | Leu | Asp | Asn | Glu | Ile | Thr | Xaa | Ala | Thr | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Glu | Val | Leu | Ile | Gln | Leu | Lys | Pro | Lys | Arg | Asn | Asn |     |     |     |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Glu | Met | Ala | Lys | Lys | Ala | Pro | Asp | Val | Gly | Asp | Tyr | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Phe | Pro | Ala | Asp | Asp | Val | Ser | Ile | Phe | Arg | Ser | Glu | Arg | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Asn | Ile | Val | Arg | Glu | Ile | Ser | Asn | Met | Lys | Asn | Glu | Pro | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Met | Leu | Asp | Phe | Arg | Leu | Lys | Ser | Leu | Lys | Leu | Phe | Tyr | Lys | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Met | Pro | Gln | Trp | Gly | Gly | Asp | Leu | Ser | Glu | Leu | Asn | Phe | Asp | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Thr | Tyr | Tyr | Val | Lys | Pro | Ser | Glu | Gln | Ala | Glu | Arg | Ser | Trp | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Pro | Glu | Glu | Ile | Lys | Arg | Thr | Phe | Asp | Lys | Leu | Gly | Ile | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Glu | Gln | Lys | Tyr | Leu | Ala | Gly | Val | Ser | Ala | Gln | Tyr | Glu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Val | Val | Tyr | His | Asn | Met | Glu | Lys | Glu | Leu | Glu | Glu | Lys | Gly | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Phe | Lys | Asp | Thr | Asp | Ser | Ala | Leu | Gln | Glu | Asn | Glu | Glu | Leu | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Lys | Tyr | Phe | Ala | Ser | Val | Val | Pro | Ala | Ala | Asp | Asn | Lys | Phe | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Asn | Ser | Ala | Val | Trp | Ser | Gly | Xaa | Ser | Leu | Ile | Tyr | Val | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asn | Ile | Lys | Leu | Asp | Thr | Pro | Leu | Gln | Ala | Tyr | Phe | Arg | Ile | Asn |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Glu | Asn | Met | Gly | Gln | Phe | Glu | Arg | Thr | Leu | Ile | Ile | Ala | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Ser | Val | His | Tyr | Val | Glu | Gly | Trp | Tyr | Cys | Thr | Ser | Leu | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Gln | His | Lys | Ala | Trp | Val | Asn | Ile | Met | Tyr | Gly | Cys | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Cys | Thr | Tyr | Cys | Ile | Val | Pro | Xaa | Thr | Arg | Ser | Lys | Asp | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Pro | Glu | Asp | Ile | Ile | Asp | Glu | Val | Arg | Glu | Leu | Ala | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Tyr | Lys | Glu | Ile | Thr | Leu | Leu | Gly | His | Asn | Val | Asn | Ser | Tyr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asp | Leu | Gln | Asp | Ile | Glu | Tyr | Asp | Leu | Gly | Asp | Leu | Leu | Gln | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ser | Lys | Ile | Ala | Ile | Pro | Arg | Val | Arg | Phe | Thr | Thr | Ser | His | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Trp | Asp | Phe | Thr | Asp | His | Met | Ile | Asp | Val | Ile | Ser | Glu | Gly | Gly | Asn |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ile | Val | Pro | His | Ile | His | Leu | Pro | Val | Gln | Ser | Gly | Asn | Asn | Ala | Val |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Leu | Lys | Ile | Met | Gly | Arg | Lys | Tyr | Thr | Arg | Glu | Ser | Tyr | Leu | Asp | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Lys | Arg | Ile | Lys | Asp | Arg | Leu | Pro | Asn | Val | Ala | Leu | Thr | Thr | Asp |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ile | Ile | Val | Gly | Tyr | Pro | Asn | Glu | Ser | Glu | Glu | Gln | Phe | Glu | Glu | Thr |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Leu | Thr | Leu | Tyr | Asp | Glu | Val | Gly | Phe | Glu | His | Ala | Tyr | Thr | Tyr | Leu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Tyr | Ser | Gln | Arg | Asp | Gly | Thr | Pro | Ala | Ala | Lys | Met | Lys | Asp | Asn | Val |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Pro | Leu | Asn | Val | Lys | Lys | Glu | Arg | Leu | Gln | Arg | Leu | Asn | Lys | Lys | Val |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Gly | His | Tyr | Ser | Gln | Ile | Ala | Met | Ser | Lys | Tyr | Glu | Gly | Gln | Thr | Val |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Thr | Val | Leu | Cys | Glu | Gly | Ser | Ser | Lys | Lys | Asp | Asp | Gln | Val | Leu | Ala |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Gly | Tyr | Thr | Asp | Lys | Asn | Lys | Leu | Val | Asn | Phe | Lys | Ala | Pro | Lys | Glu |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Met | Ile | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Gln | Tyr | Leu | Val | Thr | Thr | Phe | Lys | Asp | Ser | Thr | Gly | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Glu | His | Ile | Thr | Val | Ala | Arg | Asp | Asn | Gln | Thr | Phe | Thr | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Glu | Ser | Lys | Glu | Glu | Ala | Glu | Arg | Lys | Tyr | Glu | Ala | Gln | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Arg | Arg | Asp | Gly | Asp | Ala | Lys | Glu | Asn | Xaa | Asn | Asp |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Lys | Ala | Gln | Ala | Phe | Asp | Glu | Ile | Leu | Glu | Gly | Met | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Ile | Gln | His | Ser | Val | Lys | Xaa | Gly | Ile | Glu | Leu | Asp | Glu | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Ile | Met | Ala | Gly | Gln | Val | Val | Tyr | Lys | Tyr | Glu | Glu | Glu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asp | Met | Lys | Phe | Lys | Lys | Val | Leu | Val | Ala | Thr | Ala | Met | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Leu | Ala | Thr | Gly | Val | Val | Gly | Tyr | Gly | Asn | Gln | Ala | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Tyr | Ser | Gln | Asn | Gly | Leu | Val | Leu | His | Asp | Asp | Ala | Asn | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | His | Glu | Leu | Ser | Tyr | Ile | Asp | Val | Leu | Leu | Asp | Lys | Asn | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gln | Ala | Thr | Lys | Asp | Asn | Leu | Arg | Ser | Tyr | Phe | Ala | Asp | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | His | Ser | Ile | Lys | Asp | Ile | Ile | Asn | Lys | Ala | Lys | Gln | Asp | Gly | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Val | Ser | Lys | Tyr | Glu | His | Val | Lys |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Asn | Lys | Glu | Tyr | Glu | Ile | Glu | Pro | Gly | Lys | Arg | Glu | Cys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Met | Lys | Arg | Leu | Asn | Lys | Leu | Val | Leu | Gly | Ile | Ser | Phe | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Ile | Ser | Ile | Thr | Ala | Gly | Cys | Gly | Ile | Gly | Lys | Glu | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Lys | Lys | Ser | Phe | Glu | Lys | Thr | Leu | Ser | Met | Tyr | Pro | Ile | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Asp | Leu | Tyr | Asp | Lys | Glu | Gly | Tyr | Arg | Asp | Asp | Gln | Phe | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asn | Asp | Lys | Gly | Thr | Trp | Ile | Ile | Asn | Ser | Glu | Met | Val | Ile | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asn | Asn | Glu | Asp | Met | Val | Ala | Lys | Gly | Met | Val | Leu | Tyr | Ile | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asn | Ile | Pro | Lys | Met | Leu | Lys | Tyr | Asp | Gln | Ile | Leu | Val | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Pro | Pro | Ile | Leu | Pro | Leu | Ile | Pro | Asp | Val | Leu | His | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Lys | Lys | Tyr | Ser | Phe | Val | Val | Tyr | Asp | Ile | Ala | Pro | Asp | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Lys | Thr | Gly | Ala | Thr | Arg | Pro | Gly | Ser | Met | Ile | Asp | Lys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Met | Arg | Tyr | Ile | Asn | Arg | His | Val | Tyr | Lys | Asn | Ala | Glu | Asn | Val | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Leu | Gly | Tyr | Gly | Asn | Glu | Lys | Leu | Leu | Thr | Lys | Ser | Ser | Asn | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Lys | Met | Leu | Thr | Ile | Ser | Met |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Tyr | Ile | Glu | Ala | Pro | Tyr | Glu | Pro | His | Lys | Phe | Val | Lys | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Asp | Lys | Glu | Leu | Ala | Asp | Glu | Lys | Glu | Gly | Gly | Leu | Arg | Xaa |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Thr | Ala | Cys | Phe | Glu | Met | Arg | Leu | Asp | Ile | Val | Ala | Lys | Ala | Ala | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | His | Gly | Tyr | Asp | Tyr | Phe | Gly | Ser | Ala | Ile | Thr | Leu | Ser | Pro | Lys |
|     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |
| Lys | Asn | Ala | Gln | Leu | Ile | Asn | Glu | Leu | Gly | Met | Asp | Cys | Pro | Lys | Asn |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ile | Arg | Cys | Glu | Leu | Ile | Cys | Lys |     |     |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:



(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```
Val Leu Ala Asp Ile Thr Val Asn Ala Met Lys Gly Ile Tyr Leu Arg
 1           5           10           15
Tyr Asp Glu Asn Gly Ala Ile Thr Ser His Thr Ile Asp Lys Asp Gly
 20           25           30
Val Lys Ile Ser Gly Asp Lys Val Asp Ile Thr Ala Asn Arg Glu Phe
 35           40           45
Asn Val Phe Ala Asn Asn Ile Asn Asn Lys Val Gly Lys Asn Asp Ile
 50           55           60
Val Asn Ser Leu Asn Leu Ser Asn Glu Gly Leu Asp Ile Asn Val Asn
 65           70           75           80
Arg Ile Gly Ile Lys Gly Gly Asn Ala Asn Arg Tyr Val Gln Val Gln
 85           90           95
Asn Asp Phe Ile Glu Leu Gly Gly Ile Val Gln Arg Thr Trp Lys Gly
100          105          110
Lys Arg Ser Thr Asp Asp Ile Phe Thr Arg Leu Lys Asp Gly His Leu
115          120          125
Arg Phe Arg Asn Asn Thr Ala Gly Gly Ser Leu Tyr Met Ser His Phe
130          135          140
Gly Ile Ser Thr Tyr Ile Asp Gly Glu Gly Glu Asp Gly Gly Ser Ser
145          150          155          160
Gly Thr Ile Gln Trp Trp Asp Lys Thr Tyr Ser Asp Ser Gly Met Asn
165          170          175
Gly Ile Thr Ile Asn Ser Tyr Gly Gly Val Val Ala Leu Thr Ser Asp
180          185          190
Tyr Asn Arg Ile Ile Ile Asp Ser Tyr Ala Ser Ala Asn Ile Glu Ser
195          200          205
Arg Glu Ala Pro Ile Tyr Leu Ser Pro Asn Thr Gln Lys Leu Asn Leu
210          215          220
Xaa Leu Xaa Arg Phe Ala Phe Thr Leu Ser Asn Ala Asp Arg Xaa Ile
225          230          235          240
Thr Lys Leu Ala Val Ile Ser Cys Trp Val Gln Asp Xaa Xaa Tyr Lys
245          250          255
Xaa Gly Ala Gly Leu Arg Phe Ser Lys Arg Thr Asn Lys Gly Leu Val
260          265          270
Gln Val Val Asn Gly Asp Tyr Ala Thr Gly Gly Asp Thr Thr Ile Glu
275          280          285
Ser Gly Met Ala Lys Phe Asn Leu Val Xaa Arg Lys Arg Trp Lys
290          295          300
```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```
Val Asn Pro Thr His Val Lys Tyr Ala Ala Glu Arg Leu Ala Asp Ser
 1           5           10           15
Glu Val Leu Val Cys Thr Val Ile Gly Phe Pro Leu Gly Ala Ser Thr
 20           25           30
Thr Ala Thr Lys Ala Phe Glu Thr Glu Asp Ala Ile Gln Asn Gly Ala
 35           40           45
```



Asp Glu Ile Asp Met Val Ile Asn Ile Gly Ala Leu Lys Asp Gly Arg  
50 55 60  
Phe Asp Asp Val Gln Gln Asp Ile Glu Ala Val Val Lys Ala Ala Lys  
65 70 75 80  
Gly His Thr Val Lys Val Ile Ile Glu Thr Val Leu Leu Glu Pro  
85 90 95

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Val Lys Ile Tyr Glu Asp Thr Asn Ile Asp Thr Leu Xaa Leu Leu Asn  
1 5 10 15  
Glu Ala Xaa Ile Phe Lys Xaa Thr Leu Phe Trp Cys Xaa Xaa Ser Asn  
20 25 30

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Val Ala His Asp Asn His Ile Gly Thr Tyr Cys Ile Val Met Ser Gly  
1 5 10 15  
Arg Gly Pro Ser Asp Lys Glu Val Asp His Ile Ser Asn Pro Val Arg  
20 25 30  
Thr Ile Lys Ser Gln His Pro Gln Leu Lys Ile Cys Ala Cys Leu Gly  
35 40 45  
Leu Thr Asp Cys Arg Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Val Ile Asp Asp Leu Val Ser Asp His Ile Ala Thr Gly Gln Leu Leu  
1 5 10 15  
Val Lys Met Ser Asp Leu Thr Ser Ser Tyr Glu Pro Pro Ile Glu Ala  
20 25 30

Cys Gly Thr Trp Arg Leu Val Tyr Gln Arg Leu Lys Ala Leu Glu Val  
35 40 45  
Leu Thr His Glu His Val His Leu Glu Asn His Val Leu Phe Lys Lys  
50 55 60  
Val Ser  
65

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Val Leu Met Ile Phe Gly Pro Glu Gly Gly Leu Ser Glu Ile Glu Ile  
1 5 10 15  
Ser Leu Phe Ser Asn Thr Ser Thr Val Val Gly Leu Gly Pro Arg Ile  
20 25 30  
Leu Arg Ala Glu Thr Ala Pro Leu Tyr Ala Leu Ser Ala Ile Ser Tyr  
35 40 45  
Glu Lys Glu Leu Met Gly  
50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Val Ser Ser Ile Trp Lys Glu Lys Glu Phe Glu Pro Ser Asp Ile Val  
1 5 10 15  
Asp Ala Tyr Leu Val Ile Ala Ala Thr Asn Glu Pro Arg Val Asn Glu  
20 25 30  
Ala Val Lys Gln Ala Leu Pro Glu His Ala Leu Phe Asn Asn Val Gly  
35 40 45  
Asp Ala Ser Asn Ala Asn Val Val Phe Pro Ser Ala Leu His Arg Asp  
50 55 60  
Lys Leu Thr Ile Ser Val Ser Thr Asp Gly Ala Ser Pro Lys Leu Thr  
65 70 75 80  
Lys Ser Ile Met Ala Glu Leu Glu Ala Leu Tyr Pro Pro Ser Tyr Ser  
85 90 95  
Ser Tyr Ile Asp Phe Leu Tyr Thr Cys Arg Gln Lys Ile Lys Val Leu  
100 105 110  
Asp Ile Thr Tyr Ile Arg Lys Ala Thr Val Thr Val Thr Asn Cys Val  
115 120 125  
Thr Arg Ile Phe Lys Ser  
130

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Asn | His | Leu | Cys | His | Gly | Glu | Asp | Gln | Asp | Val | Xaa | Ala | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Thr | Asp | Leu | Glu | Asn | Lys | Gly | Ile | Ala | Leu | His | Thr | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Thr | Glu | Leu | Ser | Ser | Asp | Asp | His | His | Thr | Thr | Val | Arg | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Gly | Asn | Xaa | Glu | Ala | Asp | Ala | Val | Leu | Leu | Ala | Ile | Gly | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Pro | Asn | Thr | Ala | Leu | Ala | Leu | Glu | Asn | Thr | Asp | Ile | Glu | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Arg | Gly | Glu | Ile | Lys | Val | Asn | Ala | Gln | Leu | Gln | Thr | Ser | Val | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Ile | Tyr | Ala | Ala | Gly | Asp | Val | Lys | Gly | Gly | Leu | Gln | Phe | Thr | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ser | Leu | Asp | Asp | Tyr | Arg | Ile | Ile | Lys | Ser | Ala | Leu | Tyr | Gly | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ser | Arg | Thr | Thr | Asp | Asn | Arg | Gly | Ser | Val | Pro | Tyr | Thr | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Asp | Pro | Pro | Leu | Ser | Arg | Val | Gly | Leu | Thr | Ser | Lys | Glu | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Gln | His | Tyr | Asp | Tyr | Thr | Glu | His | Gln | Leu | Leu | Val | Ser | Ala | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Pro | Arg | His | Lys | Ile | Asn | Asn | Asp | Pro | Arg | Gly | Leu | Phe | Lys | Val | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Asn | Asn | Glu | Asn | Asn | Met | Ile | Leu | Gly | Ala | Thr | Leu | Tyr | Gly | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gln | Ser | Glu | Glu | Leu | Ile | Asn | Ile | Ile | Lys | Leu | Ala | Ile | Asp | Gln | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Pro | Tyr | Thr | Val | Leu | Arg | Asp | Ser | Ile | Tyr | Ser | His | Pro | Thr | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Arg | Ile | Ile |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Glu | Trp | Ala | Leu | Tyr | Ile | Ala | Lys | Asn | Lys | Ile | Ala | Ile | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Gly | Ser | Gly | Met | Gly | Ala | Gln | Cys | Trp | Glu | Phe | Thr |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Glu | Leu | Arg | Glu | Glu | His | Lys | Gln | His | His | Asn | Glu | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | His | Lys | Glu | Leu | Lys | Asp | Lys | Gln | Asp | Lys | Val | Val | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Glu | Gln | Thr | Lys | Ile | Leu | Asn | Arg | Ile | Glu | Glu | Arg | Tyr | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gln | Val | Xaa | Val | Xaa | Gln | Lys | Asn | Glu | Glu | Lys | Thr | Leu | Ala | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Trp | Leu | Val | Gly | Ala | Ile | Trp | Ala | Leu | Val | Thr | Ile | Val | Met |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Ala | Val | Ile | Thr | Ala | Ser | Ile | Xaa | Ala | Leu | Leu | Pro |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Ser | Thr | Leu | Ile | Arg | Ile | Gly | Asp | Ile | Ile | Gln | Ser | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Thr | Asn | Pro | Ile | Ile | Met | Gly | Ile | Ile | Leu | Gly | Gly | Ile | Ile | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Gly | Thr | Ala | Pro | Leu | Ser | Met | Ala | Leu | Thr | Ala | Leu | Leu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Leu | Thr | Gly | Val | Pro | Met | Ala | Ile | Gly | Ala | Met | Ala | Ala | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Ala | Phe | Met | Asn | Gly | Thr | Leu | Phe | His | Arg | Leu | Lys | Leu | Gly | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Lys | Ser | Thr | Ile | Ala | Val | Ser | Ile | Glu | Pro | Leu | Ser | Gln | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ile | Val | Ser | Ala | Asn | Pro | Ile | Pro | Ile | Tyr | Ile | Thr | Asn | Phe | Phe | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Ile | Ala | Gly | Leu | Ile | Ile | Ala | Met | Ser | Gly | Leu | Ile | Asn | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Thr | Gly | Thr | Ala | Thr | Pro | Ile | Xaa | Gly | Phe | Leu | Val | Met | Xaa | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Asn | His | Pro | Met | Thr | Ile | Val | Ile | Tyr | Gly | Val | Val | Met | Ala | Ile |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Gly | Cys | Ala | Cys | Arg | Val | Ile | Leu | Gly | Ser | Ile | Arg | Ile |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```
Val Gly Lys Thr Gly Phe Ala Leu Asn Met Met Leu Asn Ile Ala Arg
 1           5           10           15
Asn Gly Tyr Lys Thr Ser Phe Phe Ser Leu Glu Thr Thr Gly Thr Ser
      20           25           30
Val Leu Lys Arg Met Leu Ser Thr Ile Thr Gly Ile Glu Leu Thr Lys
      35           40           45
Ile Lys Glu Ile Arg Asn Leu Thr Pro Asp Asp Leu Thr Lys Leu Thr
      50           55           60
Asn Ala Met Gly Ser Lys Ser Leu Lys Leu Gly Ile
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```
Val Pro Asn Glu Thr Glu Ala Glu Leu Leu Ser Gly Ile Lys Val Thr
 1           5           10           15
Asn Glu Gln Ser Met Lys Asp Asn Ala Asn Tyr Phe Leu Ser Leu Gly
      20           25           30
Ile Lys Thr Val Leu Ile Thr Leu Gly Lys Gln Gly Thr Tyr Phe Ala
      35           40           45
Thr Lys Asn Gln Ser Gln His Ile Glu Ala Tyr Lys Val Asn Ala Ile
      50           55           60
Asp Thr Thr Ala Ala Gly Asp Thr Phe Ile Gly Ala Phe Val Ser Arg
65           70           75           80
Leu Asn Lys Ser Gln Asp Asn Leu Ala Asp Ala Ile Asp Phe Gly Asn
      85           90           95
Lys Ala Ser Ser Leu Thr Val Gln Lys Thr Arg Arg Ala Ser Ile Tyr
      100          105          110
Ser Ser Thr Arg Arg Ser Lys Ser Ser Leu Asn Glu Ser Asn Thr Ala
      115          120          125
Met Ile
130
```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Met | Arg | Lys | Ile | Gly | Tyr | Ala | Arg | Val | Ala | Tyr | Pro | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Asn | Leu | Asp | Thr | Gln | Leu | Thr | Lys | Leu | Leu | Ile | Asn | Gly | Cys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Tyr | Ser | Glu | Gln | Val | Asn | Val | Tyr | Tyr | Lys | Glu | Gln | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | His | Cys | Leu | Asp | Glu | Leu | Lys | Thr | Asp | Asp | Thr | Leu | Val | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Lys | Leu | Lys | Val | Leu | Gly | Phe | Thr | Pro | Lys | Lys | Leu | Met | Glu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Glu | Ser | Arg | Ile | Leu | Pro | Tyr | Asp | Ile | His | Leu | Glu | Val | Leu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Gly | Ile | Asn | Thr | Asn | Ser | Glu | Glu | Gly | Gln | Ser | Phe | Ile | Glu | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Lys | Met | Leu | Ala | Asp | Ser | Glu | Asn | Ile | Leu | Leu | Lys | Glu | Arg | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Gly | Leu | Glu | Ser | Ala | Lys | Glu | Arg | Gly | Arg | Tyr | Gly | Gly | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gln | Leu | Ser | Glu | Asp | Lys | Arg | Lys | Tyr | Ile | Lys | Gln | Leu | Phe | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ser | Arg | Met | Tyr | Thr | Pro | Asn | Glu | Ile | Ser | Lys | Trp |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ile | Met | Ile | Asn | Glu | Met | Leu | Asn | Pro | Lys | Gln | Gln | Glu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Thr | Cys | Phe | Ile | Asn | Asp | Lys | Pro | Lys | Val | Leu | Ile | Ala | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Lys | Arg | Ala | Gly | Lys | Thr | Tyr | Val | Phe | Ile | Leu | Leu | Phe | Leu | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Ile | Ala | Thr | Tyr | Lys | Asp | Lys | Gly | Leu | Asn | Phe | Ile | Ile | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Thr | Gln | Ala | Ser | Ile | Arg | Arg | Asn | Ile | Leu | Asp | Asp | Met | Glu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Leu | Gly | Arg | Glu | Leu | Thr | Leu | Asp | Lys | Ser | Asn | Ala | Val | Lys | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Gly | Asn | Lys | Val | Tyr | Val | Phe | Asp | Gly | Gln | Asn | Ser | Asp | Ala | Trp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Lys | Ala | Arg | Gly | Phe | Thr | Ser | Ala | Gly | Ala | Phe | Leu | Asn | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ala | Leu | His | Asn | Met | Phe | Ile | Lys | Glu | Val | Phe | Ser | Arg | Cys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Lys | Gly | Ala | Arg | Ile | Leu | Ile | Asp | Thr | Asn | Pro | Glu | Asn | Pro | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Pro | Val | Lys | Lys | Asp | Tyr | Ile | Asp | Lys | Ser | Gly | Gln | Arg | Leu | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Gly | Arg | Leu | Asn | Ile | Lys | Ala | Phe | Gln | Phe | Thr | Leu | Phe | Asp | Asn |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Thr | Phe | Leu | Asp | Glu | Glu | Tyr | Ile | Glu | Ser | Ile | Ile | Ala | Ser | Thr | Pro |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Thr | Gly | Met | Phe | Thr | Asp | Arg | Asp | Ile | Tyr | Gly | Lys | Trp | Val | Ser | Ala |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Glu | Gly | Val | Val | Tyr | Lys | Asp | Phe | Lys | Glu | Lys | Val | His | Tyr | Ile | Thr |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Glu | Glu | Glu | Phe | Lys | Thr | Lys | Gln | Ile | Lys | Arg | Lys | Tyr | Ala | Gly | Val |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Asp | Trp | Gly | Tyr | Glu | His | Tyr | Gly | Ser | Ile | Met | Val | Val | Ala | Glu | Asp |  |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |  |
| Phe | Asp | Gly | Asn | Lys | Tyr | Val | Ile | Glu | Glu | His | Ala | His | Arg | His | Lys |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |  |
| Glu | Ile | Asp | Asp | Trp | Val | Ala | Ile | Ala | Lys | Glu | Leu |     |     |     |     |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Ile | Arg | Ser | His | Ala | Cys | Gly | Leu | Gly | Glu | Pro | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Glu | Val | Ala | Leu | Val | Met | Met | Ile | Xaa | Arg | Leu | Asn | Thr | Leu | Leu |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Lys | Gly | His | Ser | Gly | Ala | Thr | Leu | Val | Ile | Ser | Glu | Thr | Ile | Thr | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Tyr | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | His | Val | Leu | Asp | Phe | Asn | Asp | Lys | Ile | Ile | Asp | Phe | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Asp | Asp | Pro | Ser | Leu | Val | Arg | Ala | Ile | His | Lys | Arg | Asn | Val | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Asn | Ser | Glu | Met | Leu | Glu | Leu | Leu | Ile | Ser | Ser | Glu | Arg | Ala | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Xaa | Phe | Arg | Glu | Arg | His | Arg | Val | Ile | Ile | Arg | Asp | Ser | Asn | Lys | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Trp | Arg | Glu | Phe | Ile | Ile | Asn | Trp | Val | Gln | Asp | Thr | Met | Asp | Gly | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Glu | Ile | Glu | Cys | Ile | Ala | Ser | Tyr | Leu | Ala | Asp | Ile | Thr | Thr | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Tyr | Ala | Pro | Gly | Lys | Phe | Glu | Lys | Lys | Thr | Thr | Ser | Glu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Asp | Val | Leu | Ser | Asp | Thr | Gly | Trp | Glu | Val | Ser | Glu | Xaa | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Tyr | Asp | Gly | Leu | Arg | Thr | Thr | Ser | Trp | Thr | Ser | Tyr | Xaa | Thr | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Glu | Val | Leu | Lys | Gln | Leu | Cys | Thr | Thr | Tyr | Lys | Met | Ala | Leu | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Tyr | Ile | Glu | Leu | Ser | Ser | Asn | Thr | Val | Lys | Gly | Arg | Tyr | Val | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Asn | Lys | Lys | Asn | Ser | Leu | Phe | Gln | Gly | Lys | Glu | Ile | Glu | Tyr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asp | Leu | Ala | Trp | Val | Asn |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Val | Gln | Gly | Gln | Val | Cys | Ser | His | Leu | Ser | Thr | Xaa | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Ile | Ile | Asp | Glu | Glu | His | Glu | Ser | Thr | Tyr | Lys | Gln | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Pro | Arg | Tyr | His | Ala | Arg | Glu | Ile | Ala | Gln | Trp | Arg | Ser | Glu | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | His | Cys | Pro | Val | Ile | Leu | Gly | Ser | Ala | Thr | Pro | Cys | Leu | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Ala | Arg | Ala | Glu | Lys | Asp | Val | Tyr | His | Leu | Leu | Ser | Leu | Pro | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Val | Asn | Gln | Gln | Ala | Leu | Pro | Glu | Ile | Asp | Ile | Val | Asp | Met | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Leu | Ser | Glu | Gly | Asn | Arg | Ser | Met | Phe | Ser | Lys | Asp | Leu | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Ile | Gln | Leu | Arg | Xaa | Arg | Ser | Thr | Gly | Thr | Ser | Cys | Phe | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Lys | Ser | Asp | Val | Val | Met | His | Arg | Leu | Cys | Tyr | Val | Gly | Ile | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Met | Tyr | Arg | Asn | Val | Gln | Xaa | Val | Ile | Phe | His |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Val Lys Tyr Leu Asn Asp Asp Ile Ala Lys Gly Ser Ile Phe Asp Tyr



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Glu | Ser | Asn | Met | Lys | Leu | Arg | Ile | Gly | Phe | Ser | Asp | Ile | Phe | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Val | Asp | Lys | Leu | Thr | Ser | Ser | Glu | Ala | Ser | Leu | Leu | Gln | Leu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Gly | Glu | Pro | Cys | Leu | Arg | Tyr | His | Gln | Thr | Phe | Tyr | Thr | Met | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Lys | Pro | Phe | Asp | Ser | Ser | Asp | Ile | Val | Phe | His | Tyr | Xaa | His | Ala |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Gln | Phe | Tyr | Ile | Pro | Ser | Lys | Lys |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Arg | His | Leu | His | Ile | Pro | Leu | Gln | Ser | Gly | Ser | Asp | Thr | Val | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Arg | Met | Arg | Arg | Lys | Tyr | Thr | Met | Asp | Arg | Phe | Ser | Glu | Arg | Leu |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Thr | Lys | Leu | His | Lys | Ala | Leu | Pro | Asp | Leu | Ala | Val | Thr | Ser | Asp | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ile | Val | Gly | Phe | Pro | Gly | Glu | Thr | Glu | Ala | Glu | Phe | Gln | Glu | Thr | Tyr |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Asp | Phe | Ile | Val | Lys | His | Lys | Phe | Ser | Glu | Leu | His | Val | Phe | Pro | Tyr |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |  |
| Ser | Pro | Arg | Ile | Gly | Thr | Pro | Ala | Ala | Arg | Met | Asp | Asp | Gln | Ile | Asp |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Glu | Glu | Ile | Lys | Asn | Glu | Arg | Val | His | Lys | Val | Asn | Tyr | Ala |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Val | Val | Glu | Ala | Leu | Val | Lys | Thr | Arg | Glu | Gly | His | Gly | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Glu | Leu | Leu | Asp | Lys | Glu | Val | Ala | Thr | Pro | Leu | Asp | Asp | Lys | Val |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Lys | Ile | Lys | Val | His | Tyr | Ala | Gly | Ile | Cys | Gly | Thr | Asp | Leu | His | Thr |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Tyr | Glu | Gly | His | Tyr | Xaa | Val | Asn | Phe | Pro | Val | Thr | Leu | Gly | His | Glu |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Ser | Gly | Xaa | Ile | Val | Glu | Val | Gly | Ser | Arg | Arg |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Ser | His | Val | Asn | Ser | Ile | Lys | Ile | His | Ile | Gly | Arg | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gly | Lys | Thr | Ile | Leu | Lys | Asn | Ile | Ser | Cys | His | Ile | Pro | Lys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Lys | Trp | Ile | Leu | Tyr | Gly | Leu | Xaa | Gly | Ala | Gly | Lys | Thr | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asn | Ile | Leu | Asn | Ala | Tyr | Glu | Pro | Ala | Thr | Thr | Gly | Gly | Val | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Gly | Lys | Met | Pro | Gly | Lys | Val | Gly | Tyr | Ser | Ala | Glu | Thr | Xaa |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Gln | His | Ile | Gly | Phe | Val | Ser | His | Ser | Leu | Leu | Glu | Lys | Xaa | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ile | Ser | Gly | Ala | Phe | Lys | Ser | Thr | Gly | Val | Tyr | Gln | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asp | Glu | Val | Arg | Asn | Glu | Ala | His | His | Leu | Leu | Lys | Leu | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Ala | Lys | Ala | Gln | Gln | Tyr | Ile | Gly | Tyr | Leu | Ser | Thr | Gly | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gln | Arg | Val | Met | Ile | Ala | Arg | Ala | Leu | Met | Gly | Gln | Pro | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Xaa | Gly | Val | Xaa | Pro | Lys | Pro | Leu | His | Ala | Asn | Leu | Met | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Thr | Leu | Ser | Gly | His | Ile | Gln | His | Ile | Ala | Phe | Gly | Pro | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Glu | Ser | Ile | Lys | His | Leu | Gly | Thr | Asn | Gly | Gly | Gly | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Asn | Ser | Ala | Thr | Pro | Phe | Glu | Asn | Pro | Asn | Ile | Trp | Ser | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Glu | Met | Gly | Ser | Met | Met | Leu | Leu | Pro | Met | Ser | Met | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Phe | Gly | Arg | Met | Leu | Ser | Arg | His | Gly | Lys | Arg | Val | His | Arg | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Ile | Leu | Phe | Val | Ala | Met | Phe | Phe | Ile | Phe | Ile | Ala | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Leu | Thr | Met | Trp | Ser | Glu | Tyr | Arg | Gly | Asn | Pro | Ile | Leu | Ala | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Gly | Ile | Tyr | Gly | Pro | Asn | Met | Glu | Gly | Lys | Glu | Val | Arg | Phe | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Gly | Leu | Ser | Ala | Leu | Phe | Thr | Val | Ile | Thr | Thr | Ala | Phe | Thr | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ser | Val | Asn | Asn | Met | His | Asp | Ser | Leu | Thr | Pro | Ile | Gly | Gly | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Pro | Met | Val | Leu | Met | Met | Leu | Asn | Val | Val | Phe | Gly | Gly | Glu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gly | Leu | Met | Asn | Leu | Leu | Ile | Xaa | Xaa | Leu | Leu | Thr | Val | Phe | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ser | Leu | Met | Val | Gly | Lys | Thr | Pro | Glu | Tyr | Leu | Asn | Met | Pro | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Arg | Glu | Met | Lys | Cys | Ile | Val | Leu | Val | Phe | Leu | Ile | His | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Leu | Ile | Leu | Val | Phe | Ser | Ala | Leu | Ala | Phe | Met | Ile | Pro | Gly | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Glu | Ser | Ile | Thr | Asn | Pro | Ser | Phe | His | Gly | Ile | Ser | Gln | Val | Met |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Glu | Phe | Ile | Lys | Pro | Pro | Thr | His | Val | Xaa | Gly | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Val | Gly | Gly | Tyr | Val | Xaa | Ala | Arg | Asn | Xaa | Xaa | Leu | Gln | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ser | Gln | Ala | Arg | Gln | Thr | Ala | Xaa | Asp | Ile | Val | Xaa | Gln | Ala | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Ala | Asp | Xaa | Ile | Lys | Lys | Glu | Lys | Leu | Leu | Xaa | Ala | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Xaa | Gln | Leu | Xaa | Arg | Glu | Xaa | Thr | Glu | Ala | Glu | Xaa | Arg | Glu | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

Arg Xaa Asp Leu Xaa Arg Gln Gly Asn Pro Thr Ser Ser Lys Arg Arg  
85 90 95  
Lys Leu Arg Ala His Ser  
100

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Val Arg Leu His Leu Cys Leu His Gln Arg Lys Ala Phe Leu Thr Asp  
1 5 10 15  
Trp Ser Tyr Ile Ala Gly Asn Ile Ala Ile Val Ala Ile Ile Pro Leu  
20 25 30  
Leu Ile Tyr Phe Tyr Val Pro Phe Phe Lys Lys Leu Lys Val Thr Ser  
35 40 45  
Ala Tyr Glu Tyr Leu Glu Ala Arg Phe Gly Pro Ser Ile Arg Val Xaa  
50 55 60  
Gly Ser Leu Leu Phe Val Val Tyr His Leu Gly Arg Val Ala Ile Val  
65 70 75 80  
Ile Tyr Leu Pro Thr Leu Ala Ile Thr Ser Val Ser Asp Met Asn Pro  
85 90 95  
Tyr Ile Xaa Gly Ser Leu Val Gly Leu Leu Cys Ile Xaa Xaa Thr Ser  
100 105 110  
Xaa Gly Xaa Phe Xaa Gly Val Arg Leu Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Val Tyr Lys Ile Thr Ile Asn Glu Val Phe Asn Met Thr Glu Thr Thr  
1 5 10 15  
Phe Asn Pro Ile Thr Ser Leu Thr Ile Asn Asn Glu Glu Val Lys Ala  
20 25 30  
Lys Ala Thr Phe Met Phe Asp Lys Thr Ala Lys Lys Phe Ala Thr Glu  
35 40 45  
Gln Glu Asp Asn Lys Gly Arg Lys Gln Thr Ile Ser Gly Phe Thr Asn  
50 55 60  
Val Tyr Xaa Ala Leu Leu Glu Arg Asp Thr Val Ala Ile Val Asp Phe  
65 70 75 80  
Trp Glu Cys Ala Thr Ala Tyr Leu Gly Lys Ser Ala Pro Lys Arg Glu  
85 90 95  
Asp Ile Glu Ala Glu Ile Met Glu Ile Ile Glu Arg Glu Asn Asp Thr  
100 105 110  
Leu Ile Phe Tyr Lys Val Arg Trp Thr

115

120

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ser | Asn | Lys | Val | Ala | Phe | Ile | Pro | Ser | Glu | Ala | Gln | Phe | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | Cys | Gln | Asp | Asp | Asn | Asp | Val | Lys | Gln | Ala | Ser | His | Asn | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Asp | Gly | Val | Thr | Phe | Thr |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Gly | Val | Gln | Asp | Asn | Ser | Ile | Gly | Ser | Thr | Asn | Glu | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Gly | Asn | Tyr | Ile | Val | Ile | Lys | His | Ala | Glu | Asn | Glu | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Ala | His | Leu | Gln | Gln | Tyr | Ser | Ile | Ile | Val | Asn | Glu | Gly | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Lys | Tyr | Gly | Asp | Phe | Leu | Gly | Lys | Val | Gly | Asn | Ser | Gly | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Glu | Pro | His | Ile | His | Phe | Gln | Val | Met | Asn | Asp | Lys | Asn | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | Cys | Thr | Ser | Leu | Lys | Ile | Arg | Phe | Leu | Asn | Asn | Leu | Glu | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Lys | Gly | Asp | Val | Val | Cys | Gly | Leu | Gln | Gly | Glu |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Val His Lys Glu Asn Ile Met Leu Asn Xaa Ser Ala Thr Asp Lys Glu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Val | Leu | Xaa | Gln | Met | Ser | Asp | Val | Leu | Phe | Gln | Asn | Gly | Phe | Val |  |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |  |
| Lys | Ser | Thr | Phe | Lys | Asp | Ala | Val | Ile | Asp | Arg | Glu | Lys | Glu | Xaa | Xaa |  |  |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |  |
| Thr | Gly | Leu | Pro | Thr | His | Leu | Cys | Ser | Val | Ala | Ile | Pro | His | Thr | Asp |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Val | Glu | His | Ile | Asn | His | Arg | Thr | Ile | Gly | Val | Gly | Val | Leu | Glu | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Glu | Val | Ala | Val | Ile | Gly | Met | Gly | Thr | Ile | Gly | Ser | Thr | Gly | Arg | Arg |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Arg | Ala | Ala | Phe | Gly | Lys | Asn | Gly | Gly | Asn | Met | Gly | Val | Ser | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |
| Ser | Val | Ala | Tyr | Met | Phe | Asp | His | Val | Ala | Thr | Phe | Gly | Ile | Glu | Gly |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Lys | Ser | Val | Asp | Glu | Ile | Leu | Glu | Thr | Leu | Met | Glu | Pro | Arg | Cys | Lys |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |  |
| Met | Xaa | Met | Met |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Met | Phe | Asn | Thr | Thr | Val | Asn | Ser | Asp | Thr | Asp | Val | Ile | Lys | Tyr |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |
| Gly | Arg | Leu | Leu | Val | Asp | Lys | Gly | Ala | Gln | Ser | Val | Ile | Val | Ser | Leu |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Gly | Gly | Asp | Gly | Ala | Ile | Tyr | Ile | Asp | Lys | Glu | Ile | Ser | Ile | Lys | Ala |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Val | Asn | Pro | Gln | Gly | Lys | Val | Val | Asn | Thr | Val | Gly | Ser | Gly | Asp | Ser |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Thr | Val | Ala | Gly | Met | Val | Ala | Gly | Ile | Ala | Ser | Arg | Phe | Asn | Asp |     |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Ser | Asn | Asp | Ala | Ile | Val | Glu | Leu | Val | Ser | Arg | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Val | Ser | Glu | Met | Met | Glu | Arg | Glu | Thr | Asp | Leu | Gly | Val | Ala | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Phe | Glu | Ile | Ile | Thr | Ala | Met | Met | Phe | Leu | Tyr | Phe | Gly | Glu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| His | Pro | Val | Asp | Phe | Val | Ile | Val | Glu | Ala | Gly | Leu | Gly | Ile | Lys | Asn |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Thr | Asn | Val | Phe | Thr | Pro | Val | Leu | Ser | Ile | Leu | Thr | Ser | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Leu | Asp | His | Thr | Asp | Ile | Leu | Gly | Gly | Thr | Tyr | Leu | Asp | Ile | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Asp | Lys | Gly | Ala | Ile | Ile | Lys | Pro | Asn | Val | Pro | Val | Ile | Tyr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Asn | Glu | Asp | Ala | Leu | Lys | Tyr | Val | Arg |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ile | Gly | Thr | Tyr | Met | Ile | Leu | Ser | Ile | Arg | Lys | Glu | Ser | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Ile | Thr | Asp | Thr | Asp | Glu | Ala | Leu | Lys | Gln | Val | Leu | Lys | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Xaa | Glu | Asn | Lys | Val | Ile | Ser | Gln | Asn | Asn | Lys | Glu | Val | Thr | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ala | Asp | Thr | Ile | Cys | Val | His | Gly | Asp | Gly | Glu | His | Ala | Leu | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Val | Ser | Gln | Ile | Arg | Glu | Ile | Leu | Met | Xaa | Glu | Gly | Ile | Asp | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ala | Asp | Arg | Arg | Tyr | Glu | Asp | Asp | Gly | Gln | Leu | Val | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Ser | Asp | Ala | Val | Ile | Thr | Asp | Thr | Asp | Glu | Ala | Leu | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Lys | Met | Val | Xaa | Glu | Asn | Lys | Val | Ile | Ser | Lys | Asn | Asn | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Thr | Leu | Gln | Ala | Asp | Thr | Ile | Cys | Val | His | Gly | Asp | Gly | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Ala | Leu | Leu | Phe | Val | Ser | Gln | Ile | Arg | Glu | Ile | Leu | Met | Lys | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ile | Asp | Ile | Gln | Ser | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Asp | Ile | Glu | Val | Ser | Asp | Tyr | Lys | Gly | Leu | Thr | Tyr | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ala | Phe | Arg | Gly | Lys | Val | Ile | Leu | Val | Val | Asn | Thr | Ala | Thr | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ile | Tyr | Ser | Glu | Gln | Leu | Lys | Lys | Leu | Glu | Thr | Leu | Xaa | Gln | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Lys | Asp | Arg | Gly | Phe | Val | Val | Leu | Ser | Ser | Pro | Asn | Asn | Asn | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asn | Arg | Gln | Pro | Xaa | Ser | Asn | Glu | Glu | Ile | Leu | Lys | Ile | Xaa | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Glu | Ile | Trp | Val | Leu | His | Phe | Gln | Cys |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ile | Glu | Asn | Glu | Pro | Tyr | Phe | Val | Gly | Lys | Asp | Ile | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Gly | Tyr | Ala | Arg | Ala | Asp | Asn | Ala | Ile | Arg | Asn | His | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Glu | Asp | Lys | Leu | Thr | His | Gln | Phe | Ser | Asp | Ser | Arg | Ser | Lys | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Cys | Asn | Asp | Gln | Ser | Thr | Asn | Gln | Asp | Tyr | Thr | Val |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:409:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Xaa | Leu | Ile | Xaa | Glu | Ser | Xaa | Ile | Asp | Leu | Ala | Ser | Pro | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asn | Arg | Pro | Phe | Ile | Asp | Val | Phe | Leu | Glu | Pro | Thr | Lys | Leu | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Xaa | Pro | Val | Leu | Ala | Leu | Lys | Lys | Glu | Val | Ser | Ile | Lys | Ala | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | His | Ile | Thr | Gly | Gly | Gly | Phe | Tyr | Glu | Asn | Ile | Pro | Arg | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ala | Gly | Tyr | Ala | Ala | Arg | Ile | Asp | Thr | Thr | Ser | Phe | Pro | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ile | Phe | Asp | Trp | Leu | Gln | Gln | Gln | Gly | Asn | Ile | Asp | Thr | Asn | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Tyr | Asn | Ile | Phe | Asn | Met | Gly | Ile | Gly | Tyr | Thr | Val | Ile | Val | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Asp | Ala | Ser | Thr | Arg | Phe | Glu | Asp | Phe | Ser | Arg | Thr | Lys | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Leu | Ser | Asn | Trp | Ser | Tyr | Cys | Glu | Lys |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Phe | Pro | Asn | Lys | Ala | Leu | Ile | Glu | Ser | Ala | Val | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Glu | Leu | Asp | Glu | Ser | Val | Phe | Asn | Gln | Leu | Val | Thr | Asp | Met | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | His | His | Tyr | Asn | Ile | Pro | Gln | His | Tyr | Ile | Asn | Leu | Tyr | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Asn | Ile | Lys | Thr | Leu | Lys | Asp | Val | Pro | Ala | Ser | Tyr | Met | Asn | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asn | Val | Asp | Val | Val | Ala | Asp | Leu | Leu | Leu | Glu | Lys | Ser | Lys | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Tyr | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
Val Leu Phe Ile Gly Phe Phe Val Val Ile Ile Asn Thr Ile Ala Asp
 1           5           10           15
Leu Leu Thr Leu Leu Asp Pro Lys Gln Arg Leu Gln Leu Gly Asn
      20           25           30
Pro Thr Lys His Asn Gln Tyr Thr Ile Asp Ile Arg Lys
      35           40           45
```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```
Val Leu Ile Glu Val His Asp Pro His Glu Leu Glu Arg Ala Xaa Xaa
 1           5           10           15
Val Asn Ala Lys Leu Ile Gly Val Asn Asn Arg Asp Leu Lys Arg Phe
      20           25           30
Val Thr Asn Val Glu His Xaa Asn Thr Ile Leu Glu Asn Lys Lys Pro
      35           40           45
Asn His His Tyr Ile Ser Glu Ser Gly Ile His Asp Ala Ser Asp Val
      50           55           60
Arg Lys Ile Leu His Ser Gly Ile Asp Gly Leu Leu Ile Gly Glu Ala
      65           70           75           80
Leu Met Arg Cys Asp Asn Leu Ser Glu Phe Leu Arg Gln Leu Lys Xaa
      85           90           95
Xaa Lys Val Lys Ser
      100
```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```
Val Ser Asp Glu Pro Xaa Ile Tyr Lys Phe Ile Gln His Asn Xaa Glu
 1           5           10           15
Asn Phe Ile Xaa Thr Ala Ser Xaa Ile Met Asp Gly His Thr Xaa Val
      20           25           30
Ala Pro Leu Lys Xaa Thr His Lys Leu Pro Cys Ala Phe Cys Ser Tyr
      35           40           45
Gln Ser Val Cys His Val Asp Xaa Met Ile Asp Ser Lys Arg Tyr Xaa
      50           55           60
Xaa Val Asp Glu Thr Ile Asn Pro Ile Glu Ala Ile His Asn Ile Asn
      65           70           75           80
```

Ile Asn Asp Val Phe Gly Gly Glu  
85

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | His | Leu | Xaa | Val | Thr | Leu | Arg | Ile | Asp | Arg | Glu | Asn | His | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Gly | Arg | Leu | Ala | Ser | Glu | Ser | Val | Val | Glu | Asn | Met | Phe | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | His | Asp | Asp | Asn | Leu | Lys | Asn | Glu | Val | Ile | Glu | Ala | Lys | Pro | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Glu | Arg | Ile | Thr | Asn | Trp |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | Tyr | Met | Asp | Lys | Gly | Leu | Thr | Gly | His | Ile | Met | Arg | Arg | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Thr | Glu | Ala | Asp | Ala | Ser | Ile | Asn | Trp | Ala | Leu | Gly | Leu | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Ser | Gln | Ile | Ile | Asp | Asn | Thr | Thr | Asn | Leu | Cys | Gly | Asp | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Xaa | Xaa | Leu | Lys | Ser | Gly | Gly | Xaa | Gly | Thr | Gly | Glu | Gln | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asn | Leu | Thr | Ser | Lys | Xaa | Ala | Gln | Ile | Trp |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Gln | Gly | Glu | Pro | Asn | Leu | Trp | Thr | Gly | Arg | Leu | Asp | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Asp | Pro | Lys | Lys | Phe | Arg | His | Phe | Gln | Thr | Val | Thr | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Ser | Lys | Leu | Glu | Lys | Ser | Ser | Met | Pro | Ser | Gly | Val | Gly | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Tyr | Ala | Val | Gly | Gln | Arg | Cys | Cys | Phe | Xaa | Gln | Gly | Ala | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Cys | Lys | Arg | Arg | Thr | Arg | Cys | Asp |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | His | Ile | Thr | His | Tyr | Ile | Asp | Gln | Leu | Asp | Arg | Phe | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gly | Asp | Val | Ile | Lys | Xaa | His | Ser | Gly | Gly | Tyr | His | His | Lys | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Thr | Phe | Asn | Lys | Leu | Gly | Tyr | Ile | Asn | Glu | Asn | Tyr | Ile | Glu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Val | Glu | Asn | Asn | Glu | Lys | Leu | Lys | Lys | Met | Ala | Xaa | Thr | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Glu | Gly | Gly | Val | Ala | Cys | Ala | Thr | Gln | Ile | Ala | Gln | Glu | Lys | Tyr | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Gly | Phe | Lys | Asn | Met | Cys | Val | Xaa | Thr | Asn | Asp | Ile | Glu | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Asn | Asn | Leu | Gln | Xaa | Glu | Gln | Val | Xaa | Val | Val | Ala | Pro | Thr | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Met | Glu | Arg | Asp | Thr | His | Lys | Asp | Gly | Lys | Val | Lys | Trp | Gln | Leu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Gly | Ser | Lys | Ile | Gln | Thr | Ile | Gly | Val | Ile | Leu | Pro | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asn | Pro | Phe | Phe | Ser | Ala | Leu | Met | Gln | Ser | Ile | His | Asp | His | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Ser | Asp | Val | Asp | Leu | Cys | Phe | Leu | Thr | Ser | Thr | Ala | Thr | Asp | Xaa |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Tyr | Asp | Asn | Ile | Lys | His | Leu | Ile | Asp | Arg | Gly | Ile | Asp | Gly | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Gln | Tyr | Ile | Ser | Ser | Pro | Asp | Ala | Leu | Asn | Asn | Tyr | Leu | Lys |

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |
| Lys | His | His | Val | Pro | Tyr | Val | Val | Leu | Asp | Gln | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Xaa | Asp | Glu | Xaa | Xaa | Val | Asp | Lys | Asp | Ala | Leu | Arg | Asn | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Val | Lys | Gly | Gln | Phe | Lys | Ala | Asp | His | Gln | Tyr | Gln | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Pro | Gly | Xaa | Val | Asp | Glu | Val | Tyr | Lys | Gln | Phe | Ile | Asp | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Ala | Gln | Glu | Ala | Ser | Lys | Asp | Glu | Ala | Lys | Gln | Ala | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Lys | Gly | Asn | Pro | Val | Gln | Arg | Leu | Ile | Lys | Leu | Leu | Gly | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Ile | Pro | Ile | Leu | Pro | Ala | Ile | Val | Thr | Thr | Gly | Leu | Leu | Met | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gln | Leu | Leu | Met | His | Met | Ile | His | Tyr | Gly | Thr | Ser | Val | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Arg | Thr | Gln | Ser | Ile | Leu | Asn | Asp | Asp | Lys | Val | Asn | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Asp | Tyr | Ile | Glu | Leu | His | Phe | His | Glu | Asp | Leu | Ser | Leu | Ser | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Glu | Tyr | Val | Gly | Trp | Ser | Glu | Ser | His | Leu | Ser | Lys | Lys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Glu | Ser | Leu | Gly | Val | Gly | Phe | Gln | His | Phe | Leu | Asn | Thr | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | His | Ala | Lys | Leu | Asp | Leu | Thr | Tyr | Thr | Asp | Glu | Thr | Ile | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ile | Ala | Leu | Gln | Asn | Gly | Phe | Ser | Ala | Ala | Ser | Phe | Ala | Arg |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Thr | Phe | Lys | His | Phe | Thr | His | Gln | Thr | Pro | Lys | Gln | Tyr | Arg | Gly | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Ala | Ile | Thr | Glu | Asn | Gln | Gln | Ser | Ala | Gln | His | Asn | Tyr | His |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

Asp Arg Glu Leu Ile Leu Leu Asn Asp Tyr Ile Glu Glu Met Asn  
 145 150 155 160  
 Gln Phe Asn

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Val Asn Leu Gly Gly Ser Val Thr Ser Ile Gln Pro Leu Arg Ile Asn  
 1 5 10 15  
 Leu Thr Ser Asn Glu Asn Phe Thr Asp Lys Asp Trp Gln Ile Thr Gly  
 20 25 30  
 Ile Pro Arg Thr Leu His Ile Glu Asn Ser Thr Asn Arg Thr Asn Asn  
 35 40 45  
 Ala Arg Glu Arg Asn Ile Glu Leu Val Gly Asn Leu Leu Pro Gly Asp  
 50 55 60  
 Tyr Phe Gly Thr Ile Arg Phe Gly Arg Lys Glu Gln Leu Phe Glu Ile  
 65 70 75 80  
 Arg Val Xaa Pro His Xaa Pro Gln Leu Gln Arg Gln Leu Ser Asn Xaa  
 85 90 95  
 Glu Val Arg Asn Tyr Lys Ser Ala Cys  
 100 105

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Val Ile Lys Arg Leu Ile Asn Glu Thr Phe Asp Ala Asn Tyr Ile Glu  
 1 5 10 15  
 Val Ile Glu Gly Gly Ile Glu Glu Thr Gln Thr Leu Ile His Leu Pro  
 20 25 30  
 Phe Asp Tyr Val Ser Tyr Arg Ser Glu Ile Val Gly Lys Ser Phe Ile  
 35 40 45  
 Lys Leu Gln Arg Asn Leu Val Leu  
 50 55

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
Val Ile Thr Phe Val Leu Val Pro Val Leu Ile Pro Thr Leu Lys Arg
 1           5           10           15
Met Lys Phe Gly Gln Ser Ile Arg Glu Glu Gly Pro Gln Ser His Met
      20           25           30
Lys Lys Thr Gly Thr Pro Thr Met Gly Gly Leu Thr Ile Ser Ile Lys
      35           40           45
Val Phe Val Ile Thr Val Phe Gly Gly Tyr Tyr Ile Cys Lys Ile Lys
      50           55           60
Leu Ile Gln Ser Tyr Leu Leu Leu Phe Val Thr Asp Trp Phe Trp Val
65           70           75           80
Asn Trp Phe Tyr Arg
      85
```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```
Val Met Xaa Asn Gly Xaa Leu Ile Glu His Gly Thr Arg Glu Ser Val
 1           5           10           15
Leu His His Pro Glu His Val Tyr Thr Lys Tyr Leu Leu Ser Xaa Xaa
      20           25           30
Lys Lys Xaa Asn Asp His Phe Lys His Val Met Arg Gly Asp Val His
      35           40           45
Xaa
```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```
Val Pro Thr Ile Asp Ser Val Lys Thr Tyr Gly Leu Val Ser Ile Pro
 1           5           10           15
Gly Met Met Thr Gly Leu Ile Ile Gly Gly Val Pro Pro Leu Gln Ala
      20           25           30
Ile Lys Phe Gln Leu Leu Val Val Phe Ile His Thr Thr Ala Xaa Ile
      35           40           45
Met Ser Ala Leu Ile Ala Thr Tyr Leu Ser Tyr Gly Gln Phe Phe Asn
      50           55           60
Ala Arg His Gln Leu Val Ala Arg Asn Thr Asp Val Lys Ser Glu Ser
65           70           75           80
```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```
Val Met Pro Xaa Val Phe Trp Xaa Pro Phe Pro Xaa Ile Phe Ile Gly
 1           5           10           15
Thr Ala Leu Pro Leu Ala Gly Thr Val Ala Thr Gly Ala Ile His Phe
 20           25           30
Thr Ala Asn Glu Val Ile Pro Ile Gly Xaa Met Leu Xaa Asn Asn Gly
 35           40           45
Leu Ile Ala Ile Asn Leu Ala Tyr Gln Asn Leu Asp Arg Ala Phe Val
 50           55           60
Gln Asp Gly Thr Asn Ile Glu Ser Lys Leu Ser Leu Ala Ala Thr Pro
 65           70           75           80
Lys Leu Ala Ser Lys Gly Ala Ile Arg Glu Ser Ile Arg Leu Ala Ile
 85           90           95
Gly Ala Asn Asn
          100
```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```
Val Lys Val Gly Lys Ser Met Glu Gly Leu Asn His Arg Arg Asn Thr
 1           5           10           15
Glu Lys Glu Glu Thr Thr Gln Thr Gln Ser Val Ala Pro Asn Thr Gly
 20           25           30
Glu Glu Gly Met Ser Ser Gly Lys
 35           40
```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```
Val Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val
 1           5           10           15
Lys His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro
```





(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Ala | Gly | Glu | Asn | Phe | Met | Ile | Leu | Leu | Ala | Ser | Arg | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Val | Tyr | Ser | Leu | Gly | Leu | Ala | Arg | Thr | Arg | Arg | Gln | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Val | Asn | His | Gly | His | Ile | Leu | Val | Asp | Gly | Lys | Arg | Val | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Ser | Tyr | Ser | Val | Lys | Pro | Gly | Gln | Thr | Ile | Ser | Val | Arg | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ser | Gln | Lys | Leu | Asn | Ile | Ile | Val | Glu | Ser | Val | Glu | Ile | Asn | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Val | Pro | Glu | Tyr | Leu | Asn | Phe | Asp | Ala | Asp | Ser | Leu | Thr | Gly | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Val | Arg | Leu | Pro | Glu | Arg | Ser | Glu | Leu | Pro | Ala | Glu | Ile | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Leu | Ile | Val | Glu | Tyr | Ser | Cys | Gln | Asp | Asn | Thr | Phe | Ile | Thr | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | His | Asn | Cys | Gly | Cys | Phe | Phe | Tyr |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Leu | Val | Arg | Met | Val | Tyr | Lys | Gly | Lys | Ile | Ser | Asp | His | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Val | Trp | Glu | Lys | Ala | Thr | Thr | Tyr | Gln | Met | Tyr | His | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Leu | Ile | Ile | Gly | Val | Ile | Ser | Gly | Thr | Thr | Ser | Ile | Asn | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Ala | Gly | Trp | Leu | Ile | Phe | Ala | Gly | Ile | Ile | Phe | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Tyr | Ile | Leu | Val | Leu | Thr | Gln | Ile | Lys | Val | Leu | Gly | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Pro | Ile | Gly | Gly | Val | Leu | Phe | Ile | Ile | Gly | Trp | Ile | Met | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Thr | Phe | Lys | Phe | Ala | Gly |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```
Val Leu Lys Leu Phe Gln Met Arg Ser Pro Ile Phe Arg Glu Pro Ser
 1           5           10          15
Ala Asn Asn Ala Val Lys Thr Leu Ile Ala Met Gly Ser Ile Leu Ala
 20          25          30
Phe Leu Leu Val Gly Ile Gly Gly Leu Ala Tyr Val Tyr Gly Ile Met
 35          40          45
Pro Gln Thr Glu Thr Thr Val Leu Ser Gln Leu Ala Met Gln Ile Phe
 50          55          60
Gly
65
```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```
Val Met Arg Gly Thr Ile Ile Ile Pro Thr Thr Lys Pro Gly Leu Ile
 1           5           10          15
Ala Leu Asn Ser Pro Arg Pro Asp Met Lys Asp Leu Asn Thr Gly Val
 20          25          30
Thr Lys Val Asn Ala Lys Lys Pro Asn Thr Ile Val Gly Ile Pro Ala
 35          40          45
Lys Ile Ser Asn Ile Gly Leu Ile Met Arg Arg Ala Arg Ala Leu Ala
 50          55          60
Tyr Ser Leu Lys
65
```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```
Val Ser Asp Thr Ala Val Met Ile Ala Trp Leu Val Lys Ile Pro His
 1           5           10          15
Ser Thr Met Pro Ile Leu Gly Thr Ser Gln Leu Lys Arg Xaa Asp Gln
 20          25          30
Ala Ile Glu Gly Leu Gln Leu Asn Leu Asp Asp Gln Val Val Gly
```

## (2) INFORMATION FOR SEQ ID NO:436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

Val Asp Ile Pro Leu Leu Phe Glu Asn Glu Leu Glu Asn Thr Val Asp
 1           5           10           15
Glu Val Trp Val Val Tyr Thr Ser Glu Ser Ile Gln Met Asp Arg Leu
 20           25           30
Met Xaa Arg Xaa Asp Leu Ser Leu Glu Asp Ala Lys Ala Arg Val Tyr
 35           40           45
Xaa Pro Asn Phe Tyr
 50

```

## (2) INFORMATION FOR SEQ ID NO:437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

Val Met Gln Val Phe Thr Trp Gln Gln Tyr Val Glu Ile Val Val Asn
 1           5           10           15
Glu Gly Arg Asp Ala Ala Asn Ala Ala Gln Glu Lys Ala Val Lys Glu
 20           25           30
Gly Lys Ile Ile Ile Lys Asp Ser Ile Ala Asp Ile Phe Leu Gln Gln
 35           40           45
Ile Leu Thr Arg Pro Ala Glu His Asp Val Val Ala Thr Met Asn Leu
 50           55           60
Asn Gly Asp Tyr Ile Ser Asp Ala Leu Ala Ala Gln Val Gly Xaa Ile
 65           70           75           80
Gly Ile Ala Pro Gly Ala Asn Ile Asn Tyr Glu Thr Gly His Ala Ile
 85           90           95
Phe Glu Ala Thr His Gly Leu Xaa Ser Lys Ile Cys Arg Phe Lys
 100          105          110

```

## (2) INFORMATION FOR SEQ ID NO:438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Met | Phe | Ile | Thr | Gly | Met | Gln | Tyr | Gly | Asp | Lys | Val | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Val | Ser | Arg | Gly | Ala | Val | Phe | Gly | Met | Thr | Gly | Val | Leu | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Thr | Asp | Gln | Leu | Leu | Ala | Phe | Phe | Asn | Asn | Arg | Tyr | Trp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gln | Phe | Asn | Pro | Arg | Gly | Gly | Trp | Ser | Pro | Ser | Gly | Pro | Arg | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Tyr | Ala | Asn | Gly | Gly | Leu | Ile | Thr | Lys | His | Gln | Leu | Xaa | Glu | Val | Gly |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Asp | Lys | Gln | Glu | Met | Val | Ile | Pro | Leu | Thr | Arg | Arg | Lys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ile | Gln | Leu | Thr | Glu | Gln | Val | Met | Arg | Ile | Ile | Gly | Met | Asp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Xaa | Pro | Asn | Asn | Ile | Thr | Val | Asn | Asn | Asp | Thr | Ser | Thr | Val | Glu | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Phe | Glu | Thr | Asn | Cys | Tyr | Val | Lys |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Gly | Ala | Leu | Asp | Val | Asn | Gln | Val | Asn | Val | Ser | Glu | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ala | Asn | Gln | Pro | His | Ser | Val | Leu | Leu | Ile | Asp | Thr | Gln | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Glu | Asn | Asn | Ser | Glu | Leu | Asn | Gln | Val | Gly | Thr | Ser | Thr | Lys | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ile | Ala | Phe | Cys | Ile | Asp | Val | Arg | Ser | Glu | Pro | Phe | Arg | Arg | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Ala | Ala | Gly | Pro | Phe | Glu | Thr | Ile | Gly | Ile | Ala | Gly | Phe | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Leu | Pro | Ile | Gln | Lys | Asp | Ala | Val | Asp | Glu | Gln | Phe | Lys | His | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Pro | Val | Met | Ser | Arg | Ala | Ala | Gly | Ile | Ser | His |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Phe | Gly | Val | Thr | Gly | Thr | Asn | Gly | Lys | Thr | Ser | Ile | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asp | Ser | Phe | Asn | Ser | Xaa | Lys | Val | Thr | Lys | Lys |     |     |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Gly | Thr | Ala | Asn | Gly | Val | Gly | Ser | Thr | Leu | Xaa | Leu | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Asp | Gln | Phe | Ile | Leu | Leu | Ile | Phe | Tyr | Gly | Thr | Phe | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Phe | Thr | Glu | Phe | Gly | Ser | Pro | Phe | Gly | Gly | Gly | Lys | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asn | Pro | Ser | Asn | Leu | Pro | Asp | Gly | Asp | Gly | Asn | Gly | Gly | Gly | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Glu | Phe | Gly | Leu | Thr | Lys | Ser | Ser | Arg | Thr | Ser | Leu | Thr | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Asp | Val | Tyr | Phe | Asp | Leu | Gly | Ser | Gln | Arg | Gly | Ser | Gly | Ala | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Asn | Arg | Gly | Thr | Ile | Asn | Lys | Ile | Ile | Gly | Val | Arg | Lys |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asp | Asn | Asp | Leu | Asn | Gln | Val | Thr | Leu | Ala | Asp | Tyr | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Lys | Leu | Ile | Ser | Val | Val | Pro | Ser | Ile | Asp | Thr | Gly | Val | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Gln | Thr | Arg | Lys | Phe | Asn | Ser | Glu | Ala | Ser | Lys | Glu | Glu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Leu | Thr | Ile | Ser | Ala | Asp | Leu | Pro | Phe | Ala | Gln | Lys | Arg | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Ala | Ser | Ala | Gly | Leu | Asp | Asn | Val | Ile | Thr | Leu | Ser | Asp | His | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Ser | Phe | Gly | Glu | Asn | Tyr | Gly | Val | Val | Met | Glu | Arg | Thr | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Arg | Ile | Arg | His | Glu | Leu | Val | Gln | Tyr | Leu | Tyr |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Gln | Glu | Arg | Tyr | Ser | Arg | Gln | Ile | Leu | Phe | Lys | Gln | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ile | Gly | Gln | Ser | Lys | Ile | Asn | Gln | Lys | Cys | Ala | Leu | Ile | Ile | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Gly | Ala | Leu | Gly | Thr | His | Val | Ala | Glu | Gly | Leu | Val | Arg | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Lys | Leu | Ile | Ile | Val | Asp | Arg | Asp | Tyr | Ile | Glu | Phe | Ser | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Gln | Arg | Gln | Thr | Leu | Phe | Thr | Glu | Glu | Asp | Ala | Leu | Lys | Met | Met |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Lys | Val | Val | Ala | Lys | Lys | His | Leu | Leu | Ala | Leu | Arg | Ser | Asp |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Asp | Ile | Asp | Gly | Cys | Ile | Ala | His | Val | Asp | Tyr | Tyr | Phe | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Thr | Trp | Thr | Gly | Arg | Trp | Thr | Leu | Leu | Leu | Met | Gln | Pro | Ile | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | His | Asp | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Leu | Met | Lys | Leu | Val | Phe | Val | Ala | Arg | Ala | Gly | Asn | Met | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ala | Ile | Phe | Thr | Gly | Ile | Ile | Asn | Ser | Ser | Asn | Leu | Asp | Ala | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ile | Tyr | Leu | Thr | Asn | Lys | Ser | Asn | Glu | Gln | Ala | Leu | Lys | Ala | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Lys | Leu | Gly | Val | Asn | Tyr | Ser | Tyr | Asp | Asp | Ala | Thr | Leu | Leu |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |
| Lys | Asp | Ala | Asp | Tyr |
| 65  |     | 70  |     | 75  |
| Ala | Leu | Ala | Thr | Arg |
|     |     | 85  |     | 90  |
| Met | Ser | Ile | Met | Ala |
|     |     | 100 |     | 105 |
| Glu | Cys | Gln | Asn | Pro |
|     |     | 115 |     | 120 |
| Val | Gly | His | Ser | Val |
| 130 |     |     |     | 135 |

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Arg | Ser | Leu | Met | Lys | Ile | Leu | Ile | Asn | Val | Leu | Glu | Gln | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Asn | Ala | Val | Val | Leu | Phe | Met | Gly | Ala | Gly | Asp | Ile | Gln | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Asn | Ala | Tyr | Leu | Asp | Lys | Leu | Gly | Met | Lys | Asn | Ala | Phe |     |     |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Glu | Asn | Glu | Pro | Leu | Lys | Pro | Asn | His | Glu | Leu | Tyr | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Asn | Val | Thr | Ile | Thr | Ala | His | Ile | Thr | Gly | Asn | Asp | Tyr | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Asp | Leu | Leu | Asp | Ile | Phe | Lys | Asn | Asn | Leu | Val | Asn | Phe | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asn | Lys | Asn | Gly | Leu | Ile | Glu | Asn | Glu | Val | Asp | Ala | Lys | Lys | Gly | Tyr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
Val Lys Glu Ile Thr Lys Leu Asn Gly Leu Cys Leu Lys Trp Val Ala
 1           5           10           15
Pro Gly Thr Arg Gly Val Pro Asp Arg Ile Ile Ile Met Pro Glu Gly
      20           25           30
Lys Thr Tyr Phe Val Glu Met Lys Gln Glu Lys Gly Lys Leu His Pro
      35           40           45
Leu Gln Lys Tyr Val His Arg Gln Phe Glu Asn Arg Asp His Lys Val
      50           55           60
Tyr Val Leu Trp Asn Lys Glu Gln Val Asn Thr Phe Ile Arg Met Val
65           70           75           80
Gly Gly Thr Phe Gly Asp
      85
```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
Val Trp Gly Ile Val Ile Leu Gly Gly Tyr Glu Gln Phe Ile Lys Ser
 1           5           10           15
His Leu Arg Lys Ile Tyr Ile Asp Gly Val Ser Asn Met Gln Glu His
      20           25           30
Val Val Val Thr Leu Asp Gly Lys Asp Tyr Leu Val Glu Pro Gly Thr
      35           40           45
Asn Leu Leu Glu Phe Ile Lys Ser Gln Asp Thr Phe Val Pro Ser Ile
      50           55           60
Cys Tyr Asn Glu Ser Met Gly Pro Ile Gln Thr Cys Asp Thr Cys Thr
65           70           75           80
Val Glu Ile Asp Gly Lys Ile Glu Arg Ser Cys Ser Thr Val Ile Asp
      85           90           95
Arg Pro Met Thr Val Asn Thr Val Asn Asp Val Lys Asp Ala Gln
      100           105           110
Lys Glu Pro
      115
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
Val Leu Thr Met Ile Ser Tyr Leu Leu Phe Leu Leu Ser Gly Leu Ala
 1           5           10           15
Asn Gly Leu Ile Asn Met Asn Lys Glu Gly Ile Asp Lys Trp Gln Ala
      20           25           30
```

Asp Ala Ile Xaa Leu Asn Lys Asp Ala Asn Gln Thr Val Gln Xaa Ser  
 35 40 45  
 Cys Phe  
 50

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Val Lys Lys Val Val Lys Tyr Leu Ile Ser Leu Ile Leu Ala Ile Ile  
 1 5 10 15  
 Ile Val Leu Phe Val Gln Thr Phe Val Ile Val Gly His Val Ile Pro  
 20 25 30  
 Asn Asn Asp Met Ser Pro Thr Leu Asn Lys Gly Asp Arg Val Ile Val  
 35 40 45  
 Asn Lys Ile Lys Val Thr Phe Asn Gln Leu Asn Asn Gly Asp Ile Ile  
 50 55 60  
 Thr Tyr Arg Arg Gly Asn Glu Ile Tyr Thr Ser Arg Ile Ile Ala Lys  
 65 70 75 80  
 Pro Gly Gln Ser Met Ala Phe Arg Gln Gly Gln Leu Tyr Arg Asp Asp  
 85 90 95  
 Arg Pro Val Asp Ala Ser Tyr Ala Lys Asn Arg Lys Ile Lys Asp Phe  
 100 105 110  
 Ser Leu Arg Asn Phe Lys Glu Leu Asp Gly Asp Ile Ile Pro Pro Asn  
 115 120 125  
 Asn Phe Val Val Leu Asn Asp His Asp Asn Asn Gln His Asp Ser Arg  
 130 135 140  
 Gln Phe Gly Leu Ile Asp Lys Lys Asp Ile Ile Gly Asn Ile Ser Leu  
 145 150 155 160  
 Arg Tyr Tyr Pro Phe Ser Lys Trp Thr Ile Gln Phe Lys Ser  
 165 170

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Val Ser Lys Leu Lys Lys Glu Leu Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Ile Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Val | Ile | Gly | Val | Pro | Gly | Asp | Lys | Val | Glu | Tyr | Lys | Asn | Asp | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Tyr | Val | Asn | Gly | Lys | Lys | Gln | Asp | Glu | Pro | Tyr | Leu | Asn | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | His | Lys | Gln | Gly | Asp | Tyr | Ile | Thr | Gly | Thr | Phe | Gln | Val | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Leu | Pro | Glu | Cys | Glu | Ser | Gln | Ile | Lys | Cys | Gln | Ser | Lys | Arg | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Arg | Asn | Gln | Lys | Val | Pro | Xaa | Gly | Pro | Glu | Asn | Pro | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Arg | Pro | Thr | His | Pro | Xaa | Gly | Pro | Val | Asn | Pro | Asn | Asn | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Ser | Xaa | Asp | Arg | Ala | Lys | Pro | Asn | Gly | Pro | Gly | Pro | Phe | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Trp | Ile | Lys | Met | Ile | Lys | Val | Lys | Lys | Ser | Lys | Ile | Ala | Lys | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Asn | Gln | Glu | Lys | Lys | Arg | Ala | Glu | Leu | Pro | Lys | Thr | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ser | Thr | Gln | Lys | Gly | Leu | Ile | Phe | Ser | Ser | Ile | Ile | Gly | Ile | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Met | Leu | Leu | Ala | Arg | Arg | Arg | Lys | Asn |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | His | Val | Asp | Val | Asp | Glu | Arg | Leu | Ile | Asp | Phe | Gln | Ile | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Met | Pro | Leu | Pro | Lys | Asn | Asp | Arg | Ser | Gln | Arg | Pro | Ala | Arg | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Thr | Ile | Gln | Ala | Lys | Thr | Arg | Gly | Lys | Ser | Leu | Asp | Lys | Ser | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Asp | Lys | Gly | Arg |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | His | Ile | Leu | Gln | Asn | Ile | Gly | Met | Thr | Ile | Gln | Leu | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Thr | Gly | Ile | Pro | Leu | Pro | Phe | Ile | Ser | Tyr | Gly | Gly | Ser | Ala | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Ser | Met | Met | Thr | Gly | Ile | Gly | Ile | Val | Leu | Ser | Ile | Tyr | Tyr | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Pro | Lys | Arg | Tyr | Val | Asp | Leu | Tyr | His | Pro | Lys | Ser | Asn |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Xaa | Arg | Glu | Val | Val | Asn | His | Ile | Glu | Gln | Thr | Ile | Xaa | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Gly | Val | Asn | Glu | Met | Ser | Phe | Asp | Thr | Met | Val | Leu | Phe | Gly | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Xaa | Ala | Ser | Pro | His | Gly | Thr | Pro | Gly | Asp | Arg | Arg | Leu | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Glu | Tyr | Val | Leu | Phe | Asp | Leu | Gly | Val | Ile | Tyr | Glu | His | Tyr | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asp | Met | Thr | Arg | Thr | Ile | Lys | Phe | Trp |     |     |     |     |     |     |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Val | Gly | Asp | Gly | Pro | Xaa | Gln | Arg | Glu | Ile | Val | Phe | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Asp | Xaa | Xaa | Ser | Trp | Gly | Gly | Xaa | Thr | Lys |     |     |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```
Val Gly Pro Asn Thr Glu Ala Glu Phe Arg Lys Glu Ile Gln Leu Pro
 1           5           10           15
Gly Asn Ala Ser Trp Gly Val Gly Pro Asn Thr Glu Xaa Ile Gly Phe
          20           25           30
Pro Ile Ser Ser Asp Asn Ala Ser Trp Gly Val Gly Pro Asn Lys Glu
          35           40           45
Asn Phe Glu Lys Lys Phe Tyr Arg Gln Cys Glu Leu Gly Cys Gly Pro
 50           55           60
Gln His Arg Ser Leu Arg
65           70
```

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
Val Thr Arg Leu Phe Tyr Met Phe Asp Lys Glu Thr Met Ile Ala Ser
 1           5           10           15
Met Gly Ile Gly Gly Gly Leu Gly Asn Ala Ala Leu Phe Thr Arg Phe
          20           25           30
```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```
Val Ser Ala Ile Val Xaa Tyr Xaa Ser Phe Asp Cys Xaa Ile Arg Lys
 1           5           10           15
Phe Lys Leu Lys Thr Pro Gly Arg Glu Asp Glu Glu Thr Glu Ile Arg
          20           25           30
Asn Ser Ser Val Ala Lys Leu Pro Xaa Asp Val Leu Asp Xaa Met Gly
          35           40           45
Trp Lys Arg Lys His
50
```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Arg | Met | Thr | Glu | Gln | Pro | Ser | Tyr | Tyr | Ser | Ile | Ile | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Val | Arg | Tyr | Asp | Asn | Arg | Leu | Thr | Asp | Ser | Glu | Lys | Leu | Leu | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Ile | Thr | Ser | Leu | Ser | Asn | Lys | Tyr | Gly | Tyr | Cys | Thr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Tyr | Phe | Ala | Lys | Leu | Tyr | Glu | Val | Thr | Lys | Val | Thr | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Ile | Ala | Asn | Leu | Lys | Glu | Cys | Gly | Tyr | Leu | His | Val | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Arg | Asn | Gly | Asn | Glu | Ile | Lys | Gln | Arg | Lys | Leu | Tyr | Pro | Leu | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Met | Ile | Arg | Pro | Ile | Asn | Thr | Asn | Asp | Asn | Thr | Pro | Ile | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Asn | Thr | Pro | Ile | Ile | Thr | Asn | Val | Lys | Glu | Thr | Ile | Gln | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Ile | Gln | Val | Ile | Thr | Ile |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Phe | Xaa | Ala | Ala | Ile | Arg | Met | Asp | Lys | Ser | Gly | Tyr | Ser | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Tyr | Glu | Gln | Asn | Thr | His | Ile | Gly | Gly | Lys | Val | Asn | Xaa | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Asp | Gly | Phe | Gly | Phe | Asp | Leu | Gly | Pro | Ser | Ile | Leu | Thr | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Tyr | Ile | Cys | Glu | Lys | Leu | Phe | Glu | Tyr | Ser | Lys | Lys | Gln | Met | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Tyr | Val | Thr | Ile | Lys | Arg | Leu | Xaa | His | Gln | Trp | Arg | Ser | Phe | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Asp | Gly | Thr | Thr | Ile | Asp | Leu | Tyr | Glu | Gly | Ile | Lys | Glu | Thr | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | His | Asn | Ala | Ile | Leu | Ser | Lys | Gln | Asp | Ile | Glu | Glu | Leu | Gln | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Asn | Tyr | Thr | Arg | Arg | Ile | Asp | Arg | Ile | Thr | Glu | Lys | Gly | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asn | Tyr | Gly | Leu | Asp | Thr | Leu | Ser | Gln | Ile | Ile | Lys | Phe | His | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Leu | Asn | Ala | Leu | Ile | Asn | Tyr | Asp | Tyr | Val | His | Thr | Met | Gln | Gln |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Ala | Ile | Asp | Lys | Arg | Ile | Ser | Asn | Pro | Tyr | Leu | Arg | Gln | Met | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Tyr | Phe | Ile | Lys | Tyr | Val | Gly | Ser | Ser | Ser | Tyr | Asp | Ala | Xaa | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Leu | Ser | Met | Leu | Phe | His | Met | Gln | Gln | Glu | Gln | Gly | Xaa | Xaa | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Glu | Gly | Gly | Ile | His | His | Xaa | Ala | Asn | Ala | Leu | Glu | Lys | Leu | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Glu | Glu | Gly | Val | Thr | Ile | His | Thr | Gly | Ala | Arg | Val | Asp | Asn | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Thr | Tyr | Gln | Arg | Arg | Val | Thr | Gly | Val | Arg | Leu | Asp | Thr | Gly | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Val | Lys | Ala | Asp | Tyr | Ile | Ile | Ser | Asn | Met | Glu | Val | Ile | Pro | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Lys | Tyr | Leu | Ile | His | Leu | Gly | Tyr | Ser | Thr | Ile | Lys | Gln | Ile | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Gly | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Thr | Ser | Arg | Gln | Ser | Pro | Phe | Ala | Gln | Arg | Ile | Glu | Gln | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Lys | Arg | Leu | Asn | Leu | Pro | Asp | Leu | Pro | Thr | Thr | Thr | Ile | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Pro | Gln | Ser | Arg | Glu | Val | Arg | Lys | Tyr | Arg | Ala | Asp | Trp | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Ile | Thr | Asp | Glu | Ala | Tyr | Glu | Thr | Phe | Leu | Lys | Asn | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Trp | Ile | Lys | Ile | Gln | Glu | Asp | Ile | Gly | Leu | Asp | Val | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Gly | Glu | Phe | Glu | Arg | Asn | Asp | Met | Val | Glu | Phe | Phe | Gly | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gln | Gly | Phe | Leu | Val | Thr | Lys | Phe | Gly | Trp | Val | Gln | Ser | Tyr | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Ala | Val | Lys | Pro | Pro | Ile | Ile | Tyr | Gly | Asp | Val | Lys | Trp | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Leu | Thr | Val | Asp | Glu | Thr | Val | Tyr | Ala | Gln | Ser | Leu | Thr | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Pro | Val | Lys | Gly | Met | Leu | Thr | Gly | Pro | Val | Thr | Ile | Leu | Asn | Trp |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Phe | Glu | Arg | Val | Asp | Leu | Pro | Arg | Lys | Val | Ala | Gln | Asp | Gln | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Ala | Ile | Asn | Glu | Glu | Val | Leu | Ala | Leu | Glu | Ala | Ala | Gly | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Val | Ile | Gln | Val | Asp | Glu | Pro | Ala | Leu | Arg | Glu | Gly | Leu | Pro | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Ser | Glu | Tyr | His | Glu | Gln | Tyr | Leu | Lys | Asp | Ala | Gly | Phe | Ile | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Met | Met | Pro | Arg | Lys | Phe | Arg | Val | Leu | Gln | Ile | Gly | Gly | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Glu | Pro | Ile | Phe | Gln | His | Lys | Lys | Gly | Val | Ser | Trp | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asp | Ile | Gly | Leu | Phe | Glu | Phe | Asp | Ser | Gly | Tyr | Val | Glu | Ala | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Ile | Val | Glu | Ala | Glu | Gly | Arg | Phe | Asp | Phe | Ile | Tyr | Ile | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Tyr | Ser | Glu | Thr | Leu | Thr | Asn | Leu | Leu | Gln | Met | Ile | Ser | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Tyr | Asn | Thr | Tyr | Val | Asp | Glu | Ser | Phe | Trp | Ser | Val | Glu | Tyr | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asp | Glu | Asn | Cys | Pro | Lys | Ile | Arg | Cys | Ser | Thr | Asn | Tyr | Ile | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Leu | Glu | Gly | Thr |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Lys | Gly | Tyr | Tyr | Pro | Ile | Lys | Arg | Ala | Ile | Asp | Leu | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Val | Leu | Leu | Phe | Leu | Thr | Phe | Pro | Ile | Met | Phe | Ile | Phe | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Ala | Ile | Val | Ile | Asp | Ser | Pro | Gly | Asn | Pro | Ile | Tyr | Ser | Gln | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Gly | Lys | Met | Gly | Lys | Leu | Ile | Lys | Ile | Tyr | Lys | Leu | Arg | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Cys | Lys | Asn | Ala | Glu | Lys | Asn | Gly | Ala | Gln | Trp | Ala | Asp | Lys | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asp | Arg | Ile | Thr | Asn | Val | Gly | Lys | Phe | Ile | Arg | Lys | Thr | Arg | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Glu | Leu | Pro | His | Leu | Ile | Asn | Val | Val | Lys | Gly | Glu | Met | Ser | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Pro | Arg | Pro | Glu | Arg | Pro | Glu | Phe | Val | Glu | Leu | Phe | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Val | Ile | Gly | Phe | Glu | Gln | Arg | Cys | Leu | Val | Thr | Pro | Gly | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Ala | Gln | Ile | Gln | Gly | Gly | Tyr | Asp | Leu | Thr | Pro | Gln | His | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



Leu Lys Tyr Asp Met Lys Tyr Ile His Lys Gly Ser Leu Met Met Glu  
                           165                          170                          175  
 Leu Tyr Ile Ser Ile Arg Thr Leu Met Val Val Ile Thr Gly Glu Gly  
                           180                          185                          190  
 Ser Arg

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Val Lys Ala Leu Lys Leu Tyr Gly Val Glu Asp Leu Arg Tyr Glu Asp  
 1                          5                          10                          15  
 Asn Glu Lys Pro Val Ile Glu Ser Ala Asn Asp Val Ile Val Lys Val  
                           20                          25                          30  
 Arg Ala Thr Gly Ile Cys Gly Ser Asp Thr Ser Arg Asn Xaa Xaa Met  
                           35                          40                          45  
 Gly Pro Tyr Ile Lys Gly Met Pro Phe Gly His Glu Phe Ser Gly Val  
                           50                          55                          60  
 Val Asp Ala Ile Gly Ser Asp Val Thr His Val Asn Val Gly Asp Lys  
 65                          70                          75                          80  
 Val Thr Gly Cys Pro Ala Ile Pro Cys Tyr Gln Cys Glu  
                           85                          90

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Val Gly Glu Ala Glu Ser Ser Leu Ser Phe Ile Gly Glu Leu Asp Asn  
 1                          5                          10                          15  
 Ile Asp Asp Lys Thr Tyr Gln Asp Ala Leu Val Ile Val Cys Asp Thr  
                           20                          25                          30  
 Ala Asn Ala Pro Arg Ile Asp Asp Glu Arg Tyr Ser Thr Gly Ser Lys  
                           35                          40                          45  
 Leu Ile Lys Ile Asp His His Pro Ala Val Asp Gln Tyr Gly Asp Ile  
                           50                          55                          60  
 Asn Leu Val Asn Thr Asn Ala Ser Ser Thr Ser Glu Ile Ile Tyr Asp  
 65                          70                          75                          80  
 Leu Ile Ser His Phe Asn Asp Glu Ala Ile Val Asn Lys Gly Thr Ser  
                           85                          90                          95  
 Glu Cys Phe Ile Pro Trp Tyr Arg Arg  
                           100                          105

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ser | Leu | Val | Ile | Val | Leu | Ile | Lys | Asp | Gly | Cys | Val | Ser | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Leu | Ile | Arg | Gln | Gly | Asn | Met | Ile | Lys | Arg | Asp | Xaa | Pro | Met |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Pro | Leu | His | Gln | Thr | Glu | Glu | Glu | Phe | Tyr | Thr | Phe | Ile | Gly |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Phe | Tyr | Ser | Leu | Asn | Gln | His | Ile | Leu | Pro | Lys | Glu | Val | His | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Asn | Leu | Asp | Lys | Glu | Met | Ile | Gln | Ser | Val | Val | Asp | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Val | Gln | Pro | Ala | Arg | Gly | Pro | Lys | Lys | Asp | Met | Val | Asp | Leu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | His | Asn | Ala | Lys | Val | Ser | Leu | Asn | Asn | Lys | Phe | Glu | Leu | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asp | Glu | Ser | Arg | Thr | Ile | Lys | Ala | Ile | Glu | Glu | Leu | Gly | Thr | Gln |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Gly | Ile | Gln | Thr | Pro | Ile | Arg | Ile | Glu | Ala | Phe | Asp | Asn | Ser | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gln | Gly | Val | Asp | Pro | Val | Ser | Ala | Met | Val | Thr | Phe | Val | Asp | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Pro | Asp | Lys | Lys | Asn | Tyr | Arg | Lys | Tyr | Lys | Ile | Lys | Thr | Val | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Pro | Asp | Asp | Tyr | Lys | Ser | Met | Arg | Glu | Val | Val | Arg | Arg | Arg | Tyr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Arg | Val | Leu | Asn | Glu | Gly | Leu | Pro | Leu | Pro | Asp | Leu | Ile | Ile | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Gly | Gly | Lys | Gly | His | Met | Asn | Gly | Val | Ile | Asp | Val | Leu | Gln | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Leu | Gly | Leu | Asp | Ile | Pro | Val | Ala | Gly | Leu | Gln | Lys | Asn | Asp | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Gln | Thr | Ser | Glu | Leu | Leu | Leu | Trp | Arg |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Gln | Xaa | Thr | Arg | Phe | His | Asn | Ile | Cys | Pro | His | Lys | Gln | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Ser | Glu | Gly | Thr | Val | Ser | Gly | Glu | Tyr | Val | Phe | Cys | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Asp | Gln | Lys | Ile | Asp | Leu | Asn | Thr | Gly | Ile | Val | Gln | Glu | Pro | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Glu Gly Cys Val Asp Val Tyr Glu Val Glu Val Thr Asp Gly Asn Val  
 50 55 60  
 Tyr Ile Cys Leu  
 65

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Val His Val Leu Ala Phe Leu Thr Lys His His Ser Glu Lys Phe Asn  
 1 5 10 15  
 Ser Ser Ser Leu Ala Glu Leu Thr Cys Leu Xaa Pro Val Gln Leu Arg  
 20 25 30  
 Arg Val Thr Thr Gln Leu Val Asp Leu Xaa Met Ile Asp Thr Ile Arg  
 35 40 45  
 Gly Lys Asp Gly Gly Tyr Leu Ala Asn Asp Gln Ser Ala Asp Val Ser  
 50 55 60  
 Leu Ala Thr Leu Tyr Lys His Phe Val Leu Glu Lys Glu Gln His Thr  
 65 70 75 80  
 Arg Leu Phe Thr Trp Arg Arg Arg Gln Ser Leu Ser Asn Cys Ser  
 85 90 95

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Val Gly Phe Leu Asn His Met Leu Thr Leu Phe Thr Phe His Ser Gly  
 1 5 10 15  
 Leu Ser Leu Asn Ile Glu Ala Gln Gly Asp Ile Asp Val Asp Asp His  
 20 25 30  
 His Val Thr Glu Asp Ile Gly Ile Val Ile Gly Gln Leu Leu Leu Glu  
 35 40 45  
 Met Ile Lys Asp Lys Lys His Phe Val Arg Tyr Gly Thr Met Tyr Ile  
 50 55 60  
 Pro Met Asp Glu Thr Leu Ala Arg Val Val Val Asp Ile Ser Gly Arg  
 65 70 75 80  
 Pro Tyr Leu Ser Phe Asn Ala Ser Leu Ser Lys Glu Lys Val Gly Thr  
 85 90 95  
 Phe Asp Thr Glu Leu Val Glu Glu Phe Phe Arg Ala Val Val Ile Asn  
 100 105 110  
 Ala Arg Leu Thr Thr His Ile Asp Leu Ile Arg Gly Gly Asn Thr His  
 115 120 125  
 His Glu Ile Glu Ala Ile Phe Lys Ala Phe Ser Arg Ala Leu Gly Ile  
 130 135 140  
 Ala Leu Thr Ala Thr Asp Asp Gln Arg Val Pro Ser Ser Lys Gly Val

145  
Ile Glu

150

155

160

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ala | Met | Gly | Asn | Leu | Lys | Gln | Gly | Ile | Ala | Asn | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Lys | Ala | Ser | Glu | Asn | Tyr | His | Asp | Ala | Asp | Val | Asp | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Tyr | Thr | Asn | Ala | Val | Ser | Gln | Ala | Glu | Gly | Ile | Ile | Asn | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Asn | Pro | Thr | Leu | Asn | Pro | Asp | Asp | Ile | Thr | Pro | Cys | Ile | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ala | Gln | Lys | Asp | Val | Ala | Asn | Val | Leu | Glu | Asn | Val | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asp | Ala | Xaa | Val | Gly | Ala | Thr | Asp | Thr | Ile | Ala | Leu | Ala | Ala | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Tyr | Ser | Asp | Lys | Asn | Asp | Val | Met | Lys | Pro | His | Gln | Ile | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Xaa | Gly | Gly | Asp | Pro | Met | Thr | Gln | Leu | Val | Ser | Pro | Ser | Ile | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ile | His | Tyr | Asn | Tyr | Cys | Glu | Ala | Gly | Gln | Cys | Ala | Arg | Trp | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Tyr | Asn | Arg | Cys | Leu | Lys | Ser | Lys | Ile | Cys | His | Ile | Ala | Ser | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Xaa | Asp | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | His | Glu | Val | Phe | Gln | Gln | Phe | Gly | Glu | Ser | Leu | Pro | Val | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Thr | Leu | Pro | Pro | Met | Val | Phe | Gly | Asn | Arg | Asp | Lys | Lys | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Gly | Gly | Thr | Asp | Ala | Leu | Val | Leu | Arg | Tyr | Leu | Thr | Pro | His | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Trp | Asn | Ile | His | Ser | Met | Tyr | Gln | Asp | Asn | Lys | His | Met | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Arg | Gly | Val | His | Arg | Phe | Gly | Tyr | Xaa | Met | Lys | Met | Leu | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Thr | Ile | Ser | Lys | Ile | Met | Ile | Gly |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Xaa | Arg | Asn | Gly | Val | Val | Thr | Ala | Arg | Ala | Val | Ile | Ser | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Met | Pro | Lys | Gly | Thr | Met | Phe | Met | Tyr | His | Ala | Gln | Asp | Lys | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Thr | Pro | Gly | Ser | Glu | Ile | Thr | Asp | Thr | Arg | Gly | Gly | Ser | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ala | Pro | Thr | Arg | Ile | His | Leu | Lys | Pro | Thr | Gln | Leu | Val | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Ala | Gln | Ile | Ser | Tyr | His | Phe | Asn | Tyr | Tyr | Gly | Pro | Ile | Gly | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Arg | Asp | Leu | Tyr | Val | Ala | Val | Arg | Lys | Met | Lys | Glu | Val | Asn | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Trp | Gly | Thr | Asn | Pro | Glu | Met | Gly | Val | Asn | Phe | Ser | Glu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Pro | Glu | Ile | Asn | Asp | Ile | Asn | Asp | Gln | Arg | Ala | Tyr | Asp | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Glu | Pro | Gly | Gln | Lys | Ala | Glu | Asp | Ile | Asp | Leu | Gly | Tyr | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Gly | Ser | Cys | Thr | Asn | Ala | Arg | Leu | Ser | Asp | Leu | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | His | Ile | Val | Lys | Gly | Asn | Lys | Val | His | Pro | Asn | Ile | Thr | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Val | Pro | Gly | Ser | Arg | Thr | Val | Lys | Lys | Glu | Ala | Glu | Lys | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Thr | Ile | Phe | Lys | Asn | Ala | Gly | Phe | Glu | Trp | Arg | Glu | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Ser | Met | Cys | Leu | Gly | Met | Asn | Pro | Asp | Gln | Val | Pro | Glu | Gly | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Cys | Ala | Ser | Thr | Ser | Asn | Arg | Asn | Phe | Glu | Gly | Arg | Gln | Gly | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Arg | Thr | His | Leu | Val | Ser | Pro | Ala | Met | Ala | Ala | Ala | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | His | Gly | Lys | Phe | Val | Asp | Val | Arg | Lys | Val | Val | Val |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Trp | Asn | Arg | His | Val | Leu | Xaa | Gly | Lys | Xaa | Gly | Asp | Pro | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Tyr | Ile | Asp | Leu | His | Leu | Ile | His | Glu | Val | Thr | Ser | Pro | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Glu | Gly | Leu | Arg | Leu | Gln | Asn | Arg | Lys | Leu | Arg | Arg | Pro | Asp | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Phe | Ala | Thr | Leu | Asp | His | Asn | Val | Pro | Thr | Ile | Asp | Ile | Phe | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Asp | Glu | Ile | Ala | Asn | Lys | Gln | Ile | Thr | Leu | Gln | Lys | Asn |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ile | Asp | Phe | Gly | Val | His | Ile | Phe | Asp | Met | Gly | Ser | Asp | Glu | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Val | His | Met | Val | Gly | Pro | Glu | Thr | Gly | Leu | Thr | Gln | Pro | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Thr | Ile | Val | Cys | Gly | Asp | Ser | His | Thr | Ala | Thr | His | Gly | Ala | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Ile | Ala | Phe | Gly | Ile | Gly | Thr | Ser | Glu | Val | Glu | His | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Gln | Thr | Leu | Trp | Gln | Thr | Lys | Pro | Lys | Asn | Leu | Lys | Ile | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Asn | Gly | Thr | Leu | Pro | Thr | Gly | Val | Tyr | Ala | Lys | Asp | Ile | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Leu | Ile | Lys | Thr | Tyr | Gly | Val | Asp | Phe | Gly | Thr | Gly | Tyr | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Phe | Thr | Gly | Glu | Thr | Ile | Lys | Asn | Leu | Ser | Met | Asp | Gly | Arg | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ile | Cys | Asn | Met | Ala | Ile | Glu | Gly | Gly | Ala | Lys | Tyr | Gly | Ile | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Pro | Asp | Asp | Ile | Thr | Phe | Glu | Tyr | Val | Lys | Gly | Arg | Pro | Phe | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Asp Asn Phe Ala Lys Ser Val Asp Lys Trp Arg Glu Leu Tyr Ser Asp  
245 250 255  
Gly Thr Thr Arg Tyr Leu Ile Val  
260

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Val Ile Ile Asn Lys Val Met Thr Ser Asp Thr Pro Val Thr Ile Val  
1 5 10 15  
Ala Thr Gly Pro Leu Thr Asn Val Ala Thr Ala Leu Ile Arg Asp Pro  
20 25 30  
Arg Ile Ala Glu His Ile Glu Ser Ile Thr Leu Met Gly Gly Gly Thr  
35 40 45  
Phe Gly Asn Trp Thr Ala Tyr Ser Arg Ile Leu Ser Ile Pro Thr Ser  
50 55 60  
Phe Leu Thr Lys Ser Xaa Cys Gly Phe Val Asn Met Pro Leu Gly Val  
65 70 75 80  
Ile

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Val Ala His Xaa His Val Val Asn Gly Thr Tyr Tyr Leu His Xaa His  
1 5 10 15  
Ile Val Xaa Gly Trp Gln Gly Val Lys Lys Thr Cys Asp Thr Ala Glu  
20 25 30  
Glu Leu Asp Thr Tyr Ile Lys Xaa Ser Asp Val Val Tyr Glu Glu Gln  
35 40 45  
Lys His Leu Xaa Leu Phe  
50

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | His | Ile | His | Val | Val | Asn | Gly | Thr | Tyr | Tyr | Phe | His | Gly | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Pro | Gly | Trp | Gln | Gly | Val | Lys | Lys | Thr | Phe | Asp | Thr | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Glu | Thr | Tyr | Ile | Lys | Gln | Ser | Asp | Ser | Gly | Ile |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Thr | Tyr | Cys | Gly | Val | Gly | Cys | Ser | Phe | Glu | Val | Trp | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Arg | Glu | Ile | Leu | Lys | Val | Gln | Pro | Ser | His | Asp | Ser | Pro | Ala | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Ala | Thr | Cys | Val | Lys | Gly | Lys | Phe | Ser | Trp | Gly | His | Ile | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Gln | Arg | Leu | Thr | Lys | Pro | Leu | Val | Arg | Lys | Asn | Gly | Glu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Glu | Val | Glu | Trp | Asp | Glu | Ala | Leu | Asn | Val | Ile | Ala | Asp | Asn | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ser | Ile | Lys | Glu | Lys | Tyr | Gly | Pro | Asp | Ala | Leu | Ser | Phe | Ile | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Lys | Ala | Thr | Asn | Glu | Glu | Ser | Xaa | Leu | Xaa | Gln | Lys | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gln | Val | Ile | Gly | Thr | Asn | Asn | Val | Asp | Ser | Leu | Xaa | Lys | Asp | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Lys | His | Leu | Gln | Gln | Lys | Ala | Tyr | Leu | Glu | Arg | Leu | Asp | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Asp | Ser | Arg |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Lys | Ala | Val | Gly | Glu | Arg | Ile | Pro | Ile | Thr | Ile | Ile | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ala | Leu | Ile | Val | Ala | Leu | Ile | Ile | Ala | Ile | Pro | Ile | Gly | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Ala | Met | Lys | Arg | Asn | Ser | Trp | Leu | Asp | Ile | Thr | Leu | Met | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Leu | Ile | Gly | Leu | Ser | Ile | Pro | Ser | Phe | Trp | Gln | Gly | Leu | Leu |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Ile | Leu | Ala | Xaa | Ser | Leu | Lys | Leu | Asp | Ile | Leu | Pro | Pro | Ser | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Pro | Glu | His | Pro | Ile | Ser | Val | Asp | Phe | Thr | Cys | Thr | Cys | His | Trp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Lys | Tyr | Cys | Cys | Phe | Tyr | His | Ala | Tyr |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Glu | Leu | Leu | Gly | Gly | Ser | Ala | Val | Thr | Glu | Gln | Val | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Gly | Ile | Gly | Arg | Tyr | Ile | Val | Gln | Lys | Gln | Leu | Ile | Pro | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Pro | Ala | Val | Met | Gly | Gly | Val | Val | Tyr | Ile | Tyr | Gln | Leu |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | His | Ile | Ile | Ile | Asp | Gly | Asp | Ala | Cys | Pro | Val | Xaa | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Asp | Leu | Thr | Thr | Glu | Thr | Gly | Ile | Phe | Val | Thr | Ile | Ile | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Ser | His | Phe | Ser | Asn | Gln | Leu | Tyr | Pro | Pro | His | Val | Ser | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Tyr | Val | Asp | Asp | Gly | Pro | Asp | Ala | Val | Asp | Tyr | Lys | Ile | Val | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Thr | Lys | Asp | Asp | Ile | Val | Val | Thr | Gln | Asp | Tyr | Gly | Leu | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Leu | Val | Asp | Lys | Val | Leu | Ile | Val | Met | His | His | Asn | Gly | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Tyr | Asn | Ser | Lys | Asn | Ile | Gln | Gln | Leu | Leu | Asp | Lys | Arg | Tyr | Met |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Ala | Gln | Ile | Arg | Lys | Gln | Gly | Gly | Arg | His | Lys | Gly | Pro | Pro | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Thr | Lys | Gln | Asp | Gln | Lys | Val | Phe | Glu | Gln | Ser | Leu | Leu | Lys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | His | Arg | Ile | Lys | Glu | Leu | Asp |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Glu | Ser | Leu | Pro | Glu | His | Val | Asp | Thr | Ile | Ile | Asp | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Arg | Thr | Glu | Gly | Glu | Leu | Ile | Thr | Lys | Glu | Lys | Glu | Leu | Val | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Phe | Thr | Pro | Glu | Asn | Ile | Asp | Asn | Val | Asp | Lys | Glu | Tyr | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Thr | Phe | Gly | Glu | Phe | Asp | Thr | Arg | Arg | Thr | Phe | Glu | Lys | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Ser | Ile | Ile | Leu | Asp | Ala | Ala | Gln | Thr | Pro | Leu | Val | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Pro | Arg | Leu | Gln | Ser | Asn | Leu | Phe | His | Ile | Val | Lys | Glu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asp | Thr | Leu | Ile | Glu | Asp | Val | His | Phe | Lys | Met | Lys | Lys | Thr | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Ile | Trp | Leu | Leu | Asn | Gln | Gly | Ile | Glu | Ala | Ala | Gln | Ser | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Val | Xaa | Asp | Leu | Tyr | Ser | Glu | Gln | Ala | Met | Val | Leu | Val | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ile | Asn | Leu | Ala | Leu | Arg | Ser | Cys | Arg | Met | Phe | Leu | Gly | Ser | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ser | Tyr | Arg | Cys | Lys | Asn | Val | Leu | Lys | Phe | Gly | Cys | Met | Ile | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Gln | Pro | Gly | Gly |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ser | Leu | Ala | Xaa | Val | Leu | Ile | Ile | Gly | Ile | Gly | Ala | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Ile | Ser | Xaa | Asn | Leu | Gly | Arg | Asn | Thr | Val | Leu | Val | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Leu | Pro | Xaa | Ile | Tyr | Phe | Thr | Leu | Ile | Ile | Arg | Ser | Xaa | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Xaa | Asp | Thr | Xaa | Arg | Ser | Arg | Val | Lys | Ala | Phe | Ile | Pro | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Gly | Met | Val | Phe | Trp | Ala | Ile | Gln | Glu | Gln | Gly | Ser | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Asn | Ile | Tyr | Gly | Xaa | Xaa | His | Ser | Asp | Met | Lys | Leu | Asn | Leu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Trp | Lys | Thr | Xaa | Phe | Gly | Glu | Ala | Ile | Phe | Gln | Ser | Ile | Asn | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | Ile | Leu | Leu | Leu | Ala | Pro | Ile | Ile | Ser | Leu | Leu | Trp | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Gly | Thr | Lys | Gln | Pro | Ser | Leu | Pro | Val | Lys | Phe | Ala | Ile | Gly | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Leu | Ala | Gly | Ala | Ser | Tyr | Ile | Leu | Ile | Gly | Ile | Val | Gly | Tyr | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Ser | Ser | Asn | Phe | Ser | Val | Asn | Trp | Val | Ile | Leu | Ser | Tyr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Cys | Val | Ile | Gly | Glu | Leu | Cys | Leu | Ser | Pro | Thr | Gly | Asn | Ser | Ala |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Val | Lys | Leu | Ala | Pro | Lys | Ala | Phe | Asn | Ala | Gln | Met | Met | Ser | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Tyr | Leu | Thr | Asn | Ala | Ser | Ala | Gln | Ala | Ile | Asn | Gly | Thr | Leu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Ile | Glu | Pro | Leu | Gly | Gln | Thr | Asn | Tyr | Phe | Ile | Phe | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Val | Ala | Ile | Ile | Val | Thr | Thr | Ile | Cys | Ile | Ser | Ile | Leu | Thr | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | His | Gln | Ser | Asp | Glu | Arg | Tyr | Thr | Leu | Ile | Leu | Leu | Ala |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Pro | Pro | His | Pro | Asn | Gly | Val | Ser | Gln | Glu | Val | Leu | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Tyr | Leu | Thr | Gln | Xaa | Thr | Gln | Val | Xaa | Xaa | Xaa | Gly | Gly | Ala | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Ala | Xaa | Leu | Thr | Tyr | Xaa | Ala | Xaa | Thr | Ile | Pro | Lys | Val | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Xaa | Gly | Pro | Gly | Thr | Gln | Phe | Val | Ala | Ser | Xaa | Xaa | Lys | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Gly | Gln | Val | Ala | Tyr | Cys | Ser | His | Xaa | Arg | Xaa | Thr | Xaa | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Gln | Val | Gly | Gly | Ala | Gln | Ser | Ile | Ala | Ala | Leu | Thr | Tyr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Glu | Thr | Ile | Pro | Lys | Val | Asp | Lys | Ile | Val | Gly | Pro | Gly | Asn | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Xaa | Ile | Cys | Pro | Lys | Asn | Ile | Tyr | Leu | Asp | Arg |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Met | Ser | Ile | Val | Leu | Ala | Gly | Gly | Met | Glu | Asn | Met | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Pro | Met | Leu | Xaa | Asn | Asn | Ser | Arg | Phe | Gly | Phe | Lys | Met | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ser | Met | Val | Asp | Ser | Met | Val | Tyr | Asp | Gly | Leu | Thr | Asp | Val | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gln | Tyr | His | Met | Gly | Ile | Thr | Ala | Glu | Asn | Leu | Val | Gly | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Tyr | Phe | Lys | Arg | Arg | Thr | Lys | Ile | His | Val | Ala | Gly | Asn | Leu | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Ile | Lys | Gln | Tyr | Val | His | Ser | Lys | Met | Val | Asn | Leu | Ile | Val | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Ser | Met | Lys | Trp | Leu | Ser | Arg | Ile | Leu | Thr | Val | Ile | Val | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ser | Met | Ala | Cys | Gly | Ala | Leu | Ile | Phe | Asn | Arg | Arg | His | Gln | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Thr | Lys | Thr | Leu | Asn | Phe | Asn | His | Lys | Ala | Leu | Thr | Ile | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Arg | Asn | Glu | Glu | Lys | Arg | Ile | Gly | His | Leu | Leu | His | Ser | Ile |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Gln | Gln | Gln | Val | Pro | Val | Asp | Val | Ile | Val | Met | Asn | Asp | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Asp | Glu | Thr | Ala | Arg | Val | Ala | Arg | Ser | Tyr | Gly | Ala | Thr | Val | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Val | Val | Asp | Asp | Thr | Asp | Gly | Lys | Trp | Tyr | Gly | Glu | Ile | Thr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Ser | Arg | Cys | Asp | Ala | Cys | Met | Tyr | Glu | Ser | Tyr | Cys | Leu | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Leu | Gly | Thr | Val | Phe | Thr | Ala | Leu | Thr | Gly | Pro | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Leu | Gly | Val | Leu | Ala | Gly | Leu | Ala | Val | Ala | Phe | Thr | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Lys | Lys | Ser | Glu | Thr | Phe | Arg | Asn | Cys | Val | Asn | Gly | Ala | Ile | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Lys | Gln | Thr | Phe | Ser | Asn | Phe | Ile | Gln | Phe | Ile | Gln | Pro | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asp | Ser | Val | Lys | Asn | Val | Phe | Lys | Gln | Ala | Val | Ser | Ala | Ile | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Asp | Phe | Ala | Lys | Asp | Ile | Trp | Ser | Gln | Ile | Asn | Gly | Phe | Phe | Asn | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Gly | Ile | Ser | Ile | Ala | Gln | Ala | Leu | Gln | Asn | Ile | Cys | Asn | Phe | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Ala | Ile | Phe | Glu | Phe | Ile | Leu | Lys | Phe | Cys | Asn |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Ser | Leu | Lys | Thr | Val | Ile | Gly | Met | Asn | Asn | Lys | Glu | His | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Val | Ile | Leu | Ala | Leu | Leu | Val | Leu | Met | Ser | Val | Val | Leu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Met | Val | Trp | Asn | Phe | Ser | Pro | Asp | Ile | Ala | Asn | Val | Asp | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Lys | Lys | Ser | Glu | Thr | Lys | Pro | Leu | Thr | Thr | Pro | Met | Thr | Ala |

|                         |                                             |                         |     |    |  |
|-------------------------|---------------------------------------------|-------------------------|-----|----|--|
| 50                      |                                             | 55                      |     | 60 |  |
| Lys Met Asp Thr Thr     | Ile Thr Pro Phe Gln                         | Ile Ile His Ser Lys Asn |     |    |  |
| 65                      | 70                                          | 75                      | 80  |    |  |
| Asp His Pro Glu Gly     | Thr Ile Ala Thr Val Ser Asn Val Asn Lys Leu |                         |     |    |  |
|                         | 85                                          | 90                      | 95  |    |  |
| Thr Lys Pro Leu Lys     | Asn Lys Glu Val Xaa Ser Val Glu His Val Arg |                         |     |    |  |
|                         | 100                                         | 105                     | 110 |    |  |
| Arg Asp His Asn Leu Met | Ile Pro Asp Leu Ser Ser Asp Phe Thr Leu     |                         |     |    |  |
|                         | 115                                         | 120                     | 125 |    |  |
| Phe Asp Phe Thr Phe Asp | Leu Pro Leu Ser Thr Tyr Leu Gly Gln Val     |                         |     |    |  |
|                         | 130                                         | 135                     | 140 |    |  |
| Xaa Glu His             |                                             |                         |     |    |  |
| 145                     |                                             |                         |     |    |  |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Ile Leu Pro Lys Leu Val Thr Tyr Gln Val Gln Pro Met Ser Met |  |
| 1 5 10 15                                                       |  |
| Met Leu Ile Pro Lys Gly Xaa Xaa Glu Leu Ala Leu Arg Phe Asn Gln |  |
| 20 25 30                                                        |  |
| Gly Ile Asn Xaa Gly Gly Asp Ala Leu Lys Lys Arg Thr His Phe Asn |  |
| 35 40 45                                                        |  |
| Ile Ala Gly Ala Phe Asn Pro Asp Val Arg Lys Leu Asp Gly Ala Val |  |
| 50 55 60                                                        |  |
| Xaa Arg Leu Glu Xaa Lys Asp Xaa Lys Arg Asn Val Leu Phe Xaa Asn |  |
| 65 70 75 80                                                     |  |
| Thr Thr Arg Val Gln Gln Arg Glu Asn His                         |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Leu Val Gln Pro His Ile Val Ile Lys Pro Glu Ala Gln Gln Ala |  |
| 1 5 10 15                                                       |  |
| Ile Lys Ala Thr Ala Glu Asn Gln Val Glu Ser Ile Lys Asp Thr Pro |  |
| 20 25 30                                                        |  |
| His Ala Thr Val Asp Glu Leu Asp Glu Ala Asn Gln Leu Ile Ser Asp |  |
| 35 40 45                                                        |  |
| Thr Leu Lys Gln Ala Gln Gln Glu Ile Glu Asn Thr Asn Gln Asp Ala |  |
| 50 55 60                                                        |  |
| Ala Val Thr Asp Val Arg Asn Gln Thr Ile Lys Ala Ile Glu Gln Ile |  |
| 65 70 75 80                                                     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Lys | Val | Arg | Arg | Lys | Arg | Ala | Ala | Leu | Asp | Ser | Ile | Glu | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Xaa | Lys | Asn | Gln | Leu | Gly | Cys | Asn | Pro | Glu | Ile | Arg | Gly | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Asp | Glu | Arg | Asp | Cys | Trp | Leu | Leu | Asp | Thr | Phe | Lys |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Leu | Leu | Pro | Leu | Ile | Ser | Asp | Asn | Met | Tyr | Leu | Gly | Tyr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gly | Leu | Leu | Ala | Ala | Tyr | Ala | Gly | Gly | Phe | Val | Cys | Thr | Tyr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Pro | Thr | Lys | Ala | Met | Arg | Gln | Asp | Arg | Phe | Val | Gly |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Xaa | Xaa | Ile | Met | Lys | Phe | Lys | Ala | Ile | Ala | Lys | Xaa | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Gly | Met | Leu | Ala | Thr | Gly | Val | Ile | Thr | Ser | Asn | Val | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gln | Ala | Xaa | Thr | Glu | Val | Xaa | Gln | Gln | Ser | Glu | Ser | Glu | Leu | Xaa |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Tyr | Tyr | Asn | Lys | Pro | Val | Leu | Glu | Arg | Lys | Asn | Val | Thr | Gly | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Xaa | Tyr | Thr | Glu | Lys | Gly | Lys | Asp | Tyr | Ile | Asp | Val | Ile | Val | Asp | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Tyr | Ser | Gln | Ile | Ser | Leu | Val | Arg | Ile |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asn | Ile | Glu | Leu | Val | Leu | His | Gln | Arg | Xaa | Ala | Asn | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ile | Ala | Asn | Ile | Ser | Asn | Asn | Ala | Thr | Val | Ser | Gln | Ala | Asp | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Ile | Ile | Asn | Ser | Leu | Thr | Phe | Thr | Ser | Asn | Ala | Pro | Asn | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Tyr | Ala | Thr | Ala | Ser | Ala | Asn | Glu | Ile | Thr | Ser | Lys | Thr | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Val | Ser | Arg | Thr | Gly | Asn | Asn | Ala | Asn | Val | Thr | Val | Thr | Val | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Gln | Asp | Gly | Thr | Thr | Ser | Thr | Val | Thr | Val | Pro | Val | Lys | His | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Pro | Glu | Ile | Val | Ala | His | Ser | His | Tyr | Thr | Val | Gln | Gly | Gln | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Pro | Ala | Gly | Asn | Gly | Ser | Ser | Ala | Ala | Asp | Tyr | Phe | Lys | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gly | Ser | Ala | Ile | Pro | Asp | Ala | Thr | Ile | Thr | Trp | Val | Ser | Gly | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Pro | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Glu | Asn | Ser | Arg | Pro | Glu | Arg | Asn | Glu | Ala | Thr | Met | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Met | Thr | Val | Glu | Glu | Ala | Leu | Ile | Thr | Met | Asn | Lys | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Val | Pro | Leu | Ala | Val | Arg | Lys | Ala | Ile | Pro | Gln | Leu | Thr | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ile | Lys | Lys | Thr | Ile | Ala | Gln | Tyr | Lys | Lys | Gly | Gly | Arg | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Ile | Gly | Ala | Gly | Thr | Ser | Gly | Arg | Leu | Gly | Val | Leu | Asp | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Cys | Val | Pro | Thr | Phe | Asn | Thr | Asp | Pro | His | Glu | Ile | Ile | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Gly | Gly | Gln | His | Ala | Met | Thr | Met | Ala | Val | Glu | Gly | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | His | Lys | Lys | Leu | Ala | Glu | Glu | Asp | Leu | Lys | Asn | Ile | Asp | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Asp | Val | Val | Ile | Gly | Ile | Ala | Ala | Ser | Gly | Lys | Thr | Pro | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ile | Gly | Gly | Leu | Thr | Phe | Ala | Asn | Thr | Ile | Gly | Ala | Thr | Thr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ile | Ser | Cys | Asn | Glu | His | Ala | Val | Ile | Ser | Glu | Ile | Ala | Gln | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Val | Glu | Val | Lys | Val | Gly | Pro | Glu | Val | Leu | Thr | Gly | Ser | Xaa | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Gln | Lys | Leu | Ile | Leu | Asn | Met | Ile | Ser | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Met | Val | Gly | Val | Gly | Lys | Val | Tyr | Asp | Asn | Leu | Met | Ile | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Lys | Ala | Thr | Asn | Gln | Lys | Leu | Ile | Asp | Arg | Ser | Val | Arg | Ile | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Glu | Ile | Cys | Ala | Ile | Thr | Tyr | Asp | Glu | Ala | Met | Ala | Leu | Tyr | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ser | Glu | His | Asp | Val | Glu | Ser | Cys | Asp | Ser | Tyr | Gly | Tyr | Val | Trp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | Xaa | Ile | His | Ser | Gln | Gln | Ile | Val | Ile | Ala | Pro | Asp | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Ser | Met | Xaa | Xaa | His | Gln | Val | Xaa | Asn | Ile | Ile | Lys | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Thr | Asn | Val | Tyr | Gly | Asn | Thr | Leu | His | Tyr | Asp | Ile | Ile | Pro | Met |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Asp | Gly | Gly | Glu | Gly | Thr | Xaa | Asp | Xaa | Leu | Ile | His | Ala | Xaa | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Lys | Tyr | Thr | Val | Ile | Val | Asn | Asp | Pro | Leu | Met | Arg | Pro | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ala | Cys | Tyr | Ala | Arg | Ala | Asp | Glu | Gln | Gln | Ile | Ala | Ile | Ile | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Ala | Ala | Ala | Ser | Gly | Leu | Asp | Leu | Leu | Glu | Lys | Glu | Glu | Arg | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Tyr | Thr | Ser | Ser | Tyr | Gly | Thr | Gly | Glu | Leu | Ile | Lys | Asp | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asn | His | Gly | Ala | Lys | Thr | Ile | Ile | Leu | Gly | Ile | Gly | Gly | Ser | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asn | Asp | Gly | Gly | Thr | Gly | Met | Leu | Ser | Ala | Leu | Gly | Val | Lys | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Asp | Val | Asn | Gly | Asp | Leu | Leu | Gln | Met | Asn | Gly | Ala | Asn | Leu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Ile | Ala | Gln | Ile | Asp | Ile | Thr | Asn | Leu | Ala | Asp | Ser | Arg | Xaa | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Thr | Phe | Lys | Val | Ala | Cys | Asp | Val | Ser | Asn | Pro | Leu | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Asn | Gly | Ala | Thr | Tyr | Ile | Tyr | Gly | Pro | Gln | Lys | Cys | Ala | Asp | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Met | His | Thr |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```
Val Lys Gln Cys Ile Asn Asn Asp Glu Trp Phe Val Thr Asn Asp Asn
 1          5          10          15
Gly Tyr Val Lys Glu Gln Tyr Leu Tyr Xaa Ala Gly Arg Gln Gln Asp
      20          25          30
Met Leu Ile Ile Gly Gly Arg Asn Ile Tyr Pro Ala His Val Xaa Arg
      35          40          45
Leu Leu Thr Gln Ser Ser Ser Ile Asp Glu Ala Ile Ile Ile Gly Ile
      50          55          60
Pro His Glu Arg Phe Gly Xaa Ile Gly Val Leu Leu Tyr Ser Gly Asp
      65          70          75          80
Val Thr Leu Thr His Lys Asn Xaa Lys Gln Phe Xaa Lys Lys Lys Val
      85          90          95
Lys Arg His Glu Ile Pro Phe Asp Asp Ser Ser Cys Arg Lys Asp Val
      100          105          110
Leu Xaa Cys Lys Trp
      115
```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```
Val Ser Ala Ile Phe Glu Pro Glu His Leu Glu Ala Leu Leu Ala Gln
 1          5          10          15
Val Ser Ile Lys Pro Val Ile Asn Gln Val Glu Tyr His Pro Tyr Leu
      20          25          30
Thr Gln His Lys Leu Lys Leu Tyr Leu Ala Ala Gln His Ile Val Met
      35          40          45
Glu Ser Trp Ser Pro Leu Met Asn Ala Gln Ile Leu Asn Asp Glu Thr
      50          55          60
Ile Lys Asp Ile Ala Gln Glu Leu Gly Lys Ser Pro Ala Gln Val Val
      65          70          75          80
Leu Arg Trp Asn Val Gln His Gly Val Val Ile Ile Pro Lys Ser Val
      85          90          95
Thr Pro Asn Arg Ile Ser Glu Asn Phe Gln Ile Phe Asp Phe Glu Leu
      100          105          110
Ser Asp Glu Gln Met Thr Leu Val Pro Gly Leu Asn Leu Asp Lys Arg
      115          120          125
Ile Gly Pro Asp Xaa Xaa Thr Phe Glu Gly
      130          135
```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```
Val Phe Lys Gly Ser Glu Tyr Gln Leu Ser Glu Ile Asn Ser Gly Ser
 1           5           10           15
Val Lys Tyr Glu Gln Thr Tyr Asp Asn Phe Pro Ile Leu Asn Asn Ser
          20           25           30
Lys Ala Met Leu Asn Phe Asn Ile Glu Asp Asn Lys Ala Ala Ser Tyr
          35           40           45
Lys Gln Ser Met Met Asp Asp Ile Lys Pro Thr Asp Gly Ala Asp Lys
          50           55           60
Lys His Gln Val Ile Gly Val Arg Lys Ala Ile Glu Ala Leu
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```
Val Asn Glu Thr Asn Val Gln Leu Leu Gln Pro Asn Trp Glu Ile Lys
 1           5           10           15
Val Lys His Asp Gly Lys Asp Lys Thr Asn Thr Tyr Tyr Val Glu Ala
          20           25           30
Thr Asn Asn Asn Pro Lys Ile Ile Asn His
          35           40
```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```
Val Leu Ile Tyr Phe Ile Glu Gly Leu Met Ser Xaa Asn Gln Pro Ala
 1           5           10           15
Glu Ala Leu Glu Xaa Leu Ser Tyr Val Asp Pro Ser Pro Xaa Xaa Leu
          20           25           30
Met Xaa Lys Lys
          35
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```
Val Gly Ile Asn Ser Lys Gln Gly Lys Asn Leu Ile Gly Ala Phe Tyr
 1          5          10          15
Arg Pro Thr Ala Val Ile Tyr Asp Leu Asp Phe Leu Lys Thr Leu Pro
          20          25          30
Phe Glu Gln Ile Leu Ser Gly Tyr Ala Glu Val Tyr Lys His Ala Leu
          35          40          45
Leu Asn Gly Glu Ser Thr Thr Gln Glu Ile Glu Gln His Phe Lys Asp
          50          55          60
Arg Glu Ile Leu Gln Pro Leu Asn Gly Ile Gly
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```
Val Val Thr Leu Phe Leu Cys Pro Xaa Asn Ser Phe Leu Met Ile His
 1          5          10          15
Asn Ser Trp Val Met Thr Val Gly Asn Ala Glu Glu Leu Arg Lys Thr
          20          25          30
Ala Asp Leu Leu Glu Lys Thr Asp Ala Val Ser Asn Ser Ala Tyr Leu
          35          40          45
Asp Lys Xaa Xaa Asp Leu Asp Gln Glu His Leu Lys Gln Met Leu Asp
          50          55          60
Ala Glu Thr Trp Leu Thr Ala Glu Glu Ala Leu Ser Phe Gly Leu Ile
65          70          75          80
Asp Glu Ile Leu Gly Ala Asn Glu Ile Ala Ala Ser Ile Ser Lys Glu
          85          90          95
Gln Cys Arg Arg Xaa Glu Xaa Val Pro Glu Asp Leu Lys Lys Asp Val
          100          105          110
Xaa Lys Ile Thr Lys Ile Asp Asp Xaa Arg Tyr Asp Leu Asp Trp Leu
          115          120          125
Lys Pro Pro Lys Glu Ser Met Ser Leu Glu Glu Xaa Xaa Xaa Arg Xaa
          130          135          140
Xaa Ile Val Arg Ser Asn Ala Lys Phe
145          150
```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```
Val Lys Glu Ile Pro Asp Ala Ser Ile Ser Phe Glu Val Phe Ala Asp
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Leu | Glu | Thr | Met | Glu | Lys | Glu | Ala | Ala | Ile | Leu | Lys | Gln | Tyr | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Asn | Val | Phe | Val | Lys | Ile | Pro | Ile | Val | Asn | Thr | Lys | Gly | Glu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Ile | Pro | Leu | Ile | Lys | Lys | Leu | Ser | Ala | Asp | Asn | Val | Arg | Leu | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Xaa | Ala | Val | Tyr | Thr | Ile | Glu | Gln | Gly | Lys | Glu | Ile | Thr | Glu | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | Thr | Glu | Gly | Val | Pro | Asn | Ile | Cys | Phe | Ser | Ile | Cys | Arg | Thr | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Cys | Arg | Tyr | Arg | Arg | Arg | Ser | Ile | Thr | Ile | Asn | Glu | Arg | Gly | Cys | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Tyr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Tyr | Xaa | Arg | Val | Asn | Glu | Met | Asn | Ala | Lys | Glu | Xaa | Leu | Val | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Xaa | Leu | Met | Lys | Thr | Ser | Ser | Gln | Leu | Phe | Lys | Xaa | His | Gly | Glu | Val |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Xaa | Met | Gln | Leu | Xaa | Leu | Asn | Asp | Glu | Leu | Lys | Leu | Pro | Ser | Ile | Xaa |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Glu | Ile | Cys | Val | Glu | Arg | Lys | Arg | Leu | Ser | Asp | Ile | Val | Lys | Val | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Gln | Ser | Tyr | Ala | Leu | Leu | Tyr | Ile | Asp | Lys | Gln | Asp | Gln | Ala | Arg |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Lys | Xaa | Xaa | Leu | Ser | Leu | Xaa | Lys | Ile | Ala | Lys | Val | Tyr | Val | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Asp | Asp | Thr | Ile | Met | Ser | Ile | Phe | Val | Tyr | Asp | Val | Val | Asn |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Asp | Glu | Trp | Ile | Leu | Arg | Leu | Asp | Pro | Asn | Ile | Arg | Ile | Pro | Lys | Ser |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Asn | Ile | Tyr | Phe | His | Ser | Leu | Asn | Trp | Asp | Val | Asp | Tyr | Ile | Lys | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Glu | Ile | Val | Leu | Met | Tyr | Asp | Leu | Met | Gln | His | His | Gln | Tyr | His | His |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Tyr | Ser | Asn | Tyr | Lys | Arg | Val | Ile | Asp | Xaa | Leu | Ser | Tyr | Tyr | Gln | Phe |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Phe | Ile | Leu | Lys | Phe | Val | Val | Gly | Glu | Xaa | Arg | Ile | Lys | Asp | Ala | Ile |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Gln | Lys | Asn | Asn | Lys |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Pro | Gln | Gln | Gln | Ala | Pro | Thr | Lys | Gln | Arg | Pro | Ala | Lys | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Asp | Asp | Lys | Ala | Ser | Xaa | Asp | Glu | Ser | Lys | Asp | Lys | Asp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Ser | Gln | Asp | Xaa | Ser | Asp | Asp | Thr | Gln | Lys | Lys | Thr | Asp | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Thr | His | Pro | Ala | Ala | Arg | Xaa |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Met | Leu | Lys | Met | Xaa | Leu | Ile | Lys | Lys | Leu | Thr | Gln | Met | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Val | Asn | Gln | Asn | Asp | Xaa | Leu | Thr | Asp | Glu | Glu | Lys | Gln | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Gln | Val | Ile | Glu | Glu | His | Lys | Asn | Glu | Ile | Ile | Gly | Asn | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Gln | Thr | Thr | Asp | Asp | Gly | Val | Thr | Arg | Ile | Thr | Arg | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Thr | Asp | Leu | Lys | Trp | Gly | Tyr | Cys | Asn | Thr | Gly | Cys |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Trp | Ile | Lys | Arg | Leu | Leu | Lys | Asp | Leu | Lys | Lys | Leu | Ser | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Lys | Asp | Ile | Leu | Gln | Leu | Val | Pro | Lys | Gln | Leu | Phe | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ala | Glu | Leu | Gln | Leu | Thr | Glu | Ala | Asp | Tyr | Leu | Thr | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asp | Ile | Val | Val | Gln | Pro | Gly | Lys | Lys | Leu | Gln | His | Leu | Ser |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Leu | Ser | Gly | Gly | Glu | Arg | Ala | Leu | Thr | Ala | Ile | Ala | Leu | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ala | Ile | Leu | Lys | Val | Arg | Ser | Ala | Pro | Phe | Val | Ile | Leu | Asp | Glu | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Glu | Ala | Ala | Leu | Asp | Glu | Ala | Asn | Val | Ile | Arg | Tyr | Ala | Lys | Tyr | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Asn | Glu | Leu | Ser | Asp | Glu | Thr | Gln | Phe | Ile | Val | Ile | Thr | His | Arg | Lys |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Gly | Thr | Met | Glu | Phe | Ala | Asp | Arg | Leu | Tyr | Gly | Val | Thr | Met | Gln | Glu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Ser | Gly | Val | Thr | Lys | Leu | Val | Ser | Val | Asn | Leu | Asn | Thr | Ile | Asp | Asp |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Val | Leu | Lys | Glu | Glu | Gln |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Arg | Asp | Gln | Phe | Lys | Phe | Tyr | His | Val | Arg | His | Glu | Glu | Val | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Ser | Leu | Ala | Ala | Ala | Gly | Tyr | Thr | Lys | Leu | Thr | Gly | Xaa | Ile | Gly | Val |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Ala | Leu | Ser | Ile | Gly | Xaa | Pro | Gly | Leu | Ile | His | Leu | Leu | Asn | Gly | Met |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Tyr | Asp | Ala | Lys | Met | Asp | Asn | Val | Leu | Val | Pro | Ile | Asn | Ile | Ile | Trp |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Thr | Asn | Xaa | Ile | Val | Gln | His | Leu | Glu | Arg | Lys | His | Phe | Lys | Lys | Gln |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Ile | Tyr | Lys | Asn | Tyr | Val | Lys | Met |     |     |     |     |     |     |     |     |  |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Lys | Leu | Ser | Xaa | Tyr | Tyr | Pro | Gln | Gly | Leu | Arg | Ser | Leu | Asn | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Gly | Arg | Met | Ala | Arg | Phe | Gly | Arg | Thr | Pro | Leu | Leu | Asp | Ala | Met | Glu |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Met | Ala | Asn | Glu | His | Ile | Met | Val | Ile | Ala | Met | Ile | Glu | Asp | Val | Xaa |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gly | Val | Met | Ala | Ile | Asp | Asp | Ile | Ala | Gln | Val | Glu | Gly | Leu | Asp | Met |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Ile | Val | Glu | Gly | Ala | Ala | Gly | Phe | Ile | Ala | Val | Thr | Trp | His | Thr | Xaa |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Ala | Asn | Glu | Arg | Asp | Asp | Gln | Val | Thr | Ser | His | Xaa | Gln | His | Ile | Xaa |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Val | Val | Asn | Ala | His | Gly | Lys | His | Xaa | Cys | Ala | Leu | Pro | Arg | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Glu | Asp | Ile | Ala | Lys | Trp | Gln | Ala | Gln | Gly | Val | Gln | Thr | Phe | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Thr | Ser | Gly | Lys | Ile | Tyr | Arg | His | Leu | Ser | Ala | Ser | Leu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ser | Lys | Gln | Lys | Gly | Asp | Asp | Gly |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Thr | Ser | Leu | Asp | Ala | Asp | Glu | Ala | Lys | Arg | Asn | Ala | Tyr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ala | Val | Thr | Gln | Ala | Xaa | Gln | Ile | Leu | Asn | Lys | Ala | Gln | Gly | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asn | Thr | Ala | Lys | Asp | Gly | Val | Glu | Thr | Ala | Leu | Gln | Asn | Val | Gln | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Asn | Glu | Leu | Ser | Gly | Asn | Gln | Asn | Val | Ala | Asn | Ala | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ala | Lys | Asn | Ala | Leu | Asn | Asn | Leu | Thr | Ser | Ile | Asn | Asn | Ala | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ala | Ala | Leu | Lys | Ser | Gln | Ile | Glu | Gly | Ala | Thr | Thr | Val | Ala | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Asn | Gln | Val | Ser | Thr | Met | Ala | Ser |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ala | Lys | Thr | Ala | Leu | Asn | Gly | Asp | Ala | Arg | Leu | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Lys | Asn | Thr | Ala | Lys | Gln | Gln | Leu | Ala | Thr | Met | Ser | His | Leu | Thr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Ala | Gln | Lys | Ala | Asn | Leu | Thr | Glu | Gln | Ile | Glu | Arg | Gly | Thr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Ala | Gly | Val | Gln | Gly | Ile | Gln | Ala | Asn | Ala | Gly | Thr | Leu | Asn | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Met | Asn | Gln | Leu | Arg | Gln | Ser | Ile | Ala | Ser | Lys | Asp | Ala | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ser | Glu | Asp | Tyr | Gln | Asp | Ala | Asn | Ala | Asp | Leu | Gln | Asn | Ala | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Asp | Ala | Val | Thr | Asn | Ala | Gly | Gly | Ile | Ile | Ser | Ala | Xaa | Asn | Asn |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Met | Asn | Pro | Asp | Thr | Ile | Xaa | Gln | Lys | Ala | Ser | Gln | Val | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ala | Lys | Ser | Ala | Leu | Xaa | Gly | Asp | Glu | Lys | Leu | Ala | Ala | Ala | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Thr | Ala | Lys | Ser | Asp | Ile | Gly | Arg | Val | Thr | Asp | Leu | Asn | Asn | Ala |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Gln | Arg | Thr | Ala | Xaa | Asn | Ala | Glu | Val | Asp | Gln | Ala | Pro | Xaa | Leu | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Val | Thr | Ala | Ala | Lys | Asn | Lys | Ala | Thr | Ser | Leu | Asn | Thr | Ala | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asn | Val | Lys | His | Ala | Leu | Ala | Glu | Lys | Asp | Asn | Thr | Xaa | Arg | Ser |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Val | Asn | Tyr | Thr | Asp | Ala | Asp | Gln | Pro | Xaa | Gln | Gln | Ala | Xaa | Asp | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gly | Thr | Gln | Ala | Glu | Ala | Ile | Thr | Asn | Ala | Asn | Gly | Ser | Xaa | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Glu | Thr | Gln | Val | Gln | Ala | Ala | Leu | Asn | Gln | Leu | Asn | Gln | Ala | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Asn | Asp | Leu | Glu | Trp | Val | Ile | Ile | Lys | Leu | Leu | Lys | Arg | Lys | Lys | Gln |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Asn | Val | His |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Thr | Lys | Ala | Ala | Leu | His | Gly | Asp | Val | Lys | Leu | Gln | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Lys | Asp | His | Ala | Lys | Gln | Thr | Val | Ser | Gln | Leu | Ala | His | Leu | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Gln | Lys | His | Met | Glu | Asp | Thr | Leu | Ile | Asp | Ser | Glu | Thr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Thr | Ala | Val | Lys | Gln | Asp | Leu | Thr | Glu | Val | Gln | Ala | Leu | Asp | Gln |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Leu | Met | Asp | Ala | Leu | Gln | Gln | Ser | Ile | Ala | Asp | Lys | Asp | Ala | Thr | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ser | Ser | Ala | Tyr | Val | Asn | Ala | Glu | Pro | Asn | Lys | Lys | Gln | Ala | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Glu | Ala | Val | Gln | Asn | Ala | Glu | Ser | Ile | Ile | Ala | Gly | Leu | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Ile | Asn | Lys | Gly | Asn | Val | Ser | Ser | Ala | Thr | Gln | Ala | Val | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Lys | Asn | Ala | Leu | Asp | Gly | Val | Glu | Arg | Leu | Ala | Gln | Asp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Thr | Ala | Gly | Asn | Ser | Leu | Asn | His | Leu | Asp | Gln | Leu | Thr | Pro | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Gln | Gln | Ala | Leu | Glu | Asn | Gln | Ile | Asn | Asn | Ala | Thr | Thr | Arg | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Val | Ala | Glu | Ile | Ile | Ala | Gln | Ala | Gln | Ala | Leu | Asn | Glu | Ala | Met |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |
| Lys | Ala | Leu | Lys | Xaa | Ser | Ile | Lys | Asp | Gln | Pro | Gln | Thr | Glu | Ala | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |     |
| Ser | Lys | Phe | Ile | Asn | Glu | Asp | Gln | Ala | Gln | Lys | Asp | Ala | Tyr | Thr | Gln |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Gln | His | Ala | Arg | Arg | Cys | Leu | Xaa |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Glu | Ile | Ile | Ala | Gln | Ala | Gln | Ala | Leu | Asn | Glu | Ala | Met | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Lys | Glu | Ser | Ile | Lys | Asp | Gln | Pro | Gln | Thr | Glu | Ala | Ser | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Phe | Ile | Asn | Glu | Asp | Gln | Ala | Gln | Lys | Asp | Ala | Tyr | Thr | Gln | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Gln | His | Glu | Arg | Lys | Ile |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Leu | Arg | Met | Ala | Ser | Asn | Met | Pro | Ser | Leu | Xaa | Lys | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Val | Glu | Met | Ile | Ala | Phe | Cys | Asp | Val | Asp | Ile | Ser | Lys | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Ser | Ala | Ala | Glu | Ala | Tyr | Gly | Thr | Asp | Asn | Ala | Lys | Val | Tyr | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Tyr | Lys | Ala | Leu | Leu | Lys | Asp | Asp | Thr | Ile | Asp | Val | Ile | His | Val |
| 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |
| Cys | Thr | Pro | Asn | Asp | Ser | His | Cys | Glu | Ile | Thr | Val | Ala | Gly | Leu | His |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Lys | His | Val | Met | Cys | Glu | Lys | Pro | Met | Ala | Lys | Thr | Thr | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ala | Gln | Lys | Met | Ile | Asp | Thr | Ala | Lys | Ser | Thr | Gly | Lys | Lys | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ile | Gly | Tyr | Gln | Asn | Arg | Phe | Arg | Pro | Asp | Ser | Gln | Phe | Leu | His |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Ala | Ala | Gln | Arg | Gly | Asp | Leu | Gly | Asp | Ile | Tyr | Phe | Gly | Lys | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| His | Ala | Ile | Arg | Arg | Arg | Ala | Val | Pro | Thr | Trp | Gly | Val | Phe | Leu | Asn |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Glu | Ala | Gln | Gly | Gly | Gly | Pro | Leu | Ile | Asp | Ile | Gly | Thr | His | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Leu Asp Leu Thr Leu Trp Met Met Asp Asn Tyr Glu Pro Glu Ser Val  
                   180                                  185                  190  
 Met Gly Ser Thr Phe His Lys Leu Asn Lys Gln His Asp Ala Pro Asn  
                   195                                  200                  205  
 Ala Trp Gly Ser Trp Asn Pro Asp Glu Leu Thr Val Glu Asp Ser Ala  
                   210                                  215                  220  
 Phe Gly Phe Ile Lys  
 225

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Val Asp Glu Ala Lys Cys Ser Leu Leu Gly Thr Lys Ala Gly Ala Asp  
 1                                  5                                  10                                  15  
 Met Lys Asp Val Leu Arg Ile His Gly Glu Asp Met Gly Thr Leu Tyr  
                   20                                  25                                  30  
 Thr Lys His Val Glu Xaa Glu Asn Lys Gly Val Asp Phe Tyr Glu Gly  
                   35                                  40                                  45  
 Asn Glu Val Asp Glu Ala Glu Glu Glu Xaa Lys Ala Trp Ile Asp Ala  
                   50                                  55                                  60  
 Val Val Asn Asp Thr Glu Pro Val Val Lys Pro Glu Gln Ala Met Val  
 65                                  70                                  75                                  80  
 Val Thr Lys Ile Leu Glu Ala Ile Tyr Gln Ser Ala Lys Ser Gly Lys  
                   85                                  90                                  95  
 Ala Ile Tyr Phe Glu  
                                   100

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Val Asp Pro Pro Gly Cys Arg Asn Ser Thr Arg Thr Arg Ala Ala Phe  
 1                                  5                                  10                                  15  
 Thr Val Ala Ser Ile Asp Leu Gly Ala His Pro Glu Phe Leu Gly Lys  
                   20                                  25                                  30  
 Asn Asp Ile Gln Leu Xaa Lys Lys Glu Ser Val Glu Asp Thr Xaa Lys  
                   35                                  40                                  45  
 Val Leu Gly Arg Met Phe Asp Gly Ile Glu Phe Lys Leu  
                   50                                  55                                  60

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Val Ile Pro Asn Glu Phe Leu Lys His Ser Gly Lys Val His Ala Gln
 1           5           10           15
Ala Phe Phe Thr Gln Asn Gly Ser Asn Asn Val Val Val Glu Arg Gln
      20           25           30
Phe Ser Phe Asn Ile Glu Asn Asp Leu Val Ser Gly Xaa Asp Gly Ile
      35           40           45
Thr Lys Leu Val Tyr Ile Lys Ser Ile Gln Asp Thr Ile Glu Ala Val
 50           55           60
Gly Lys Asp Phe Asn Gln Leu Lys Gln Asn Met Ala Asp Thr Gln Thr
65           70           75           80
Leu Ile Ala Lys Val Asn Asp Ser Ala Thr Lys Gly Ile Gln Gln Ile
      85           90           95
Glu Ile Lys Gln Asn Glu Ala Ile Gln Ala Ile Thr Ala Thr Gln Thr
      100           105           110
Ser Ala Thr Gln Ala Val Thr Ala Glu Val Gly
      115           120

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```

Val Met Asn Ile Ile Asn Leu Glu Lys Pro Lys Gly Val Val Val Gln
 1           5           10           15
Phe Gly Gly Gln Thr Ala Ile Asn Leu Ala Asp Lys Leu Ala Lys His
      20           25           30
Gly Val Lys Ile Leu Gly Thr Ser Leu Glu Asn Leu Asn Arg Ala Glu
      35           40           45
Asp Arg Lys Glu Phe Glu Ala Leu Leu Arg Lys Ile Asn Val Pro Gln
 50           55           60
Pro Gln Gly Lys Ser Ala Thr Ser Pro Glu Glu Ala Leu Ala Asn Ala
65           70           75           80
Ala Glu Ile Gly Tyr Pro Val Val Val Arg Pro Ser Tyr Val Leu Gly
      85           90           95
Gly Arg Ala Met Glu Ile Val Asp Asn Asp Lys Glu Leu Glu Asn Tyr
      100           105           110
Met Thr Gln Ala Val Lys Ala Ser Pro Glu His Pro Val Leu Val Asp
      115           120           125
Arg Tyr Leu Thr Gly Lys Glu Ile Glu Val Asp Ala Ile Cys Asp Gly
      130           135           140
Glu Thr Val Ile Ile Pro Gly Ile Met Glu His Ile Glu Arg Ala Gly
145           150           155           160
Val His Ser Gly Asp Ser Ile Ala Val Tyr Pro Pro Gln Thr Leu Thr
      165           170           175
Glu Asp Glu Leu Ala Thr Leu Glu Asp Tyr Thr Ile Lys Leu Ala Lys
      180           185           190

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Asn | Ile | Ile | Gly | Leu | Ile | Asn | Ile | Gln | Phe | Val | Ile | Ala | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Gly | Val | Tyr | Cys | Phe | Arg | Ser | Lys | Pro | Thr | Val | Leu | Val | Glu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Xaa | His | Ser | Arg | Ala |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Phe | Met | Thr | Asn | Asn | Lys | Val | Ala | Leu | Val | Thr | Gly | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gly | Ile | Gly | Phe | Lys | Ile | Ala | Glu | Arg | Leu | Val | Glu | Asp | Gly | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Ala | Val | Val | Asp | Phe | Asn | Glu | Glu | Gly | Ala | Lys | Ala | Ala | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Leu | Ser | Ser | Asp | Gly | Thr | Lys | Ala | Ile | Ala | Ile | Lys | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Asn | Arg | Asp | Asp | Val | Phe | Asn | Ala | Val | Arg | Gln | Ala | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ala | Ile | Trp | Arg | Phe | Pro | Cys | His | Gly |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ile | His | Tyr | Val | Asp | Ile | Ile | Met | Phe | Lys | Asp | Val | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Glu | Val | Cys | Leu | Ile | Arg | Leu | Leu | Val | Ile | Lys | Val | Leu | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ile | Phe | Ala | Arg | Ala | Lys | Phe | Glu | Lys | Glu | Tyr | Gly | Val | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Lys | Ala | Gly | Lys | Asp | Asn | His | Glu | Met | Val | Glu | Gly | Ile | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gly | Glu | Val | His | Ser | Leu | Tyr | Leu | Tyr | Gly | Glu | Asp | Thr | Gly | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Asp | Ser | Asn | Ile | Asn | Phe | Val | Gln | Ala | Ala | Phe | Glu | Lys | Leu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Met | Val | Val | Gln | Asp | Glu | Phe | Leu | Thr | Phe | Thr | Ala | Thr | Tyr | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Val | Val | Leu | Pro | Ala | Ser | Pro | Ser | Leu | Glu | Lys | Asp | Gly | Thr | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Thr | Glu | Arg | Arg | Ile | Gln | Arg | Leu | Tyr | Gln | Ala | Leu | Glu | Pro |

|                     |                 |                 |             |     |  |
|---------------------|-----------------|-----------------|-------------|-----|--|
| 130                 |                 | 135             |             | 140 |  |
| Leu Gly Asp Ser Lys | Pro Asp Trp Lys | Ile Phe Gln Ala | Ile Ala Asn |     |  |
| 145                 | 150             | 155             | 160         |     |  |
| Arg Leu Gly Ile Trp | Ile Gly Ile Thr | Ser Ile Leu Val | Lys Leu Trp |     |  |
|                     | 165             | 170             | 175         |     |  |
| Ile Glu Gly Arg Thr | Leu Asn Thr Ser | Ile Cys Trp Gly | Lys Leu     |     |  |
|                     | 180             | 185             | 190         |     |  |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Pro Ile Arg His Glu Arg Xaa Asp Lys Cys Glu Xaa Ile Met Tyr |  |
| 1 5 10 15                                                       |  |
| Ala Asp Asn Met Thr Asp Xaa Met Lys Tyr Ala Ile Asp Glu Thr Gln |  |
| 20 25 30                                                        |  |
| Arg Arg Arg Glu Ile Gln Met Lys His Asn Glu Lys His Gly Ile Thr |  |
| 35 40 45                                                        |  |
| Pro Lys Thr Ile Asn Lys Xaa Val His Asp Leu Ile Ser Ala Thr Val |  |
| 50 55 60                                                        |  |
| Glu Asn Asp Glu Asn Xaa Asp Xaa Ala Gln Thr Val Ile Pro Lys Lys |  |
| 65 70 75 80                                                     |  |
| Met Pro Lys Arg Ala Arg Xaa Lys Thr Ile Asp Asn Ile Glu Lys Glu |  |
| 85 90 95                                                        |  |
| Met Lys Gln Ala Ala Lys Asp Leu Asp Phe Glu Lys Ala Xaa Glu Leu |  |
| 100 105 110                                                     |  |
| Arg Asp Met Leu Phe Glu Leu Lys Ala Xaa Gly                     |  |
| 115 120                                                         |  |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Xaa Ala Asn Glu Ile Xaa Lys Xaa Lys Ile Asp Ala Asn Lys Asp |  |
| 1 5 10 15                                                       |  |
| Val Asp Lys Gln Val Gln Ala Leu Ile Asp Glu Ile Asp Arg Asn Pro |  |
| 20 25 30                                                        |  |
| Asn Leu Thr Asp Lys Glu Lys Gln Ala Leu Lys Arg Ser Tyr         |  |
| 35 40 45                                                        |  |

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```
Val Ser Glu Phe Asn Glu Ile Ile Ile Ala Thr Pro Ala Gln Trp Ile
 1          5          10          15
Ser His Thr Gln Asp Ile Leu Lys Lys Tyr Asn Ile Thr Asp Gln Arg
 20          25          30
Val Lys Val Val Ala Gly Gly Xaa Asp Arg Asn Glu Thr Ile Met Asn
 35          40          45
Ile Ile Asp His Ile Arg Asn Val Asn Gly Ile Asn Asn Asp Asp Val
 50          55          60
Ile Val Thr His Asp Ala Val Arg Pro Phe Leu Thr Gln Arg Ile Ile
 65          70          75          80
Lys Glu Asn Ile Glu Val Ala Xaa Xaa Tyr Gly Ala Val Asp Thr Val
 85          90          95
Ile Glu Ala Ile Asp Thr Ile Val Met Ser Lys Asp Lys Gln Asn Ile
100          105          110
His Ser Ile Pro Val Arg Asn Glu Met Tyr Gln Gly Gln Thr Pro Gln
115          120          125
Ser Phe Asn Ile Lys Leu Leu Gln Asp Ser Tyr Arg Ala Leu Ser Ser
130          135          140
Glu Pro Xaa Arg Asn Leu Ile Arg Cys Met
145          150
```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```
Val Leu Phe Thr Ser Asp Ser Arg Pro Thr Met Ser Gly Asn Phe Glu
 1          5          10          15
Tyr Ile Tyr Asn Glu Met Leu Arg Gln Asn Leu Asp Lys Lys Tyr Asp
 20          25          30
Ile His Thr Val Phe Lys Ala Asn Ile Thr Asp Arg Arg Gly Ile Ile
 35          40          45
Asp Lys Phe Arg Leu Pro Tyr Leu Leu Gly Lys Ala Asp Tyr Ile Phe
 50          55          60
Val Asp Asp Phe His Pro Leu Ile Tyr Thr Val Arg Phe Arg Arg Ser
 65          70          75          80
Gln Glu Val Ile Gln Val Trp His Ala Val Gly Ala Phe Lys Thr Val
 85          90          95
Gly Phe Ser Arg Thr Gly Lys Lys Gly Gly Pro Phe Ile Asp Ser Leu
100          105          110
Asn His Arg Ser Ser Cys Gln Ser Leu Cys Ile Ile
115          120
```

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | His | Ala | Val | Gly | Ala | Phe | Lys | Thr | Val | Gly | Phe | Ser | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Xaa | Lys | Gly | Gly | Pro | Phe | Ile | Asp | Ser | Leu | Lys | Pro | Ile | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Lys | Ala | Tyr | Val | Ser | Ser | Glu | Thr | Arg | Tyr | Ser | Ile | Leu | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Phe | Asp | Leu | Gly | Lys | Thr | Ser | Gly | Ser | Gly | Thr | Asn | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Val | Thr | Ile | Thr | Lys | Ile | Met | Gly | Trp | Lys |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ile | Met | Lys | Ile | Thr | Val | Asn | Asp | Lys | Asn | Glu | Val | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Tyr | Val | Asn | Thr | Gly | Gly | Leu | Arg | Asn | Ser | Leu | Asp | Val | Asp | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Pro | Ile | Lys | Phe | Lys | Glu | Glu | Phe | Glu | Pro | Arg | Lys | Phe | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Thr | Asn | Gly | Glu | Ile | Lys | Tyr | Asn | Ser | Asn | Phe | Glu | Lys | Glu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Pro | Asn | Ala | Ser | Ser | Gln | Gln | Ser | Glu | Ser | Asp | Leu | Ser | Asp | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Leu | Arg | Gly | Met | Val | Ala | Ser | Met | Gln | Met | Gln | Val | Ala | Gln | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Val | Leu | Thr | Met | Glu | Leu | Ala | Gln | Asn | Ala | Met | Leu | Thr | Gln |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gln | Leu | Thr | Glu | Leu | Lys | Thr | Asn | Lys | Thr | Ser | Thr | Glu | Gly | Asp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |



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|            |            |            |            |            |     |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val<br>1   | Arg        | Gln        | Leu        | Ala<br>5   | Gln | Ala        | Lys        | Lys        | Lys<br>10  | Ser        | Thr        | Ala        | Lys        | Lys<br>15  | Lys        |
| Thr        | Ala        | Ser        | Lys<br>20  | Lys        | Arg | Thr        | Asn        | Ser<br>25  | Arg        | Lys        | Lys        | Lys        | Asn<br>30  | Asp        | Asn        |
| Pro        | Ile        | Arg<br>35  | Tyr        | Val        | Ile | Ala        | Ile<br>40  | Leu        | Val        | Val        | Val        | Leu<br>45  | Met        | Val        | Leu        |
| Gly        | Val<br>50  | Phe        | Gln        | Leu        | Gly | Ile<br>55  | Ile        | Gly        | Arg        | Leu        | Ile<br>60  | Asp        | Ser        | Phe        | Phe        |
| Asn<br>65  | Tyr        | Leu        | Phe        | Gly<br>70  | Tyr | Ser        | Arg        | Tyr        | Leu        | Thr<br>75  | Tyr        | Ile        | Leu        | Val        | Leu<br>80  |
| Leu        | Ala        | Thr        | Gly<br>85  | Phe        | Ile | Thr        | Tyr        | Ser        | Lys<br>90  | Arg        | Ile        | Pro        | Lys        | Thr<br>95  | Arg        |
| Arg        | Thr        | Ala        | Gly<br>100 | Ser        | Ile | Val        | Leu        | Gln<br>105 | Ile        | Ala        | Leu        | Leu        | Phe<br>110 | Val        | Ser        |
| Gln        | Leu        | Val<br>115 | Phe        | His        | Phe | Asn        | Ser<br>120 | Gly        | Ile        | Lys        | Ala        | Glu        | Arg        | Glu        | Pro        |
| Val<br>130 | Leu        | Ser        | Tyr        | Val        | Tyr | Gln<br>135 | Ser        | Tyr        | Gln        | His        | Ser<br>140 | His        | Phe        | Pro        | Asn        |
| Phe<br>145 | Gly        | Gly        | Gly        | Val<br>150 | Leu | Gly        | Phe        | Tyr        | Leu        | Leu<br>155 | Glu        | Leu        | Ser        | Val        | Pro<br>160 |
| Leu        | Ile        | Ser        | Leu<br>165 | Phe        | Gly | Val        | Cys        | Ile        | Ile<br>170 | Thr        | Ile        | Leu        | Leu        | Leu<br>175 | Cys        |
| Ser        | Ser        | Val<br>180 | Ile        | Leu        | Leu | Thr        | Asn<br>185 | His        | Gln        | His        | Arg        | Asp        | Val<br>190 | Ala        | Lys        |
| Val        | Ala        | Leu<br>195 | Glu        | Asn        | Ile | Lys        | Ala<br>200 | Trp        | Phe        | Gly        | Ser        | Phe<br>205 | Asn        | Glu        | Lys        |
| Met        | Ser<br>210 | Glu        | Arg        | Asn        | Gln | Glu<br>215 | Lys        | Gln        | Leu        | Lys        | Arg<br>220 | Glu        | Glu        | Lys        | Ala        |
| Arg<br>225 | Leu        | Lys        | Glu        | Glu<br>230 | Gln | Lys        | Ala        | Arg        | Gln        | Asn<br>235 | Glu        | Gln        | Pro        | Gln        | Ile<br>240 |
| Lys        | Asp        | Val        | Ser<br>245 | Asp        | Phe | Thr        | Glu        | Val        | Pro<br>250 | Gln        | Glu        | Arg        | Asp        | Ile<br>255 | Pro        |
| Ile        | Tyr        | Gly        | His<br>260 | Thr        | Glu | Asn        | Glu<br>265 | Ser        | Lys        | Ser        | Gln        | Cys<br>270 | Gln        | Pro        | Ser        |
| Arg        | Lys<br>275 | Lys        | Arg        | Val        | Phe | Asp        | Ala<br>280 | Glu        | Asn        | Ser        | Ser        | Asn<br>285 | Asn        | Ile        | Val        |
| Asn        | His<br>290 | Gln        | Ala        | Asp        | Gln | Gln<br>295 | Glu        | Gln        | Leu        | Thr        | Glu<br>300 | Gln        | Thr        | His        | Asn        |
| Ser<br>305 | Val        | Glu        | Ser        | Glu<br>310 | Asn | Thr        | Ile        | Glu        | Glu        | Ala<br>315 | Gly        | Glu        | Val        | Thr        | Asn<br>320 |
| Val        | Ser        | Tyr        | Val<br>325 | Val        | Pro | Pro        | Leu        | Thr<br>330 | Leu        | Leu        | Asn        | Gln        | Pro        | Ala<br>335 | Lys        |
| Gln        | Lys        | Ala        | Thr<br>340 | Ser        | Lys | Ala        | Glu        | Val<br>345 | Gln        | Arg        | Lys        | Gly        | Gln<br>350 | Val        | Pro        |
| Lys        | Arg        | Tyr<br>355 | Xaa        | Lys        | Arg | Phe        | Trp<br>360 | Gly        | Xaa        | Ile        | Xaa        | Lys<br>365 | Xaa        | Thr        | Gln        |
| Xaa        | Lys<br>370 | Leu        | Ser        | Xaa<br>375 | Ser | Asn        | Ser        | Ile        |            |            |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Val<br>1   | Met        | Thr        | Glu        | Glu<br>5   | Xaa | Cys        | Leu        | Leu        | Lys<br>10  | Arg        | Val        | Phe        | Met        | Arg<br>15  | Met |
| Lys        | Arg        | Phe        | Leu<br>20  | Thr        | Ile | Val        | Gln        | Ile<br>25  | Leu        | Leu        | Val        | Val        | Ile<br>30  | Ile        | Ile |
| Ile        | Phe        | Gly<br>35  | Tyr        | Lys        | Ile | Val        | Gln<br>40  | Thr        | Tyr        | Ile        | Glu        | Asp<br>45  | Lys        | Gln        | Glu |
| Arg        | Ala<br>50  | Xaa        | Tyr        | Glu        | Lys | Leu<br>55  | Gln        | Xaa        | Lys        | Phe        | Xaa<br>60  | Met        | Leu        | Met        | Xaa |
| Lys<br>65  | His        | Gln        | Glu        | His<br>70  | Val | Arg        | Pro        | Gln        | Phe        | Glu<br>75  | Ser        | Leu        | Glu        | Lys<br>80  | Ile |
| Asn        | Lys        | Asp        | Ile<br>85  | Val        | Gly | Trp        | Ile        | Lys<br>90  | Leu        | Ser        | Gly        | Thr        | Ser<br>95  | Leu        | Xaa |
| Tyr        | Pro        | Val<br>100 | Leu        | Gln        | Gly | Lys        | Thr<br>105 | Asn        | His        | Asp        | Tyr        | Leu<br>110 | Asn        | Leu        | Asp |
| Phe        | Glu<br>115 | Arg        | Glu        | His        | Arg | Arg<br>120 | Lys        | Gly        | Ser        | Ile        | Phe<br>125 | Met        | Asp        | Phe        | Arg |
| Asn<br>130 | Glu        | Leu        | Xaa        | Asn<br>135 | Leu | Asn        | His        | Asn        | Thr        | Ile<br>140 | Leu        | Tyr        | Gly        | His        | His |
| Val<br>145 | Gly        | Asp        | Asn<br>150 | Thr        | Met | Phe        | Asp        | Val        | Leu<br>155 | Glu        | Asp        | Tyr        | Leu        | Lys<br>160 | Gln |
| Ser        | Phe        | Tyr        | Glu<br>165 | Lys        | His | Lys        | Ile        | Ile<br>170 | Gly        | Phe        | Asp        | Asn        | Lys<br>175 | Tyr        | Gly |
| Lys        | Tyr        | Gln<br>180 | Leu        | Gln        | Val | Phe<br>185 | Ser        | Ala        | Tyr        |            |            |            |            |            |     |